

STIC Search Report Biotech-Chem Library

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TO: Jeffrey Parkin

Location: rem/3D39/3C18

Art Unit: 1648

Friday, February 17, 2006

Case Serial Number: 09/669187

From: Toby Port

Location: Biotech-Chem Library

REM-1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Parkin,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port X22523



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STIC-Biotech/ChemLib

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From:

Parkin, Jeffrey

Sent:

Friday, February 03, 2006 6:25 PM

To: Subject:

STIC-Biotech/ChemLib U.S. Serial No. 09/669,187

Aloha!

Please search **SEQ ID NOS.: 73, 80, 81, 148, and 906** from U.S. Serial No. **09/669,187** v. all relevant databases, including interference. Please limit search results to oligonucleotides less than 50 nt in length, if possible. Place results on both paper and electronic format (i.e., disk, e-mail, etc.). Thanks!

Jeffrey S. Parkin, Ph.D. Primary Examiner Art Unit 1648 REM 3D39 2-0908

3C/8

Searcher:
Searcher Phone:
Date Searcher Picked up:
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Type of Search

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VERSION AX103881.1 GI:13920078 KEYWORDS SOURCE ORGANISM Synthetic construct other sequences; artificial sequences. REFERENCE TITLE IMMUNOStimulatory nucleic acids JOURNAL PARENTY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical GmbH (DE) Source Location/Qualifiers Location/Qualifiers		ACESSION AX546934 ACESSION AX546934 VERYORDS SURVEY SOURCE JOURNAL AUTHORS SOURCE JOORNAL FRATURES Coley Pharmaceutical Group, Inc. (US) FRATURES Location/Qualifiers Jooranism="supthetic construct" AUTHORS Location/Qualifiers Jooranism="supthetic construct" Jooranism="supthetic construct" AUTHORS Location/Qualifiers Location/Qualifiers Joranism="supthetic construct" Authors Joranism="supthetic construct" Authors Joranism="supthetic construct" Authors Joranism="supthetic Sequence" Authors Joranism="supthetic Sequence"	Okidin Query Match Query Match Best Local Similarity 100.0%; Score 20; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy	RESULT 3 CS077910 LOCUS LOCUS DEFINITION Sequence 28 from Patent WO2005035579. ACCESSION VERSION VERSION CS077910.1 GI:63092998 KEYWORDS SOURCE SOURCE ORGANISM Synthetic construct
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1 Bates,P.J., Miller,D.M., Trent,J.O. and Xu,X. A method for the treatment of malignant diseases by inhibiting nucleolin

REFERENCE AUTHORS TITLE

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AX103881 20 bp Sequence 73 from Patent WO0122972. AX103881

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Hanecak, C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
Imbach, J. Louis.
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Wyatt, J.R.
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Patent: EP 101715-A 121 05-UUL-2000;
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Nucleic Acids Res. 10 (9), 2911-2924 (1982)
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Method for inhibiting nf-kappa b signaling and use to treat or prevent human diseases
Patent: WO 200503733-A 29 28-APR-2005;
University of Louisville Research Foundation, Inc. (US)
Location/Qualifiers
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Dawson, D. and Herrick, G.
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REFERENCE AUTHORS

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THOMAS
GREG B
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C1201/48,C1201/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
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CI2N15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
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  RS Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M., Calvin, B.H. and William, H.A.
Calvin, B.H. and William, H.A.
Calvin, B.H. and William, H.A.
Human telomerase catalytic subunit promoter
Human telomerase catalytic subunit promoter
Patent: JP 199253177-A-226 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 199253177-A/226
PD 21-SEP-1999
PR 15-OCT-1998 JP 1989320169
PR 15-OCT-1998 UP 1989320169
PR 10-OCT-1998 UP 198724-643, 18-APR-1997 US 08/851.843, PR 25-APR-1997 US 08/854, 050, 14-AUG-1997 US 08/854, 050, 14-AUG-1997 US 08/912.503 PI THA A-AUG-1997 US 08/912.503 PI THA A-AUG-1997 US 08/912.951, 14-AUG-1997 US 08/912.503 PI THA A-AUG-1997 US 08/912.951, 14-AUG-1997 US 08/912
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Patent: US 6610839-A 568 26-AUG-2003;
Geron Corporation; Menlo Park, CA
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/organism='Unidentified'
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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Sequence 568 from patent US 6610839.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unknown"
/mol_type="genomic DNA"
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Morin, G.B. and Andrews, W.H.
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Human telomerase catalytic subunit promoter.
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Patent: US 6093809-A 42 25-JUL-2000;
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Patent: US 6309867-A 42 30-OCT-2001;
Location/Qualifiers
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Sequence 42 from patent US 6093809.
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/organism="unknown"
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1 (bases 1 to 44)
Cech,T.R. and Nakamura,T.
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Cech, T.R. and Lingner, J.
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PAT 31-JAN-2002

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CALVIN B HARLEY, WILLIAM H ANDREWS
A61K38/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,
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S Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
Human tellomerase catalytic subunit

L Patent: JP 2001081042-A.226 27-MAR-2001;
GERNN CORP,UNIVESITY TECHNOLOGY CORP
OS Unidentified
PD 27-MAR-2001
PF 27-JUL-2000 JP 200227474
PR 01-OCT-1995 US 08/844419 PR 25-APR-1997 US 08/844419 PR 25-APR-1997 US 08/846017,06-MAY-1997 US 08/81843 PR 14-AUG-1997 US 08/81843 PR 09-MAY-1997 US 08/81843 PR 09-MAY-1997 US 08/81843 PR 14-AUG-1997 US 08/812951.14-AUG-1997 US 08/911312 PR 14-AUG-1997 US 08/911391 US 08/911391
                                                                                                                                       Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Andrews, W.H.
Human telomerase catalytic subunit
Patent: EP 1331094-A 568 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12,
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100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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CC Topology: Linear;
FH Key
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AX810603.1 GI:38524092
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unclassified sequences.
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PC A61K3
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Cech,T.R., Lingmer,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
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Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,
Harley, C. and Andrews, W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 42 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
                                                                                                                                                                                                                                                                                                                                                                                                                          drug screening
Patent: US 6617110-A 568 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo
Park, CA
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Sequence 42 from patent US 6808880.
AR592667
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Sequence 568 from Patent EP1333094.
AX810603
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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CALVIN B HAREI, WILLIAM H ANDREWS
CILOLIS(09, AGIK31/70, AGIK38/55, AGIK39/395, AGIK39/395, AGIK48/00,
CILOLI/02,
CILOLI/68, CILOLI/68, GOIN33/15, GOIN33/48, GOIN33/50//CO7K14/47, PC
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100.0%; Score 20; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Morin,G.B. and Andrews,W.H.
Promoter for telomerase reverse transcriptase
Patent: US 661083-A 567 26-AUG-2003;
Geron Corporation; Menlo Park, CA
Location/Qualifiers
                                                                                                               Toru, N., Karen, B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ce 1. .46
/organism='Unidentified'
Location/Qualifiers
                                                          unclassified.

1 (bases 1 to 46)
Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C. Calvin,B.H. and William,H.A.
Human telomerase catalytic subunit promoter
Patent: JP 1999253177-A 225 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
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Sequence 567 from patent US 6610839.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 1999253177-A/225
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Human telomerase catalytic subunit promoter.
E37017.1 GI:13022980
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1 (bases 1 to 46)
Cech,T.R. and Nakamura,T.
Telomerase
Telomerase 10S 6309867-A 41 30-OCT-2001;
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Sequence 41 from patent US 6093809.
AR104529
AR104529.1 GI:12817237
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 41 from patent US 6309867.
AR175790 AR175790.1 GI:17917089
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Cech, T.R. and Lingner, J.
                                              20; Conservative
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Matches 20; Conserv
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Matches 20; Conserv
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E37017
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AR104529
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TITLE
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AR175790
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PAT 25-NOV-2003
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C07K5/10,
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S Schi,T.R. Lingners.

S Schi,T.R., Lingners. J., Nakamura,T., Chapman,K.B., Mori,G.B., Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit
Human telomerase catalytic subunit
ERRON CORP, UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 2001081042-A/225
PD 27-MAR-2001
PR 27-MAR-2001
PR 27-MAR-2001
PR 27-MAR-2001
PR 27-WAR-2001
PR 27-WAR-2001
PR 27-WAR-2001
PR 27-WAR-2001
PR 27-WAR-2001
PR 28-WAY-1997 US 08/844617,06-MAY-1997 US 08/851843 PR 09-MAY-1997 US 08/851843 PR 14-WG-1997 US 08/851813 PR 14-WG-1997 US 08/8512951,14-AUG-1997 US 08/9512951,14-AUG-1997 US 08/9512997 US 08/9512997 US 08/9512997 US 08/9512997 US 08/95129
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Human telomerase catalytic subunit
Patent: EP 133094-A 567 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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BD011268
BD011268
BD011268.1 GI:18639641
JP 2001081042-A/225.
unidentified
unidentified
              46 bp 1
Sequence 567 from Patent EP1333094.
AX810602

    .46
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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G01N33/53,
PC G01N33/56,G01N33/
Strandedness: Single;
CC Topology: Linear;
FH Key Lo
FT source 1.
                                                                                           AX810602.1 GI:38524091
                                                                                                                                       unidentified
unidentified
unclassified sequences.
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Matches 20; Conservative
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PC C07K5
PC C07K5
C12N15/09,
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Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
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1 (bases 1 to 46)

Cech,T.R., Lingmer,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C. and Andrews,W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 41 26-OCT-2004;

Geron Corporation and Regents of the University of Colorado; Menlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug screening
Patent: US 6617110-A 567 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo
Park, CA
  Gaps
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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AR393308
  Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
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                                              1 TTTTGGGGTTTTGGGGTTTT 20
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Matches 20; Conservative 0
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AR393308
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JP 1999253177-A/222.
unidentified
unidentified
unclassified.

B 1 (bases 1 to 48)
S Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M.,
Calvin, B.H. and William, H.A.
Human telomerase catalytic subunit promoter
Datent: JP 1999253177-A 222 21-SEP-1999;
Unidentified
OS Unidentified
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      linear
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100.0%; Score 20; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Human telomerase catalytic subunit promoter.
E37014
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
      DNA
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                                                                                                                                Telomerase
Patent: US 6309867-A 37 30-OCT-2001;
Location/Qualifiers
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Cech, T.R. and Nakamura, T.
Telomerase
Patent: US 6309867-A 40 30-OCT-2001;
Location/Qualifiers
48 bp 1
Sequence 37 from patent US 6309867.
AR175786
AR175786.1 GI:17917085
                                                                                                                                                                              1. .48
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Sequence 40 from patent US 6309867.
AR175789 1G1:17917088
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/organism="unknown"
/mol_type="unassigned DNA"
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Cech, T.R. and Nakamura, T.
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Matches 20; Conservative 0; Mismatches 0; Indels
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Patent: US 6093809-A 37 25-JUL-2000;
Location/Qualifiers
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Patent: US 6093809-A 40 25-JUL-2000;
Location/Qualifiers
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AR104528
AR104528.1 GI:12817236
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Sequence 37 from patent US 6093809.
AR104525 GI:12817233
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/organism="unknown"
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/mol_type="unassigned DNA"
      /mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                          Unclassified.
1 (bases 1 to 48)
Cech, T.R. and Lingner, J.
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Cech, T.R. and Lingner, J.
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AR104525
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PAT 15-DEC-2004
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Cech,T.R. Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C. and Andrews,W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 37 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo Park, CA
                                                                            Unclassified.

1 (bases 1 to 48)

1 (bases 1 to 48)

1 (bases 2 to 48)

Harley, C.B. and Andrews, W.H.

Cells immortalized with telomerase reverse transcriptase for use
                                                                                                                                                         drug screening
Patent: US 6617110-A 564 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo
Park, CA
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1 (bases 1 to 48)
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
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Sequence 40 from patent US 6808880.
AR592665
AR592665.1 GI:56641385
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Sequence 37 from patent US 6808880.
AR592662
AR592662.1 GI:56641382
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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Matches 20; Conservative 0
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AR393305
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AR592665
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AR592662
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C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
                                                                                                                                                                                                                                                                PC (C12N1/21,C12R1:19), (C12N9/12,C12R1:19), (C12N9/12,C12R1:84), PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC Strandedness: Single;
                                                 PR
PN JP 1999253177-A/222
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 JP 1998320169
PR 01-OCT-1996 JP 1998320169
25-APR-1997 US 08/846.017,06-MAY-1997 US 08/851.843, PR 09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/851.312, PR 14-AUG-1997 US 08/911.312, PR PS DF 1997 US 08/911.312, PR PS DF 1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI TR SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GR
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CO2N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19,
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Patent: US 6610839-A 564 26-AUG-2003;
Geron Corporation; Menlo Park, CA
Location/Qualifiers
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'organism='Unidentified'
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Sequence 564 from patent US 6617110.
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Sequence 564 from patent US 6610839.
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/organism="unidentified"
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Morin, G.B. and Andrews, W.H.
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                                                                                    PI CALVIN B HARLEY, WILLIAM H ANDREWS
PC AGIN38/00, AGIN31/7088, AGIN39/00, AGIP48/00, AGIP35/00, AGIP43/00
PC CO7K5/10,
PC CO7K5/107, CO7K5/117, CO7K7/06, CO7K7/08, CO7K16/40, C12N9/12, PC C12N15/09,
PC C12U15/09,
PC C12Q1/02, C12Q1/48, C12Q1/68, G01N33/15, G01N33/53, PC G01N33/53,
PC G10N33/53,
PC G01N33/54,
PC G01N33/56, G01N33/573/C12P21/08, AGIK37/02, C12N15/00 CC
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25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR 09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR 14-AUG-1997 US 08/912551,14-AUG-1997 US 08/915503 PI R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI MORIN,
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Matches 20; Conservative 0; Mismatches 0;
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                          Location/Qualifiers
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Patent: US 6093809-A 39 25-JUL-2000;
Location/Qualifiers
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Sequence 39 from patent US 6309867.
AR175788.1 GI:17917087
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/wol_type="unassigned DNA"
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Sequence 39 from patent US 6093809.
AR104527 GI:12817235
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                             source 1..48 /organism='Unidentified'.
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Cech, T.R. and Lingner, J.
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CC Topology: Linear;
FH Key Loc
FT Source 1.
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         Harley, C. and Andrews, W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 40 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit
Patent: EP 1331094-A 564 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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BD011265
BD011265.1 GI:18639638
JP 2001081042-A/222.
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unclassified.
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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                                                                                      Location/Qualifiers
                                                                                                                      /organism="unknown"
                                                                                                                                                                                                                                            unidentified unclassified sequences.
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Matches 20; Conservative
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AX810599
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Unclassified.
1 (bases 1 to 50)
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
                                                                                               PAT 18-DEC-2003
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Patent: US 6617110-A 566 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo Park, CA
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Patent: US 6610839-A 566 26-AUG-2003;
Geron Corporation; Menlo Park, CA
Location/Qualifiers
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ilarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0;
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Sequence 566 from patent US 6617110.
                                                                                             AR390693 566 from patent US 6610839.
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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Morin, G.B. and Andrews, W.H.
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AR592664
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C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
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CI2N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
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PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
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PD 1999233177-A/224
PD 1999233177-A/224
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,431,18-APR-1997 US 08/844.419,
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851.843, PR 09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/911.312, PR 14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/912.951,14-AUG-199
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1 (bases 1 to 50)
Thomas.R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
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Human telomerase catalytic subunit promoter.
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Patent: JP 1999253177-A 224 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
                                                                                                                                                                                                                                                Query Match 100.0%; Score 20; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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1 (bases 1 to 50)
Cech, T.R. and Nakamura, T.
Telomerase Patent: US 6309867-A 39 30-OCT-2001;
                                                                                          Location/Qualifiers
1. 50
/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 1999253177-A/224.
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C12R1:84)
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                       AUTHORS
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SOURCE
                                                                                                    FEATURES
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GREG B

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Query Match Best Local 8

ORIGIN

Matches

AX810601 LOCUS DEFINITION

RESULT 41

g 8

ORGANISM

VERSION KEYWORDS SOURCE

ACCESSION

source

PEATURES

TITLE JOURNAL

AUTHORS

REFERENCE

ORGANISM

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PAT 14-FEB-2001
PN JP 2001081042-A/224

PD 27-MAR-2001

PF 27-JUL-2000 JP 2000227474

PF 27-JUL-2000 JP 2000227474

PF 01-OCT-1996 US 08/724643,18-APR-1997 US 08/81843 PR 01-OCT-1997 US 08/84617 US 08/84613 PR 09-MAY-1997 US 08/84610,1997 US 08/851843 PR 14-AUG-1997 US 08/81251,14-AUG-1997 US 08/91312 PR PR 01-CT-1996 US 08/91252,14-AUG-1997 US 08/913503 PI THOMA R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B NORIN,

PI CALVIN B HARLEY, MILLIAM H ANDREWS

PC AGINSS/10, CO7K5/117, CO7K7/06, CO7K7/08, CO7K16/40, CI2N9/12, PC C12N15/09,

PC C1201/48, C12Q1/68, G01N33/15, G01N33/53, PC G01N33/53,
                                                                                                                                                                                                                                                                                A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
C07K5/10,
C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
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ilarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0:
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Patent: US 6093809-A 39 25-JUL-2000;
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Sequence 39 from patent US 6309867.
AR175788.1 GI:17917087
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Seguence 39 from patent US 6093809.
AR104527
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unidentified"
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/db_xref="taxon:32644"
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Cech, T.R. and Lingner, J.
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CC Topology: Linear;
FH Key Love
FT Source 1 1
FT /organism='Unidenti
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Matches 20; Conserv
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Les 18; Conserv
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AR104527/c
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VERSION
KEYWORDS
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AUTHORS
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                                                Unclassified.

1 (Dases 1 to 50)

1 (Dases 1 to 50)

Harley, C. and Andrews, W.H.

Method for detecting polynucleotides encoding telomerase

Batch: US 6808880-A 39 26-OCT-2004;

Geron Corporation and Regents of the University of Colorado; Menlo

Park, CA
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Human telomerase catalytic subunit
Patent: EP 133099-A 566 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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patent: JP 2001081042-A 224 27-MAR-2001;
GERON CORP UNIVERSITY TECHNOLOGY CORP
OS Unidentified
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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/wol_type="unassigned DNA"
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Sequence 566 from Patent EP1333094.
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JP 2001081042-A/224.
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Best Local Similarity
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                             Unknown.
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Matches

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FEATURES

TITLE JOURNAL

AUTHORS

REFERENCE

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

DEFINITION ACCESSION

RESULT 42

BD011267

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Unknown.
Unclassified.
1 (bases 1 to 50)
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
                                                                                                                          PAT 18-DEC-2003
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Geron Corporation and University Technology Corporation; Menlo
Park, CA
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Patent: US 6610839-A 566 26-AUG-2003;
Geron Corporation; Menlo Park, CA
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Sequence 39 from patent US 6808880.
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Morin, G.B. and Andrews, W.H.
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AR592664/c
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GREG B
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C12Q1/48, C12Q1/68, G01N33/15, G01N33/48, G01N33/50//C07K14/47, PC
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CI2N15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
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PP 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 UB 08/724.613,18-APR-1997 US 08/844.419, PR 25-APR-1997 US 08/854.617,06-MAY-1997 US 08/854.050,14-AUG-1997 US 08/813.312, PR 09-MAY-1997 US 08/813.957 US 08/811.312, PR 14-AUG-1997 US 08/911.312, PR R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG MORIN,
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JP 1999253177-A/224.
unidentified
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unclassified.

E 1 (bases 1 to 50)

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Calvin, B. H. and William, H. A.
Human telomerase catalytic subunit promoter
Patent: JP 1999253177-A 224 21-SEP-1999;
OS Unidentified
PN UP 1999253177-A/224
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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Human telomerase catalytic subunit promoter.
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Cech, T.R. and Nakamura, T.
Telomerase
Patent: US 6309867-A 39 30-OCT-2001;
Location/Qualifiers
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                                                                                              1 (bases 1 to 50)
Cech,T.K., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C. and Andrews,W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 39 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
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Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit
Patent: EP 333094-A 566 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
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Sequence 566 from Patent EP1333094.
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AX810601.1 GI:38524090
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BD011267.1 GI:18639640
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AR592664
AR592664.1 GI:56641384
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unclassified sequences.
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C07KS/10,
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                                                                                                                                                       OS Unidentified

PN JP 20010101042-A/224

PD 27-MAR-2001

PF 20-1011.0200 JP 2000227474

PR 01-0CT-1996 US 08/846017,06-MAY-1997 US 08/851843 PR 27-UUL-2000 JP 200027474

PR 01-0CT-1996 US 08/846017,06-MAY-1997 US 08/911312 PR 09-MAY-1997 US 08/846017,06-MAY-1997 US 08/911312 PR 14-AUG-1997 US 08/912851,14-AUG-1997 US 08/912853 PI TT R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GRINGALN,

PI CALVIN B HARLEY,WILLIAM H ANDREWS

PC AGINSS 00, AGIRS 1/7088, AGIRS 9/00, AGIRS 9/00, AGIPS 1/20, COTKS/10, COTKS/10, COTKS/117, COTKT/06, COTKT/08, COTKS/10, COTKS/10, COTKS/107, COTKS
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Human telomerase catalytic subunit
Patent: JP 2001081042-A 224 27-MAR-2001;
GERON CORP,UNIVERSITY TECHNOLOGY CORP
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Location/Qualifiers
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Addy 8482 MAP3K9 ma
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ALIGNMENTS

Aav09446 CpG-conta Aav09582 MSP ampli

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                                                              Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection, bacterial infection; fungal infection; parasitic infection, cancer; asthma, infectious disease; allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiogenesis inhibitor; 88; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 39; 338pp; English.
                               Immunostimulatory nucleic acid #64.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Krieg AM, Schetter C, Vollmer J;
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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AAF98948 standard; DNA; 20 AAF98948 RESULT 1
AAF98948
ID AAF9
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AC AAF9

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The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contect dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                   Treating non-allergic inflammatory diseases, such as psoriasis, eczeallergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds, allergy, asthma, poly-G nucleic acid, aerosol formulation, hypo-responsive subject, immunostimulatory.
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(PETE/) PETERSEN D M.
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                                                                                                                                                                                             WPI; 2003-521815/49
                                                                                                                                                      Krieg AM, Berg DJ;
                                                                                   (KRIE/) KRIEG A M. (BERG/) BERG D J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     administering at least one antitangle mortaic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasis, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to inhibiting angiogenesis in a subject,
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                                                                                                                                                                                                                                                                             14-DEC-2000; 2000US-0255534P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACD99381 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-566690/60
                                                                                                                                                 WO200253141-A2
                                                                                                                                                                                                                                                                                                                                                               Bratzler RL;
                                                                                                                                                                                           11-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting
                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Best Loc Matches

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Gaps

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9; Length 20; 0; Indels

Score 20; DB Pred. No. 52; 0; Mismatches Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.

Disclosure; Page 6; 221pp; English

US2003050268-A1

Synthetic.

13-MAR-2003.

Fouron Y;

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Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;

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especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G mucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy
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Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;

Gaps . 0 9; Length 20; 0; Indels 100.0%; Score 20; DB 100.0%; Pred. No. 52; Mismatches ; 0 Conservative Query Match Best Local Similarity Local 20; Conserve

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RESULT

ADG76003 standard; DNA; 20

ADG76003;

(first entry) 11-MAR-2004

Non-CpG DNA oligonucleotide 4.

ss; non-CpG; immunostimulatory; non-palindromic; immune response; proliferation; differentiation; cytokine; antibody production; B-cell; plasmacytoid dendritic cell; immunomodulator; gene therapy; chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma; renal cell carcinoma.

Synthetic.

WO2003101375-A2.

11-DEC-2003

30-MAY-2003; 2003WO-EP005691.

30-MAY-2002; 2002CA-02388049

(IMMU-) IMMUNOTECH SA

Lopez RA;

WPI; 2004-053333/05.

New immunostimulatory oligonuclectide comprising non-palindromic nucleic acid sequence motif, useful for inducing B-cell activation, treating, preventing or ameliorating immune system disorder or tumoral disease e.g. melanoma

Example 17; Page 80; 139pp; English.

This invention relates to novel immunostimulatory oligonucleotides that contain a non-palindromic sequence motif. Specifically, it refers to DNA coligonucleotides (without a CPG motif), which can stimulate an immune response in animals of the order of primate, including humans. The immune response is characterised by the proliferation, differentiation, cytokine and antibody production in B-cells, as well as cell differentiation and cytokine production in plasmacytoid dendric cells. The present invention describes immunomodulator compositions that also comprise an antigen selected from, for example, viruses, bacteria, parasites, tumour cells and glycolipides. As such, these DNA oligos can be used in gene therapy for inducing B-cell activation, treating, preventing or ameliorating an immune system disorder or a tumoural disease including chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell carcinoma. This oligonucleotide sequence is a non-CpG DNA oligo of the invention. 

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Gaps

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Score 20; DB 13; Length 20; Pred. No. 52; ); Mismatches 0; Indel8

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Conservative

Similarity

Query Match Best Local Simi Matches 20;

100.0%;

TTTTGGGGTTTTGGGGTTTT 20 TTTTGGGGTTTTGGGGTTTT 20

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Seguence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;

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Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                      Gaps
                                                                                                                                                                                                                                                                                                                 ss, antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagoniat; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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Score 20; DB 12; Length 20; Pred. No. 52; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     Allergic response suppressor oligonucleotide #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 73; 235pp; English.
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                                                                     1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                       ADU89389 standard; DNA; 20 BP
   100.0%;
ilarity 100.0%;
Conservative 0
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02-FEB-2001; 2001US-00776479.
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                                                                                                                                                                                                                                                       10-FEB-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method of the invention.
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PETERSEN D
     Query Match
Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004235774-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                        ADU89389;
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(FOUR/)
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sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to method for determining neoplastic state of a cell, involves detecting the presence of plasma membrane nucleotide in the cell or quantifying the amount of plasma membrane nucleolin in the cell. The invention is useful for diagnosing pre-malignant cells, malignant cells and lung small cell carcinoma. The present sequence is a non-antisense oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Determining neoplastic state of cell, involves detecting presence or plasma membrane nucleotide in cell or quantifying amount of plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 10; Length 28; 100.0%; Pred. No. 53; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; linear polynucleotide; cation; telomere repeat.
                                                                                                                               Neoplastic, malignancy; lung carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                      Xu X;
                                                                                                     GRO J1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 28; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide of the invention #26
                                                                                                                                                                                                                                                                                                                                                      Trent JO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                     Non-antisense oligonucleotide,
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                         AAD64883 standard; DNA; 28 BP
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                                                                                                                                                                                                                                   08-APR-2002; 2002US-00118854
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                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane nucleolin in cell.
                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                      Miller DM, Bates PJ,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-875400/81
                                                                                                                                                                                                                                                                                    MILLER D M.
                                                                                                                                                                                                                                                                                                 (BATE/) BATES P J. (TREN/) TRENT J O. (XUXX/) XU X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                JS2003194754-A1
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                                                                                                                                                         Unidentified
                                                                                                                                                                                                         16-OCT-2003
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                                                   AAD64883;
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(BATE/) H
(TREN/)
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              AAD64883
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The invention relates to a novel quantitative method for adding linear polynucleotide to solution containing a cation. The linear polynucleotide contains telomere repeat sequence with donor at one edge portion and acceptor at another edge portion. The optical detection is performed using this linear polynucleotide. The method of the invention is useful in medical fields such as clinical laboratory test and fields with cation fixed assay. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting apoptosis comprises preparing a sample from which cells have been removed and detecting at least one of nucleolin and PARP-I in the
                                                                                                                                                                                                                         Quantitative method of cation for clinical laboratory test, involves adding linear polynucleotide containing telomere repeat sequence with donor and acceptor at edge portions, to solution containing cation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guanosine-rich oligonucleotide GRO J, used in apoptosis detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis; nucleolin; AIDS; cancer; neurodegenerative disease; autoimmune disease; infection; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 20; DB 10; Length 28; Best Local Similarity 100.0%; Pred. No. 53; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYLO-) UNIV LOUISVILLE RES FOUND INC. (BATE/) BATES P J. (MIYY/) MI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; SEQ ID NO 28; 66pp; English
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 29; 8pp; Japanese
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                   05-DEC-2001; 2001JP-00371975.
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                                                                05-DEC-2001; 2001JP-00371975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2002; 2002US-0392143P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI28732 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                         (TAKE/) TAKENAKA S.
(TUMK-) TUM KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-083166/08.
                                                                                                                                                                                 WPI; 2003-639772/61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004003554-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sates PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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The present sequence is that of guanosine-rich oligomucleotide GRO J, which can be used in the method of the invention. The method is for the detection of apoptosis. It involves preparing a sample from which cells have been removed, and detecting nucleolin and/or poly(ADP-ribose) polymerase (PARP-1) in the sample, where the sample is blood, serum, plasma, tissue, tissue culture medium or sputum. Detection of nucleolin involves detection of a complex between nucleolin and a nucleolin binding molecule, preferably an anti-nucleolin antibody or a GRO, such as GRO J, which is characterised as a good plasma membrane nucleolin-binding GRO. The method allows detection of excessive apoptosis in a subject suspected of having AIDS, a neurodegnerative disease, an ischaemic injury, an
                                                                                                                                                                                                                                                                                                                                                            autoimmune disease, a tumour, a cancer (especially endocervical adenocarcinoma, prostatic carcinoma, breast cancer, leukaemia and nonsmall cell lung carcinoma), a viral infection, an acute inflammatory condition or sepsis (all claimed).
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Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 20; DB 12; Length 28; 100.0%; Pred. No. 53; 0; Indels 0; Mismatches 20 rrrrecectrirecectrir 24 TTTTGGGGTTTTT Local Similarity 100. Les 20; Conservative Query Match Matches 8

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ADY53924 standard; DNA; 28 BP

19-MAY-2005 (first entry) ADY53924;

Non-antisense GRO nucleolin-binding oligonucleotide GRO29A.

Diagnosis; therapy; tumor; cancer; neoplasm; cytostatic; nucleolin; ss; guanine-rich oligonucleotide; gene silencing; RNA interference; melanoma; lymphoma; sarcoma; glioma; leukemia; hepatocellular carcinoma.

Synthetic

US2005053607-A1.

10-MAR-2005.

09-OCT-2003; 2003US-00683480

08-APR-2002; 2002US-00118854

BATES P J. MILLER D M. TRENT J O. (BATE/)

(xuxx/) xu x. (MILL/) (TREN/)

Trent JO, Bates PJ, Miller DM,

Xn X

WPI; 2005-213006/22.

Treating cancer in a subject comprises administering to the subject a therapeutically effective amount of an anti-nucleolin agent and a Disclosure, SEQ ID NO 28; 32pp; English. carrier.

The invention relates to treating cancer in a subject comprises administering to the subject a therapeutically effective amount of an anti-nucleolin agent and a carrier. Also included is a pharmaceutical composition comprising a nucleolin antibody or an inhibitory RNA against nucleolin, and a carrier. The method and antibodies, RNA and composition are useful for treating cancer, such as melanoma, lymphoma, plasmocytoma, sarcoma, glioma, thymoma, leukemia, hepatoma, or breast, prostate, colon, RESULT 10
ADY53924
ID ADY53924
XX ADX531
XX DE Non-al
XX BUADH
XX UNDH
XX Synth
XX Synth
XX OS Synth
XX OS OS
XX Synth
XX OS OS
XX Synth
XX DE NON-Al
XX DE NON-A

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This invention relates to a novel method for treating inflammation in a patient which comprises administering to the patient a composition comprising a GRO (guanosine-rich oligonucleotide). The invention may be useful for the development of compounds with an antinflammatory.

C analgesic, gynecological, hepatotropic, neuroprotective, nootropic, antisterintic, antistemmatic, gastrointestinal-Gen. or antiulorer activity whilst the disclosed sequence may prove useful for gene therapy. The methods are useful for treating inflammation associated with an acute inflammatory condition. The acute inflammatory condition is selected from primary dysmenorrhea, acute alcoholic liver disease and acute from particles. The inflammation may also be of Alzheimer's disease or associated with a chronic inflammacory disease. The chronic inflammatory disease is selected from rheumatoid arthritis, asthma, gastrointestinal crack disease, psoriasis, atherosclerosis, Crohns disease, ulcerative clisease, psoriasis, atherosclerosis, Crohns disease, ulcerative clisease, psoriasis, atherosclerosis, Crohns disease, ulcerative clisease is elected GRO J which was used during the development of the order method of the invention.
                                                                                                                                                               ö
liver, esophageal, brain, lung, ovary, or cervical cancer. The present sequence is a GRO (guanine-rich oligonucleotide) which binds to nucleolin (thereby inhibiting cancer cell growth).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating inflammation, e.g. acute or chronic inflammation such as rheumatoid arthritis, asthma, psoriasis, and atherosclerosis, in a patient comprises administering to the patient a composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation; antiinflammatory; analgesic; gynecological; hepatotropic; neuroprotective; nootropic; antiarthritic; antirheumatic; gastrointestinal-Gen.; antiulcer; gene therapy; dysmenorrhea; alcoholic hepatitis; pancreatitis; Alzheimers disease; rheumatoid arthritis; atchan; gastrointestinal disease; psoriasis; attherosclerosis; Crohns disease; ulcerative colitis; GRO J; ss.
                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inflammation treatment-related GRO J oligonucleotide SegID29.
                                                                                                                           Score 20; DB 14; Length 28;
                                                                                                                                                                 Indels
                                                                                  Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
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                                                                                                                                            53;
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                                                                                                                                            Pred. No.
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                                                                                                                                                                                                          1 TITIGGGTTITGGGGTTIT 20
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                                                                                                                                                                                                                                     TTTTGGGGTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                    ADZ58647 standard; DNA; 28 BP.
                                                                                                                         100.08;
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                                                                                                                                            100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                            Local Similarity 100.
les 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-315628/32.
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                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stabilize the intramolecular G-quadruplex structure of human relomeres. The folding of telomeric DNA into G-quadruplexes inhibits telomerase, the enzyme present in over 8% of tumor cells which adds nuclectides to telomeres, preventing them from reducing in length during cell division. The carbazole compounds of the invention may be used to treat telomereral addiesase, e.g., cancer. Sequences ADZ25610-ADZ25619 represent DNA sequences capable of duplex or quadruplex formation which were demonstrated to be bound by a carbazole compound of the invention. The present sequence represents a G-quadruplex-formation which were bound by a carbazole compound. Note: The specification states that this sequence forms a G-quadruplex structure; however, further details on how
                                                                                                                                                                                                                                                                                                                                                                    Telomere; stabilizer; telomerase inhibitor; cancer; neoplasm; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New carbazole compound stabilizing G-quadruplex of telomere, useful to treat telomerase-related disease e.g. cancer.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel carbazole compounds which thermally
                                                                                                                                                                                                                                                                                                                                       G-quadruplex-forming carbazole-binding DNA Oxy28, SEQ ID NO:11.
                                                                       ö
                               100.0%; Score 20; DB 14; Length 28; 100.0%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 14; Length 28; 100.0%; Pred. No. 53;
                                                                     Indels
Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the structure is formed has not been provided
                                                 Local Similarity 100.0%; Pred. No. 53; es 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; SEQ ID NO 11; 12pp; English
                                                                                                        1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                            5 TTTTGGGGTTTTGGGGTTTT 24
                                                                                                                                                                                                                                ADZ25617 standard; DNA; 28 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2003; 2003US-00690984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2003; 2003US-00690984
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wα J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-331984/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHAN/) CHANG T.
(CHAN/) CHANG C.
(WUJJ/) WU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2005090671-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                    14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-2005
                                    Query Match
                                                                                                                                                                                                                                                                 ADZ25617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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method has been developed for binding quadruplex nucleic acids. The method comprises contacting a quadruplex nucleic acid with a monoclonal antibody that selectively binds to quadruplex nucleic acid to form an antibody-quadruplex nucleic acid complex. The method can be used for detecting antibodies that bind to quadruplex nucleic acids and to collect attibodies that bind to quadruplex nucleic acids and to collect cartibodies that bind to quadruplex nucleic acids and to collect suitable for detecting, isolating and purifying quadruplex nucleic acids. The method is also suspected of containing quadruplex nucleic acids. The method can be used for the purification of quadruplex nucleic acids from solutions and to suspected of containing quadruplex nucleic acids from solutions and to purify aptamers from combinatorial libraries or heterogenous solutions, in particular to purify or detect DNA aptamers that specifically bind the thrombin molecule critical in the thrombin-catalysed, fibrin-clot cormation cascade of blood platelets. The antibodies can then be used to detect levels of a known therapeutic aptamer in a patient and monitor clearance and dosage levels in a treatment protocol involving the aptamer. The present sequence trepresents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quadruplex nucleic acid and antibody binding assay useful for detecting and purifying antibodies and nucleic acids from a biological sample.
                                                                                                                                              Quadruplex DNA; antibody; binding; detection; isolation; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 3; Length 32; 100.0%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                             Exemplary quadruplex nucleic acid SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hardin CC,
                                                                                                                                                                                                                                                                                                                                                                                         UYNC-) UNIV NORTH CAROLINA STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 3; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTTTT 20
AAZ57146 standard; DNA; 32 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                  96US-00729598
                                                                                                                                                                                                                                                                                                                                                     95US-0005242P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ61979 standard; DNA; 39
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pelsue SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-096139/08.
                                                                                                                                                                                                                                                                                                                                                                                                            JACK-) JACKSON LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                  11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                     12-OCT-1995;
                                                                         24-MAR-2000
                                                                                                                                                                                                                                           US6001657-A
                                                                                                                                                                                                                                                                               14-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               Roberts JF,
                                                                                                                                                                                                        Synthetic.
                                      AAZ57146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ61979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
AAQ61979
ID AAQ61
XX
AC AAQ61
XX
DT 25-MA
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Gaps

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0; Indels

100.0%; Preu. ...

20; Conservative

Matches

Local Similarity

TTTTGGGGTTTTGGGGTTTT 24 1 TTTTGGGGTTTTGGGGTTTT 20

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The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (frRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hrRT, by detecting the change in hrRT cecombinant protein or polymucleoride, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hrRT with a telomerase RNA component; (C) detection of hrRT with a sample by binding a relevant probe to the sample of hrRT RNA or protein in a sample by binding a relevant probe to the sample of maplifying the product and correlating the presence of complex or amplifying the product with presence of hrRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hrRT expression; and (B) the use of an agent that causes an increase in cell correlation to create a medicament that inhibits ageing. A protein preparation of hrRT and the polymucleotide encoding hrRT can be used in the manufacture of medicaments for inhibiting the cancer inhibitors of telomerase activity can be used
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a guanine rich sequence derived from the Oxytricha telomeric region. This sequence forms an unusual structure termed a G quartet. The formation of this structure is monovalent cation dependant and is disrupted by high temperature. Sequences which share the guanine rich nature of this telomeric sequence may be used to inhibit human type II phospholipase A2 activity. Oligonucleotides such as these may also be used for inhibiting activity of HSV, HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant calls by modualting telomere length, which may also retard aging. (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                    Inhibition; replication; herpes simplex virus; HSV; HIV; aging; human cytomegalovirus; influenza virus; influenze length; neurological disorders; phospholipes A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Bennett CF, Chiang M, Brown-Driver VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 39 BP; 0 A; 0 C; 20 G; 16 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     Wyatt JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 36; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAR-2003 to correct PN field.)
                                   Oxytricha telomeric sequence.
                                                                                                                                                                                                                                                                        93WO-US009297.
                                                                                                                                                                                                                                                                                                          92US-00954185.
04-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Anderson KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                   Vickers TA,
                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-135613/16.
                                                                                                                                                              Oxytricha sp
                                                                                                                                                                                                WO9408053-A1
                                                                                                                                                                                                                                                                        29-SEP-1993;
                                                                                                                                                                                                                                                                                                            29-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                  Hanecak RC,
                                                                                                                                                                                                                                    14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                   Ecker DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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cell

Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of oppoliferation conditions especially cancer and ageing.

Example 1; Page 200; 387pp; English

Morin GB, Harley CB;

Chapman KB,

Lingner J, Nakamura T,

WPI; 1998-171633/16.

Andrews WH;

Cech TR,

UNIV TECHNOLOGY CORP.

CORP

GERON

(GERO-) (UYTE-)

97US-00915503

14-AUG-1997;

97US-00844419. 97US-00846017. 97US-00851843. 97US-00854050. 97US-00911312.

25-APR-1997 06-MAY-1997 09-MAY-1997 14-AUG-1997 14-AUG-1997

97GB-00020890 96US-00724643

01-OCT-1997;

08-APR-1998

GB2317891-A.

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                                                                                                                                                                                                                                                                            Human, telomerase reverse transcriptase, hTRT, TRT, diagnosis, prognosis, cell proliferation, cancer, ageing, ribonucleoprotein, primer, ss.
                                                    Gaps
                                                    .
0
                       Score 20; DB 2; Length 44;
Pred. No. 54;
                                                   0; Indels
Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                     Telomerase substrate utilisation primer 25-27.
                                                   0; Mismatches
                                                                              20
                                                                                                      44
                      natch 100.0%;
Local Similarity 100.0%;
les 20; Conservative 0:
                                                                              1 TTTTGGGGTTTTT
                                                                                                       25 rrrregegerrrregegerrrr
                                                                                                                                                                       AAV17008 standard; DNA; 46
                                                                                                                                                                                                                            13-AUG-1998
                                                                                                                                                                                                   AAV17008;
                        Query Match
                                                    Matches
                                                                                                                                                RESULT 16
                                                                                                                                                             AAV17008
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Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.

Synthetic. Homo sapiens.

Telomerase substrate utilisation primer 28-30.

13-AUG-1998 (first entry)

AAV17009;

AAV17009 standard; DNA; 44 BP

RESULT 15 AAV17009

TITIGGGTTTTGGGGTTTT 20 rrrrececrrrrececrrrr 27

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8

high telomerase activity. A

protein preparation of hTRT can also be used in the new methods

to treat conditions that are associated with

us-09-669-187a-73.szlm50.rng

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13-AUG-1998 (first entry)
                                                                                                                                                                                                                                                           GERON
                                             Homo sapiens.
                                                                                                                       01-OCT-1997;
                                                                       GB2317891-A.
                                                                                                                                                                                                                                   4-AUG-1997;
                                                                                              38-APR-1998
                                                                                                                                              01-0CT-1996
                                                                                                                                                                                    1997
                                                                                                                                                                                                                        1997
                                                                                                                                                                       1997
                                                                                                                                                                                                           14-AUG-1997
                                                                                                                                                           18-APR-1997
                                                                                                                                                                                                                                                                                                            Andrews WH;
                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV17004;
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                                                                                                                                                                                                                                                                        (UYTE-)
                                                                                                                                                                                    36-MAY-
                                                                                                                                                                                                                                                           GERO-)
                                                                                                                                                                       25-APR-
                                                                                                                                                                                                                       14-AUG-
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AAV17004
                                                                                                                                                                                                                                                                                                Cech
HXXXH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT cast compound is a modulator of hTRT, by detecting the change in hTRT cast combinant protein or polymucleotide, on administration of the compound; (B) preparation of hTRT with a telomerase by contacting a protein of the TRT with a telomerase BNA component; (C) detection of the TRT with a telomerase BNA component; (C) detection of the TRT with a telomerase BNA component; (C) detection of the TRT with a telomerase BNA component; (C) detection of the TRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT cast and (B) the use of an agent that causes an increasing hTRT cast send in the maniferance of medicament that inhibits ageing. A protein preparation of hTRT and the polymucleotide encoding the fact of ageing or cancer. Inhibitors of telomerase activity and be used to the maniferance of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity and the new methods protein preparation of hTRT can also be used in the new methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                       Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                             Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 2; Length 46; 100.0%; Pred. No. 54;
                                                                                                                                                                                                                                                             Chapman KB, Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46 BP; 10 A; 12 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Telomerase substrate utilisation primer 22-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 200; 387pp; English
                                                                                                                                                                                                                                                           Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 TTTTGGGGTTTTGGGGTTTT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TITTGGGGTTTTGGGGTTTT 20
                                                                                                                       97US-00844419.
97US-00846017.
97US-00851843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV17007 standard; DNA; 48 BP
                                                                                                                                                          97US-00854050.
97US-00911312.
97US-00912951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                        GERON CORP.
UNIV TECHNOLOGY CORP.
                                                                                    97GB-00020890
                                                                                                           96US-00724643
                                                                                                                                                                                                97US-00915503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
                                                                                                                                                                                                                                                                                                  WPI; 1998-171633/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
              Homo sapiens
                                                                                    01-OCT-1997;
                                                                                                                                                          09-MAY-1997;
14-AUG-1997;
14-AUG-1997;
14-AUG-1997;
                                    GB2317891-A
                                                           08-APR-1998
                                                                                                             01-OCT-1996
                                                                                                                                   25-APR-1997
06-MAY-1997
                                                                                                                                                                                                                                                                          Andrews WH;
 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV17007;
                                                                                                                                                                                                                                                             Sech TR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                       (GERO-)
                                                                                                                                                                                                                                     (UYTE-)
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The present sequence represents a primer from the present invention which describes human telomerase transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a teat compound is a modulator of hRRT, by detecting the change in hRRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein of the preparation of the compound; (C) detection of the hRRT with a telomerase RNA component; (C) detection of the hRRT with a relomerase RNA component; (C) detection of the hRRT with a telomerase RNA component; (C) detection of the hRRT with a product and correlating the presence of complex or amplifying the product and correlating the presence of hRRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hRRT cappearation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding correct conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
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Human, telomerase reverse transcriptase, hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 200; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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97US-00846017.
97US-00851843.
97US-00854050.
97US-00911312.
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                                                                                                                                                                                                                                                                                                                                                                                                             96US-00724643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00915503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-171633/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORP
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Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;

Pelomerase substrate utilisation primer 19-21.

13-AUG-1998 (first entry)

AAV17006;

cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.

Homo sapiens.

Synthetic

GB2317891-A 08-APR-1998

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The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of hTRT with a telomerase by contacting a protein of the hTRT with a telomerase by contacting a protein of the hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample, and (D) increasing the proliferation of a vertebrate cell by increasing hTRT camplification product with presence of an agent that causes an increasing hTRT carporate cell proliferation to create a medicament that inhibits of hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
                                                 Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chapman KB, Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
                 Telomerase substrate utilisation primer 13-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 200; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cech TR, Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                         970S-00846017
970S-00851843.
970S-00854050.
970S-00911312.
970S-00912951.
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97US-00844419
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GERON CORP
                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                      01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-1997;
                                                                                                                                                              GB2317891-A
                                                                                                                                                                                                                                                                                                            25-APR-1997
06-MAY-1997
                                                                                                                                                                                                    08-APR-1998
                                                                                                                                                                                                                                                                          01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                    14-AUG-1997
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                                                                                                        Synthetic.
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variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.

Example 1; Page 200; 387pp; English.

Pure and recombinant human Telomerase Reverse Transcriptase and its

Chapman KB, Morin GB, Harley CB;

Nakamura T,

Lingner J,

Andrews WH;

Cech

WPI; 1998-171633/16.

UNIV TECHNOLOGY CORP.

(GERO-) GERON CORP

UYTE-)

14-AUG-1997;

96US-00724643. 97US-00844119. 97US-00846017. 97US-00854050. 97US-0091312. 97US-00912513.

06-MAY-1997

97GB-00020890

01-OCT-1997;

01-OCT-1996 25-APR-1997 09-MAY-1997 14-AUG-1997 14-AUG-1997

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The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (C) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT WNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, and detecting the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT and sequing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
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0
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Matches
8
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RESULT 20

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Gaps

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0; Indels

0; Mismatches

Local Similarity 100. ses 20; Conservative

Matches

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Query Match

48

59

AAV17006 standard; DNA; 50 BP.

RESULT 19
AAV17006
ID AAV17
XX

1 TTTTGGGGTTTTGGGGTTTT 20

100.0%; Score 20; DB 2; Length 48; 100.0%; Pred. No. 54;

ADF69702

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The present invention relates to a method for detecting differential methylation patterns in an helicase-like transcription factor (HLTF, also called HIPILGA, 2D1, RUSHIA and Samarca) nucleotide sequence. The method involves obtaining samples from a patient and a healthy subject, assaying the samples for the presence of methylation within a nucleotide sequence and comparing the methylation patterns in the sample from the subject to those in the normal sample. HLTF modulator is useful for treating an HLTF-associated proliferative disease in a subject, where the disease is associated with methylation of an HLTF nucleic acid sequence, i.e. colon neoplasia and the compound induces HLTF expression. The method of the invention is useful in gene therapy. The present sequence is the human HLTF's unmethylated DNA fragment amplifying PCR primer.
                                                                                                                                                                                                                                                            Detecting differential methylation patterns in an HLTF nucleotide sequence, useful for diagnosing or treating colon neoplasia, comprises assay samples for the presence of methylation within a specific nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA methylation; HLTF; helicase-like transcription factor; HIP116a; RUSH1a; Smarca; proliferative disease; colon neoplasia; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HLTF unmethylated DNA amplifying forward PCR primer, 1347UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
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Pred. No. 2.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 50; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TITIGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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                                         07-OCT-2002; 2002US-00266103.
                                                                                   05-OCT-2001; 2001US-0327537P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-2002; 2002US-00266103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADV09348 standard; DNA; 29
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                                                                                                                               (MARK/) MARKOWITZ S D.
                                                                                                                                                                                                                       WPI; 2005-011663/01.
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                                                                                                                                                                           Markowitz SD;
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02-DEC-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes the human SLC5A8 protein (1), which is a cell surface protein. (1) has cytostatic activity, and can be used in gene therapy. (1) can be used in detecting and treating SLC5A8-associated cancer. e.g. colon cancer, breast cancer, thyroid cancer or stomach cancer. (1) is also useful in screening assays, predictive medicine and in diagnostic and prognostic assays. The human SLC5A8 gene is located on chromosome 12. The present sequence is used in the exemplification of the
                                                                                                                                                                                           human; SLC5A8; cell surface protein; cytostatic; gene therapy; SLC5A8-associated cancer; colon cancer; breast cancer; thyroid cancer; stomach cancer; cancer; HLTF; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New SLCSA8 polypeptide, useful for detecting and treating SLCSA8-
associated cancer, e.g. colon, breast, thyroid or stomach cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                      Human HLTF methylation detection PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 77; Page 99; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYCA-) UNIV CASE WESTERN RESERVE
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                       ВР.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2003; 2003WO-US018239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2002; 2002US-0386653P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
                       ADF69702 standard; DNA; 29
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                          11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
                                                                                                                                                                                                                                                                                          Synthetic
                                                                   ADF69702;
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Gaps

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Length 29; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT28317-T28347 represent multi-G oligonucleotides. AAT28336-T28347 are multi-G oligonucleotides with multiple G strings, or G strings of 4 bases and over. These sequences are oligonucleotides of the invention. These sequences can be modified to become more nuclease resistant, using phosphorothioate, phosphorodithioate, or 3'-carbon modified links. To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multi-G oligonucleotide; antisense sequence; c-myb; nuclease resistant; phosphorothioate linkage; phosphorodithioate linkage; inhibitor; therapy; cell proliferation; smooth muscle cell; proliferation protein; vascular restenosis; arterial restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified oligo:nucleotide(s) contg. consecutive guanine residues -inhibit proliferation of smooth muscle cells, esp. to prevent arterial restenosis.
                                nce, useful for diagnosing or treating colon neoplasia, comprises samples for the presence of methylation within a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Detecting differential methylation patterns in an HLTF nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%; Score 18.4; DB 14; Length 29; 95.0%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unmethylated DNA amplifying PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multi-G oligonucleotide T3-G4-T4-G4-T3.
                                                                                                                                                                      Claim 10; SEQ ID NO 13; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fisher EF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 32; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT28342 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US012770.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 95.0
les 19; Conservative
                                                                                                         nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-209848/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1996
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                                       sequence,
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AAT28342
AAT28342
XX
AC AAT28
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DT 20-NO
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DE Multi
XX
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screen for modified multi-G sequences that inhibit cell proliferation, cultured smooth muscle cells that are arrested in the GO phase, are induced to proliferate in the presence of the multi-G sequence. The cultured smooth muscle cells used in this method are attached to a solid support, and growth arrest is achieved on a starvation medium, followed by transfer to a normal growth medium to induce proliferation. The compounds that provide over 50% inhibition at a set dosage are selected as being useful for inhibiting vascular restenosis. The multi-G oligonucleotides are used to inhibit proliferation of smooth muscle cells, such as to prevent arterial restenosis. These sequences are not antisense sequences, but are thought to work in a similar way. The sequences are thought to act by binding to proteins involved in the proliferation process. Compounds contening these multi-G oligonucleotides are not toxic, and their effect on cell proliferation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, telomerase reverse transcriptase, hTRT, TRT, diagnosis, prognosis,
cell proliferation, cancer, ageing, ribonucleoprotein, primer, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a primer from the present invention which
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                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of c proliferation conditions especially cancer and ageing.
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                                                                                                                                                                                                                                                                           DB 2; Length 18; 3.4e+02;
                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                   Sequence 18 BP; 0 A; 0 C; 8 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telomerase substrate utilisation primer 19-21.
                                                                                                                                                                                                                                                                                       100.0%; Pred. ....
                                                                                                                                                                                                                                                                               Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 200; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                            2 TITGGGGTTTTGGGGTTT 19
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97US-00846017.
97US-00851843.
97US-0091312.
97US-00912951.
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                                                                                                                                                                                                                                                                                 90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV17006 standard; DNA; 50
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-171633/16.
                                                                                                                                                                                                                      fully reversible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV17006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GERO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
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describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT. by detecting the change in hTRT recombinant protein or polynuclectide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein properation of hTRT with a telomerase RNA component; (C) detection of the TRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product with presence of hTRT in the sample, or amplifying the product with presence of hTRT in the sample, and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits or ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used
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                                                                                                                                                                                                                                                                                                                           high telomerase activity. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligo:nucleotide(s) forming triple helix with target nucleic acid contain purine and pyrimidine tracts in specific orientations, useful therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                protein preparation of hTRT can also be used in the new methods
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                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%; Score 18; DB 2; Length 50; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50 BP; 12 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                             treat conditions that are associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 14a; 101pp; English
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92US-00826934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TITIGGGGTTTTGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Target sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9312230-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming colinear triplex to control transcription process in gene-specific fashion.
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                 Sequence binding to and inhibiting the gene controlling Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                               C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimers disease; EGF; epidermal growth factor; GSTpi; HWGCoA; thallasemia; Herpes simplex virus; nerve growth factor receptor; globin; ss.
the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                            1; Indels
                                                            Score 17.4; DB 2; Length Pred. No. 6e+02; 0; Mismatches 1; Indels
                              Sequence 26 BP; 2 A; 1 C; 13 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 35; Page 30; 40pp; English.
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90.0%;
                                                            Query Match 87.0%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                      AAQ04992 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                    disease plaque formation.
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                                                                                                                                                                                                                                                                                                      (revised)
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Best Local Similarity
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31-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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The APP770 gene is the precursor protein responsible for production of plaque in Alzheimer's disease. Expression of this gene may be prevented by the formation of a triplex between the duplex target DNA sequence and an anti parallel or parallel synthetic oligonucleotide. A suitable target sequence is that from base -434 to -407 of the APP770 gene and a suitable antiparallel synthetic oligonucleotide sequence is shown. See also AAQ36219-362. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, telomerase reverse transcriptase, hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition which bind to target sequence in duplex DNA forming colinear triplex by binding to major groove.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morin GB, Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 16.8; DB 2; Length 90.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chapman KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telomerase substrate utilisation primer 28-30
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lingner J, Nakamura T,
                                                                                                                                                                                                                   Example 6; Col 22; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTGGGGTTTT 20
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97US-00846119.
97US-00846017.
97US-00854050.
97US-00911312.
97US-00912951.
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                                     89US-00453532
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                                                             88US-00287359
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ID AAV17009 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                               Kessler DJ;
                                                                                                                                        WPI; 1993-035718/04.
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                                     22-DEC-1989;
                                                              20-DEC-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1997;
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            05-JAN-1993
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25-APR-1997
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                                                                                                               Hogan ME,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GERO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The APP770 gene is the precursor protein responsible for production of plaque in Alzheimer's disease. Expression of this gene may be prevented by the formation of a triplex between the duplex target DNA sequence and an anti parallel or parallel synthetic oligonucleotide. A suitable target sequence is that from base -434 to -407 of the APP770 gene and a suitable parallel synthetic oligonucleotide sequence is shown. See also AAQ36219-362. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                    Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition which bind to target sequence in duplex DNA forming colinear triplex by binding to major groove.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APP4anti, targetted to a region of APP770 gene.
                                                                                                                             APP4par, targetted to a region of APP770 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTGGGGTTTTTGGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE
                                     AAQ36268 standard; DNA; 28 BP
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90.0%;
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                                                                                                    (first entry)
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                                                                                        (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                      22-DEC-1989;
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                                                                                     25-MAR-2003
07-JUN-1993
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07-JUN-1993
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                                                                                                                                                                                                                                             05-JAN-1993
                                                                                                                                                                   duplex; ss
                                                                                                                                                                                                                                                                                                                                                 Hogan ME,
                                                                                                                                                                                           Synthetic.
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                                                              AAQ36268;
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(UYTE-) UNIV TECHNOLOGY CORP.
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AAV17007/c
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                                                                                                                                                                                                                The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (E) preparation of recombinant telomerase by contacting a protein or protein in a sample by binding a relevant probe to the sample hTRT RNA or protein in a sample by binding a relevant probe to the sample or mightlying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT captebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polymucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to the name are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                     Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                Example 1; Page 200; 387pp; English
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97US-00846017.
97US-00851843.
97US-0091312.
97US-00912951.
97US-00912951.
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                                              WPI; 1998-171633/16.
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06-MAY-1997;
09-MAY-1997;
14-AUG-1997;
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The present sequence represents a primer from the present invention which describes human telomerase transcriptase (hTRT). The present transcribes human telomerase reverse transcriptase (hTRT). The present transcribes human telomerase transcriptase (hTRT). The present transcriptase determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (C) preparation of recombinant telomerase by contacting a protein protein of preparation of hTRT with a telomerase By contacting a protein of the hTRT RNA or protein in a sample by binding a relevant probe to the sample of hTRT RNA or protein in a sample by binding a relevant probe to the sample complex formed or in the case of RNA detection, and detection the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT capperation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity and the new methods
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                                                                                                                                                                Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
Harley CB;
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   Chapman KB, Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46 BP; 10 A; 12 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                           Example 1; Page 200; 387pp; English.
   Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TITIGGGGTTTTGGGGTTTT 20
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97US-0084419.
97US-0081617.
97US-00851843.
97US-00911312.
97US-00911312.
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Matches 18; Conservative
                                                                                                       WPI; 1998-171633/16.
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14-AUG-1997;
14-AUG-1997;
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06-MAY-1997
Cech TR, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1997
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14-AUG-1997;
            14-AUG-1997;
14-AUG-1997;
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                                                                                                                Andrews WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ05743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                    Cech TR,
                                                              GERO-)
                                                                            (UYTE-)
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ05743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                     The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase by contacting a protein protein in a sample by binding a relevant probe to the sample hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) corrected in the use of an agent that causes an increase in cell expression; and (E) the use of an agent that causes an increase in cell expression; and (E) the use of an agent that that inhibits ageing. A protein preparation of effect of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used the constant of a protein preparation of the medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, telomerase reverse transcriptase, hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
                                                                                                                             Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                               Chapman KB, Morin GB, Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8; DB 2; Length 48; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Telomerase substrate utilisation primer 13-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                  Example 1; Page 200; 387pp; English
                                                              Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTTTGGGGTTTTGGGGTTTT 20
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97US-0084419.
97US-00846017.
97US-00851843.
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90.0%;
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 97US-00915503
                                      UNIV TECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                    WPI; 1998-171633/16
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                           GERON CORP
 14-AUG-1997;
                                                                          Andrews WH;
                                                               Cech TR,
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                         (GERO-)
                                      (UYTE-)
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the present sequence reverse transcriptase (hTRT). The present incepresent and escribes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (B) preparation of hTRT with a telomerase BNA component; (C) detection of the TRT RNA or protein in a sample by binding a relevant probe to the sample of hTRT RNA or protein in a sample by binding a relevant probe to the sample of and etecting the complex formed or in the case of RNA detection, amplification product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) concreasing the proliferation of a vertebrate cell by increasing hTRT concreasing in the use of an agent that causes an increase in cell contract can be used in the manufacture of medicament that inhibit againg or cancer. Inhibitors of telomerase activity and the new methods activity. A protein preparation of hTRT can also be used in the new methods in the new methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents a primer from the present invention which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                           Chapman KB, Morin GB, Harley CB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 200; 387pp; English.
                                                                                                                                                                                                                                                                                                                      Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTTTGGGGTTTTGGGGTTTT 20
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97US-00854050.
97US-00911312.
97US-00912951.
97US-00915503.
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                                                                                                                                                                                                                                           UNIV TECHNOLOGY CORP
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-171633/16.
                                                                                                                                                                                                     GERON CORP
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invention
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                                                                                                                                                                            The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ008152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulatory sequence; eukaryotic protist; telomere; alpha-tubulin; primer;
                                                                                                           New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                       Prentice J, Phillips J;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                    B4.0%; Score 16.8; DB 6; Length 50; Local Similarity 90.0%; Pred. No. 1.1e+03; Conservative 0; Miematel
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                                                      Altman P, Pr, Johnson F;

    lemnae alphal-tubulin telomerase primer DNA.

                                                      muth J, Fry K, Matcuk G, A
Woodward R, Quertermous T,
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                                                                                                                                                                                                                                                                                                                                                                                                                14 TGTTGGGTTTTTGGGGTTTT 33
                                                                                                                                                         Claim 1; Page 513; Opp; English.
20-OCT-2000; 2000US-0241994P
08-JUN-2001; 2001US-0296764P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-EP007958
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98DE-01048486
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AAA39694 standard; DNA; 20
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                                 (BIOC-) BIOCARDIA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-339703/29.
                                                                                        WPI; 2002-636525/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stylonychia lemnae.
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                                                       Wohlgemuth J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-2000
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Matches
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This invention describes a novel expression vector (A) for eukaryotic protists comprises a sequence (I) encoding a protein and having, at its 3' and 5'-ends, native flanking regulatory sequences (RS) selected from Stylonychia lemnae and with terminal telomeric sequences. (A) are used for production of proteins in protists, particularly functional heterologous proteins. (A) provide overexpression of foreign proteins in protists, e.g. at 7.15 of total proteins. Bukaryotic protists can be protists, e.g. at 7.15 of total proteins. Bukaryotic protists can be grown simply and on a large scale to high cell density with short generation times and have metabolic and other properties similar to those of multicellular organisms (contrast prokaryotes). In the macronucleus genome of protists, most genes are amplified, resulting in high expression rates even under normal conditions. This sequence represents a primer used in the construction of the expression vector described in the
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Pred. No. 2.2e+03;
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    lemnae expression vector construct primer XbaApatel.

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Claim 4; Page 45; 51pp; German.
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98DE-01048486.
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Les 16; Conservative
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of multicellular organisms (contrast prokaryotes). In the macronucleus genome of protists, most genes are amplified, resulting in high expression rates even under normal conditions. This sequence represents a primer used in the construction of the expression vector described in the
                                                                                                             invention
        88888888
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Sequence 30 BP; 10 A; 13 C; 5 G; 2 T; 0 U; 0 Other;

ö Score 16; DB 3; Length 30; Pred. No. 2.3e+03; 0; Indels 80.0%; Scc... 100.0%; Pred. No.... 0; Mismatches 16 TTTTGGGGTTTTGGGG Conservative Local Similarity les 16; Conserv Н 28 Query Match Best Loca Matches 셤 ઠ

rrrrececrrrrecee 13

ADV45884 standard; DNA; 19

ADV45884;

ВЪ

(first entry) 10-MAR-2005 Human CpG site probe SEQ ID NO 1411.

DNA methylation; ss; probe; cancer; neoplasm; squamous cell carcinoma.

Homo sapiens

WO2004110246-A2.

23-DEC-2004.

14-MAY-2004; 2004WO-US015382.

15-MAY-2003; 2003US-0471488P.

(ILLU-) ILLUMINA INC.

Bibikova M; Fan J,

WPI; 2005-057693/06

Identifying differentially methylated genomic CpG dinucleotide sequences associated with cancer, comprises measuring level of methylated genomic CpG dinucleotide sequences for genomic targets in sample and comparing to reference level.

Claim 28; SEQ ID NO 1411; 89pp; English.

The invention relates to a mehtod of identifying differentially methylated genomic CpG dinucleotide sequences associated with cancer, comprising measuring the level of methylated genomic CpG dinucleotide equences for two or more of the genomic targets in sample, and comparing the level of methylation at genomic CpG dinucleotide sequences in the sample to a reference level of methylated genomic CpG dinucleotide sequences. The method is useful for identifying differentially methylated genomic CpG dinucleotide sequences associated with cancer in an individual. The level of methylation of the differentially methylated genomic CpG dinucleotide sequences is used to diagnose cancer in the individual, predict the course of cancer, predict the susceptibility of cancer, stage the progression of cancer, predict the likelihood of overall survival, and predict the likelihood of recurrence of cancer for individual. The level of methylation of the differentially methylated genomic CpG dinucleotide sequences in the sample is also used to determine the effectiveness of a treatment course undergone by the individual. The cancer is preferably adenocarcinoma or squamous cell carcinoma. The probes are useful for detecting methylation of genomic CpG dinuclectide sequences of two or more genomic targets. The present sequence represents a CpG site probe. 

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Gaps
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                            Length 19;
                                                            Indels
Sequence 19 BP; 11 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
                          77.0%; Score 15.4; DB 14;
llarity 94.1%; Pred. No. 3.9e+03;
Conservative 0; Mismatches 1;
                                                                                           20
                                                                                           4 TGGGGTTTTGGGGTTTT
                              Query Match
Best Local Similarity
Matches 16; Conserv
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recerririectrir 3

RESULT 37 ACF58129

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Gaps

ACF58129 standard; DNA; 43 BP

ACF58129;

15-JAN-2004 (first entry)

HLTF non-methylation-specific PCR forward primer.

Disease diagnostic, CpG; nucleic acid amplification; cancer detection; p14; HLTF; MINT31; MINT2; methylation; PCR; primer; 88.

Homo sapiens.

WO2003087390-A2

23-OCT-2003

11-APR-2003; 2003WO-US011023.

11-APR-2002; 2002US-00123071.

(EXAC-) EXACT SCI CORP

Shuber AP;

WPI; 2003-845337/78.

Detecting an indicium of a disease in a heterogeneous biological sample comprises contacting the nucleic acid sample with an agent that modifies unmethylated cytosine, and detecting hypermethylated or hypomethylated nucleic acid.

Example 4; Page 17; Opp; English.

The invention relates to detecting an indicium of a disease in a heterogeneous biological sample. The method involves (a) isolating a comparison and calcacid sample comprising a CpG-containing target template from a nucleic acid sample comprised a CpG-containing target template from a heterogeneous biological sample; (b) contacting the nucleic acid sample with an agent that modifies unmethylated cytosine; (c) performing an amplification reaction on the target template using at least one chimeric primer that comprises a first portion that is not specific for the target template and a second portion, where the second portion is specific for the CpG-containing target template if the template comprises an unmodified cytosine at predetermined position, and (d) detecting the presence of an predetermined position, and indicium of a disease. The method is useful for detecting indicia of cancer in a biological sample, for detecting cancer detection in a homogenous sample, such as a biopsy sample. The method is especially suitable in clinical assays involving sporadic cancer detection, for infectious disease diagnostics, or inherited disease diagnostics. The new method makes it possible to detect a disease assaying of hypermethylation markers on genes pl4, HLTF, MINT31 and MINT2, used in detection of hypermethylation at multiple loci, which indicate a higher risk of colorectal cancer

Sequence 43 BP; 4 A; 5 C; 16 G; 18 T; 0 U; 0 Other;

Query Match

DB 10; Length 43; 77.0%; Score 15.4; the haplotype, and reagents for detection of the label, and a reagent kit for assaying a sample for the presence of at least one haplotype comprising 2 or more alleles comprising: at least one nucleic acid comprising at least one nucleotide sequence that is at least partially

complementary to a part of nucleotide sequence of MAP3K9, capable of acting as a primer for a primer extension reaction and capable of detecting 2 or more specific alleles of the haplotype. The MLK family

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                                                                                                                                                  mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9; antiasthmatic; respiratory-gen.; antinflammatory; antirheumatic; antipsoriatic; neuroprotective; gastrointestinal-gen.; respiratory disease; chronic obstructive pulmonary disease; chronic botructive pulmonary disease; chronic bronchitis; inflammation; ss; primer; PCR.
          Gaps
          ö
          Indels
          ;
                                                                                                                                   MAP3K9 marker amplification reverse primer #1146.
Pred. No. 4e+03;
          Mismatches
                                                                                                                                                                                                                                                                                                             Hakonarson H, Gurney ME, Halapi E;
          .
0
                         20
                                                                                   BP
                                                                                                                                                                                                                                                                    14-JUL-2003; 2003US-0487072P. 05-APR-2004; 2004US-0559611P.
                                                                                                                                                                                                                                                     14-JUL-2004; 2004WO-US022446.
 94.1%;
                                                                                                                                                                                                                                                                                             (DECO-) DECODE GENETICS EHF.
                          4 TGGGGTTTTGGGGTTTT
                                          TGGGGTTTTGTGGTTTTT
                                                                                   ADW84828 standard; DNA; 20
                                                                                                                    (first entry)
          16; Conservative
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                    WO2005007144-A2.
                                                                                                                                                                                                   Unidentified.
                                                                                                                   07-APR-2005
                                                                                                                                                                                                                                    27-JAN-2005
                                                                                                    ADW84828;
                                                                  RESULT 38
ADW84828/c
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cherecting 2 or more specialists attended to the interpretary chinase inhibitor has the following activities: antiaethmatic, respiratory equ., antinflammatory antirheumatic, antiarthritic, antiasculus activities: antiaethmatic, respiratory equ., and agastrointestinal-gen. The MLK family kinase inhibitor is useful for the treatment of asthma associated with a risk factor selected from at-risk haplotype for asthma, at-risk haplotype in MAPRY of gene, polymorphism in MAPRY midler activity and/or increased MLKI protein expression, dysregulation of MAPRY mRNA isoform, increased MLKI protein soform expression; and in diagnosis or identification of susceptibility to asthma. The inhibitor is also useful for the treatment of other respiratory diseases associated with MAPRY or other members of the JNK pathway such as chronic obstructive pulmonary disease, chronic bronchitis and other inflammatory diseases such as rheumatoid arthritis, polymorary diseases until inflammatory diseases. This production dequence represents a reverse primer which is used in amplifying a marker of the MAPRYS innase, where MAPRYS is a part of mitogen-Activated Protein Kinase (MAPK) signal transduction pathways, of

the invention.

Use of mixed lineage kinase family kinase inhibitor in the manufacture of a medicament for treatment of asthma associated at-risk haplotype for asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein expression or activity.

WPI; 2005-122681/13.

Disclosure; Fig 12; 640pp; English.

The invention relates to the movel use of a mixed intase (wilk) the invention relates to the invention relates to the invention relates to the invention relates to the invention sethma, at-risk haplotype in MARIX9 gene, polymorphism in MARIX9 mixed acid, dysregulation of a MARIX9 gene, polymorphism in MARIX9 mixed acid, dysregulation of a MARIX9 gene, polymorphism in MARIX9 mixed acid, dysregulation of a MARIX9 gene, polymorphism in MARIX9 gene, polymorphism in MARIX9 gene, polymorphism in a sample, a method for the diagnosis or identification of molecule for diagnosing asthma or susceptibility to asthma in a sample, and the presence of a first nucleic acid molecule in a sample, amethod for assessing the response to treatment with an MIX family kinase nucleic acid inhibitor in a target population or in an ample, a method for assessing the response to treatment with an at-risk haplotype for asthma, at-risk haplotype in the MARIX9 gene, polymorphism in the MARIX9 mucleic acid, dysregulation of MARIX9 gene, polymorphism in the MARIX9 mixed acid, dysregulation of MARIX protein isoform expression, increased MIXI biochemical activity or increased MIXI protein isoform expression; a method for assessing the response to treatment with an MIXI inhibitor in a target population including an individual with an at-risk haplotype for asthma, as above; a kit for assaying a sample for the presence of at least one haplotype comprising 2 or more alleles associated with asthma comprising: at least one specific allele; a reagent kit for assaying the presence of at least one haplotype comprising 2 or more alleles associated we have a sees in the comprising 2 or more alleles associated we have a sees one apecific allele of detecting at least one specific allele of a reagent kit for assaying at least one haplotype comprising 2 or more alleles associated we have a sees one specific allele of detecting at least one specific alled nucleic acid capable of detecting at least one apecific alled a reagent kit least one specific alled a reage invention relates to the novel use of a mixed lineage kinase (MLK)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 20 BP; 11 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2; DB 14;
Pred. No. 4.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate cancer gene PCR primer SEQ ID NO 376.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TITIGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%;
85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2003; 2003EP-00090414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2004; 2004EP-00090292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA51773 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neoplasm; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Best Local {
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The invention relates to a novel quantitative method for adding linear polynucleotide to solution containing a cation. The linear polynucleotide contains telomere repeat sequence with donor at one edge portion and acceptor at another edge portion. The optical detection is performed using this linear polynucleotide. The method of the invention is useful in medical fields such as clinical laboratory test and fields with cation fixed assay. The present sequence is used in the exemplification of the
adding linear polynucleotide containing telomere repeat sequence wi
donor and acceptor at edge portions, to solution containing cation.
                                                                                                                                                                                                                                                                                                                Sequence 31 BP; 3 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; linear polynucleotide; cation; telomere repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonuclectide of the invention #12.
                                                                   Disclosure; Page 16; Bpp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 rrraddddrrrraddddrr 25
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                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                        invention
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                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                              The invention describes a method of detecting and/or differentiating between prostate cell proliferative disorders in a subject comprising contacting genomic DNA isolated from a biological sample with at least contacting genomic DNA isolated from a biological sample with at least cone reagent, or series of reagents that distinguishes between methylated cone reagent, or series of reagents that distinguishes between methylated cards e.g. HISTONE H4. Also described are: a treated mucleic acids e.g. HISTONE H4. Also described are: a treated concerts at leas one unmethylated cytosine base of the casponent converts at leas one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectable comprising at lest 16 contiguous nucleotides of a treated genomic DNA sequences complementary to them; an oligomer comprising a sequence of sequences complementary to them; an oligomer comprising a sequence of at least 9 contiguous nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a treated genomic DNA sequence above; as et of oligomers comprising at least two coligomers above; and a kit useful for detecting and/or distinguishing between or among prostate cell proliferative disorder of a subject comprising a contiguous sequence at least or complementary to, or hybridizes complements or sequence complements. The concludes that is complementary to, or hybridizes under moderately stringent conditions to a sequence selected from SEQ ID NO: 60-295, 1029-1076, 1117-1120, 1172-1175 and their complements. The concludent capted caid, oligomer, set of oligomorlectibes that second molecule comprising a contiguous sequence at least or method or among cell candul for detecting and/or differentiating between or among cell contingent or stringent cardidoling a prostate cell proliferation a seculated from SEQ ID NO: confidential disorders. This sequence selected from SEQ ID NO: confidention of gene encoding a prostate cell proliferation associated a primer 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%; Score 15.2; DB 14; Length 22; 85.0%; Pred. No. 4.7e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 3 A; 0 C; 7 G; 12 T; 0 U; 0 Other;
                                              Example 3; SEQ ID NO 376; 164pp; English.
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Matches
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ADJ94146
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Gaps

.; 0

Length 31; Indels

Score 15.2; DB 10; Pred. No. 4.8e+03; 0; Mismatches

76.0%; 85.0%;

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The invention relates to a novel quantitative method for adding linear polynucleotide to solution containing a cation. The linear polynucleotide contains telomere repeat sequence with donor at one edge portion and acceptor at another edge portion. The optical detection is performed using this linear polynucleotide. The method of the invention is useful in medical fields such as clinical laboratory test and fields with cation fixed assay. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                      Quantitative method of cation for clinical laboratory test, involves adding linear polynucleotide containing telomere repeat sequence with donor and acceptor at edge portions, to solution containing cation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 76.0%; Score 15.2; DB 10; Length 36; 1 Similarity 85.0%; Pred. No. 4.8e+03; 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36 BP; 4 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 15; 8pp; Japanese.
                                                                                                                                                                                                                                                                                         TAKENAKA S.
TUM KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                          WPI; 2003-639772/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                         (TAKE/) (TUMK-)
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ds; linear polynucleotide; cation; telomere repeat.

JP2003169676-A. Unidentified.

17-JUN-2003.

Oligonucleotide of the invention #13

(first entry)

06-MAY-2004

ADJ94146;

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Quantitative method of cation for clinical laboratory test, involves

05-DEC-2001; 2001JP-00371975. 05-DEC-2001; 2001JP-00371975

(TAKE/) TAKENAKA S. (TUMK-) TUM KENKYUSHO KK.

4PI; 2003-639772/61

(first entry)

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Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; munuostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infections disease; allergy; immune deficiency; phosphorothioate; ss.
                                        Immunostimulatory nucleic acid #616.
                                                                                                                                                                                                                                                     25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                           25-SEP-2000; 2000WO-US026383
                                                                                                                                                                    WO200122972-A2.
           12-JUN-2001
                                                                                                                                                                                                05-APR-2001.
                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for predicting a disease, monitoring (rate of) progression of a disease, predicting therapeutic cutcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                           17, leukocyte, gene expression profiling, allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus; rheumatoid arthritis, osteoarthritis, cytomegalovirus; infection, probe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prentice J, Phillips
                                                                                                                                                                                  Human leukocyte gene expression profiling probe SEQ ID NO 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%; Score 15.2; DB 6; Length 50; 85.0%; Pred. No. 4.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 50 BP; 13 A; 6 C; 14 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altman P, P;
, Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nuth J, Fry K, Matcuk G, A
Woodward R, Quertermous T,
TTTTGGGGTTTTGGGGTTTT 20
              ||| ||||||||| ||| ||| TTTAGGGGTTT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 357; Opp; English.
                                                                                               ABZ01038 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-2000; 2000US-0241994P.
                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001; 2001WO-US047856
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 85.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOC-) BIOCARDIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-636525/68.
                                                                                                                                                                                                                                                                                                              WO200257414-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wohlgemuth J,
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                       09-JAN-2003
                                                                                                                                                                                                                                                                                                                                          25-JUL-2002
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                                                                                                                          ABZ01038;
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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich prich or thymidine (T) rich The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae) had to thomyvoritidae), bacterial antigens (e.g. toxoplasma, and/or orthomyxoritidae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells. Note: the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection, bacterial infection, fungal infection, parasitic infection, cancer; asthma,
                                                                                                                                                                                              Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 0 A; 0 C; 7 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory nucleic acid #794.
                                                                                                                                                                                                                                                                                               Claim 101; Page 52; 338pp; English.
                                                                                       ņ
                                                                                          Vollmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTTTGGGGTTTTGGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 88.9%;
Conservative
   FOUND
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(IOWA ) UNIV IOWA RES FO
(COLE-) COLEY PHARM GMBH
                                                                                       Schetter C,
                                                                                                                                                 WPI; 2001-273485/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-2001
                                                                                          Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF99678;
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Gaps

.. 0

3; Indels

0; Mismatches

Matches

20

1 TITIGGGGTTTTGGGGTTTT

TTTTGTTATTTTGGGGTTTT 28

AAF99500 standard; DNA; 24 BP.

RESULT 43
AAF99500
ID AAF99
XX
AC AAF99

AAF99500

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strand displacement amplification; primer; detection; probe; reporter; fluorescent donor; quencher dye; ss.
                                                                                                                                                                                                                                                                                                        Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 74.0%; Score 14.8; DB 4; Length 24; 1 Similarity 88.9%; Pred. No. 6.9e+03; 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strand displacement amplification reporter primer SEQ ID 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 0 A; 1 C; 7 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                    Vollmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BECT ) BECTON DICKINSON & CO.
25-SEP-2000; 2000WO-US026383.
                                            25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                    COLE-) COLEY PHARM GMBH
                                                                                                                                                                                                                 Schetter C,
                                                                                                                                                                                                                                                              WPI; 2001-273485/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-259636/27
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1087020-A2
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                                                                                                                                                                                                                    Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF61386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 46
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  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae haemophilus, campylobacter, closcridium, Bscherichia coli and/or staphylococus), fungal antigens and/or parastitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or firm when deficiency. The present sequence can also be used to redirect a Thi to a Thi immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
  infectious disease; allergy; immune deficiency; phosphorothioate; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;
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Claim 101; Page 55; 338pp; English.

Vollmer J;

Schetter C,

Krieg AM,

WPI; 2001-273485/28

25-SEP-1999; 99US-0156113P. 27-SEP-1999; 99US-0156135P. 23-AUG-2000; 2000US-0227436P.

25-SEP-1999;

(IOWA ) UNIV IOWA RES FOUND.

(COLE-) COLEY PHARM GMBH

25-SEP-2000; 2000WO-US026383

WO200122972-A2

Synthetic

05-APR-2001

Immunostimulatory nucleic acid #614.

RESULT 45
AAF99498
XX
XX
AC AAF99
XX
DT 12-JU
XX
XX
DE Immun
XX
XW Vaccii
XW Vaccii
XW immun

WO200122972-A2

Synthetic

05-APR-2001,

(first entry)

12-JUN-2001

AAF99498;

AAF99498 standard; DNA; 24 BP.

1 TTTTGGGGTTTTTGGGGTT 18

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Query Match

Best Loca Matches

24

7 rrrreregrirreregri

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Gaps

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This invention describes a novel signal primer (I) comprising a reporter probe (II) and an adapter oligonucleotide (III) hybridized to (II), such that (I) comprises intermolectularly base-paired portion and a single-catranded target binding sequence. (I) comprises (II), which in the absence of hybridization to a complementary sequence assumes a conformational structure which brings a fluorescent donor/quencher dye pair linked to it into sufficiently close spatial proximity to quench conformational structure which brings a fluorescent donor/quencher dye pair linked to it into sufficiently close spatial proximity to quench conformation into sufficiently close spatial proximity to quench conformation (I) such that (I) comprises an intermolectide (III) hybridized to conclet arget sequence: (I) by: (a) hybridizing with the target sequence such that formation of a secondary structure as an indication of secondary structure as an indication of the presence of the target sequence; or (2) by: (a) hybridizing (I) to the presence of the target sequence; or (2) by: (a) hybridizing (I) to the target sequence; or (2) by: (a) hybridizing (I) to the presence of the target sequence; or (2) by: (b) hybridized to a second oligonucleotide complementary to (I) which forms a secondary structure when not hybridized to a complementary sequence; (b) separating the second oligonucleotide complementary sequence (I) as an indication of the presence of target sequence. Detection of a variety of different targets is simplified as the adapter polynucleotide to the target, as a result the 5° adapter sequence may consider such that it is the same in a variety of oligonucleotide with different target binding sequences. A single colligonucleotide with different target binding sequences. A single colligonucleotide by the presence of the second oligonucleotide of or detection of a variety of inferent target sequence. A single colligonucleotide by the presence of the second oligonucleotide same in a variety of inference target sequences. A single c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancercus lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; blade neovascularisation; telangiectasia; heemophiliac joint; anglofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     less costly, to synthesize than reporter probes as they do not require labeling for use
Novel signal primer for detecting nucleic acid target sequences by fluorescence quenching mechanisms, comprising a reporter probe and an adaptor oligonucleotide hybridized to the probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiogenesis inhibitory oligonucleotide #692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                            Example 2; Page 11; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TITGGGGTTTTGGGGTTT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 rrrrcccrrrrcccrrrr 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS78208;
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administering at least one antianglogenic nucleic acid molecule. Also included is a kit comprising efficit container housing the antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy relinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                       Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                        The invention relates to inhibiting angiogenesis in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 6; Length 24; Pred. No. 6.9e+03; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 0 A; 1 C; 7 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiogenesis inhibitory oligonucleotide #883.
                                                                                                                                                                                                                                                    Claim 2; Page 31; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scleroderma; hypertrophic scar.
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                                                                          (COLE-) COLEY PHARM GROUP INC.
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88.9%;
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14-DEC-2001; 2001WO-US048458.
                                      14-DEC-2000; 2000US-025534P.
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Matches 16, Conservative
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                                                                                                                 Bratzler RL;
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                     Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; plaque neovascularisation; telangiectasia; heemophiliac joint; anglofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%; Score 14.8; DB 6; Length 24; 88.9%; Pred. No. 6.9e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;
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                                                                                                            Claim 2; Page 35; 276pp; English
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Les 16, Conservative
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Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.

WPI; 2002-566690/60.

Bratzler RL;

Claim 2; Page 31; 276pp; English

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Gaps

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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous leaston, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic ö The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of Gaps Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss. ö Score 14.8; DB 6; Length 24; Pred. No. 6.9e+03; Indels Sequence 24 BP; 0 A; 0 C; 7 G; 17 T; 0 U; 0 Other; /note= "phosphorothioate backbone" Immunostimulatory nucleic acid SEQ ID NO: 735. 0; Mismatches Disclosure; Page 283; 312pp; English. Location/Qualifiers base= OTHER 18 24 BP. 22-JUN-2001; 2001WO-US020154 22-JUN-2000; 2000US-0213346P 74.0%; 88.9%; 7 rrrigredrirrigregrr (IOWA ) UNIV IOWA RES FOUND. 1 TTTTGGGGTTTTTGGGGTT ABL39306 standard; DNA; 24 Ø (first entry) Query Match (12.2)
Best Local Similarity 88.9
Matches 16; Conservative Hartmann G; pom/ WPI; 2002-154611/20. developing cancer WO200197843-A2 modified base 16-APR-2002 27-DEC-2001 Synthetic Weiner G, ABL39306; RESULT 50 ABL39306 ò

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treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cornective tissue cancer, cesphageal cancer, colon and rectum cancer, connective cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, pymphoma, non-dodkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
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74.0%; Score 14.8; DB 6; Length 24;
Best Local Similarity 88.9%; Pred. No. 6.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels
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GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd.  OM nucleic - nucleic search, using sw model  Run on: February 15, 2006, 18:07:43; Search time 1330.25 Seconds  (without alignments) 10, 2006, 18:07:43; Search time 1330.25 Seconds	idues 179606	Database: EST:*  1: gb_est1:* 2: gb_est2:* 3: gb_est3:* 4: gb_htc:* 5: gb_est4:* 6: gb_est5:* 7: gb_est6:* 11: gb_gss1:* 10: gb_gss1:* 11: gb_gss2:* 11: gb_gss3:*  Regult of the total score distribution.  **SUMMARIES**  **SUMMARIES**  **Besult**  **Core distribution.  **ADMARIES**  **ADMARIES**	No. Score Match Length DB ID  C 2 16 84.0 37 1 AA916364 C 33 1 16.88 44.0 37 1 AA916364 C 3 16 80.0 37 1 AA916364 C 4 15.2 76.0 31 1 A468834 C 14.8 74.0 31 1 A468834 C 14.8 72.0 32 9 AZ994869 C 2 11 14.4 72.0 39 10 AJ590961 C 3 14.4 72.0 40 1 AA51639 C 11 14.4 72.0 40 1 AA51639 C 11 14.4 72.0 40 1 AA51639 C 12 14.4 72.0 40 1 AA51639 C 13 14.4 72.0 40 1 AA51639 C 14 14.4 72.0 40 1 AA51639 C 15 14.4 72.0 48 10 C2918128 C 16 14.2 72.0 49 10 AJ93577 C 17 14.2 72.0 49 10 AJ93577 C 18 14.4 72.0 49 10 AJ93577 C 19 14.2 72.0 49 10 AJ93577 C 17 14.2 72.0 49 10 C2918128 C 25 14.4 72.0 49 10 C2518128 C 25 14.4 72.0 49 10 C252588 C 25 15 14.4 72.0 49 10 C252588 C 25 15 14.4 72.0 49 10 AJ943577 C 15 14.2 71.0 37 11 DR63F217 C 17 14.2 71.0 50 10 C252598 C 2729319 111907309 C 271 13.8 69.0 46 8 H71330 H71330 yus55408.51

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Oryza sativa (japonica cultivar-group)

Eukaryota; diaponica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhatoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Extim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-eacla Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Fax: 82 31 320 6193

Fax: Bazion/Qualifiers
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1 (Dases 1 to 37)

1 (Dases 1 to 37)

1 (Dases 1 to 37)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 1205 Std Error: 0.00

Seg primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.
                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/mol_type="Nackdong"
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA916364 1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441241 3' similar to TR:Q29427 Q29427 PROLINE-RICH PROTEIN: ;, mRNA sequence.
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84.0%; Score 16.8; DB 6; Length 37;
Best Local Similarity 90.0%; Pred. No. 1.4e+04;
Matches 18; Conservative 0; Mismatches 2; Indels
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AA916364.1 GI:3055756
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BJ0880710 BJ0880710
AG396420 Pan L51017
AG396430 Pan trogil
AW698626 G578 Glan
CF301078 TLEAP-05
BX189109 Danio ret
CZ484701 F02189-5p
CZ484701 F02189-5p
CZ484702 F02190-5p
AJ549055 AJ649055
AV947752 AV947752
BHC3051 100707680
BHC3051 100707680
BHC3051 100707680
HC4541 Y130F66.r1
NS5368 YV479C2.s1
AZ404140 1M0172215
AZ404140 1M0172215
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AZ404140 1M0172215
AZ404140 1M0172215
BHS95634 SALK 1075
AJ588341 ARABIÓOPS
CO77749 NT028-D0
BX130415 Danio ret
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BH909144 SALK 0522
AL758859 AARBIGOPS
BJ083833 BJ083833
CF276937 14ETL--02
AZ803783 ZM0064B22
BH865521 SALK 0987
BX153515 Danio rer
BX946089 Arabidops
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AA908388 og77c01.s
AV965080 AV965080
T49499 ya76a12.rl
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A1000996 os45h07.s
A1567122 tq85e11.x
CZ476003 d07939-5p
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37 bp mRNA linear EST 15-AUG-2003
7LEAF--07-A07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa (japonica cultivar-group) cDNA clone 7LEAF--07-A07, mRNA
                 CZ478672 e00833-3p
BZ595207 SALK 0863
CG726545 1119090E0
AL978672 Danio rer
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BZ596617 SALK 0928
A1633299 ta866C05.x
AZ587121 1M0394G05
AZ796681 2M0052G05
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1M0159D22
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H3002B08-
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BH755392 SALK 0490
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CZ484703
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AG196430
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BJ080710
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BH629051
BH902063
H24541
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BG063099
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AI633299
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BZ595207
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AI679997
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BH865521
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CF301952
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1. .37 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1441241"

i de la companya de l

sequence. CF301952 CF301952,1 GI:33673713 EST.

ACCESSION VERSION KEYWORDS

RESULT 3 AI813791/c LOCUS

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DEFINITION

ACCESSION

VERSION KEYWORDS

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                A1468834 1NCI CGAP Lyml2 Homo sapiens CDNA clone IMAGE:1999 ti42008.x1 NCI CGAP Lyml2 Homo sapiens CDNA clone IMAGE:2133135 3' similar to SW:FRP2 RAT P10164 ACTDIC PROLINE-RICH PROTEIN PRECURSOR ;contains element MSR1 repetitive element ;, mRNA sequence.
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Arabidopsis thaliana T-DNA flanking sequence GK-111H11-012331,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/clone lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sal; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                follicular mixed small and large
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1 (bases 1 to 31)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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85.0%; Pred. No. 5.8e+04;
iive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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Best Local Similarity 85.0
Matches 17; Conservative
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//lab_nost="DHIOB"
//clone lib="NDI CGAP Pan1"
//note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Br7"
/note="Organ: breast; Vector: pCMV-SPORT4; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.2 kb. Life Technologies catalog
#:10985-018"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                 Length 37;
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                                                                                                                                                                                                              80.0%; Score 16; DB 1; Le
100.0%; Pred. No. 2.8e+04;
ive 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2421637"
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100.0%; Pre
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Unpublished (1997)
                                                                                                                                                                                                                                                               16; Conservative
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Best Local Similarity
Matches 16; Conserv
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AZ807733
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the right border of the T-DNA. It indicates an insertion close to or within gene At1g17190. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project (GABI-Kat is part of the German Plant Genomics program designated http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                        An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-11H11-012331"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                    High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003) 14682050
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                                                                     Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
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Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
Bioinformatics 19 (11), 1441-1442 (2003)
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(http://www.iax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil #132114 [gb] AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2 (bases 1 to 27)
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2M0070H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD47nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 Tow: O column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC2M0048017"
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Location/Qualifiers
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Fax: 801 585 7177
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Submitted (13-007-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versaillee). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.info.gen.fr).
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LZ17h03.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2288885 3'
similar to TR:000599 000599 CONI. ;contains element MER22
repetitive element;, mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                   I-DNA integration into the Arabidopsis genome depends on sequences
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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/db_xref="taxon:3702"
/clone="577E03"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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1 (Dases 1 to 40)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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    .39
    /organism="Arabidopsis thaliana"

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1. .39
/note="T-DNA flanking sequence
           Lepiniec, L., Caboche, M. and Lecharny, A.
                                                                                   of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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                                                                                                                                                                                               2 (bases 1 to 39)
Balzergue, S.
Direct Submission
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|q'132114 gip|AFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the innext adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ad590961 Arabidopsis thaliana T-DNA flanking sequence, left border, clone 577E03, genomic survey sequence.
577E03, genomic survey sequence.
577E03, genomic survey sequence.
577E03, genomic survey sequence.
575E00961. I G1:37940585
GSS; left border; T-DNA flanking sequence.
578E1 for border; T-DNA flanking sequence.
578E1 for border; T-DNA flanking sequence.
578E1 for border; T-DNA flanking sequence.
578E2 for flanking 
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                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 row: H column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 27.
Location/Qualifiers
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                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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                                           TITLE
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/mol_type="manANA"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Emmil: cgapbs-remail.nih.gov
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
borderline ovarian carcinoma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified.
                                                                                                                                                                                                                                                                                                                                                                                                                           AI564592 46 bp mRNA linear EST 13-MAY-195 tp98d09.x1 NCI CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207345 3' similar to SW:PRP3_MOUSE P05143 PROLINE-RICH PROTEIN MP-3 ;, mRNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                       0; Mismatches
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/organism="Homo sapiens"
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                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
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/clone="IMAGE:2288885"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
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46 bp mRNA linear EST 03-FEB-1999

qx66h12.x1 NCI_CGAP_Ov36 Homo sapiens cDNA clone IMAGE:2006375 3'

similar to SW:NHPX_HUMAN P55769 NHP2/RS6 FAMILY PROTEIN YEL026W
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.B. Consortium, LiNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
/clone lib="NCI_CGAP_Ov36"
/note="Organ: ovary; Vector: pAMP1; mRNA made from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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     Trace considered overall poor quality Insert Length: 1514 Std Brror: 0.00 Seq primer: -40UP from Gibco High quality sequence scop: 1. Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:2006375"
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// Lissue_type="leaf"
/db xref="taxxon:4577"
/ Lissue_type="leaf"
/db host="dault"
/lab_host="DH108"
/clone lib="4011" - RescueMu Grid V"
/clone lib="4011" - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site !: BamHi; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHi
and BglII, and ligated to form circular plasmids. DH108
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1475390 49 bp mRNA linear EST 14-APR-1999 t18291.x1 NCI CGAP CO14 Homo sapiens CDNA clone INAGE:2153616 3' similar to SW:PRPM HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO ;contains element MSR1 repetitive element ;, mRNA sequence.
                                      CZ918128 48 bp DNA linear GSS 08-AUG-2005 4021008B10.1EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                     Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Very probable ligation site of per-ligation sequence from source sequence.
Plate: 4021008 row: 1
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                        Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 48)
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/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
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AI475390.1 GI:4328435
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93.8%;
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Homo sapiens (human)
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Matches 15; Conservative
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                                                                                 survey sequence
                                                                                                   CZ918128 CZ918128.1
                                                                                                                                                                 Zea mays
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RESULT 12
CZ918128
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Email: cgapbs-remail.nib.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
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Arabidopsis thaliana T-DNA flanking sequence GK-275E01-015095,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="maxNA"
/db xref="taxon:9606"
/dlone="IMAGE:2153616"
/tissue_type="moderately-differentiated adenocarcinoma"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab host="Plub"NCI CGAP_CO14"
/note="Organ: colon; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                            Hominidae, Homo.

1 (bases 1 to 2)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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AL943577.1 GI:24400175
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Unpublished (1997)
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Best Local Similarity
Matches 15; Conserva
ORGANISM
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Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                   recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
                         Email: RHoskins@lbl.gov
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Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At5g11660.

Details on the protocols used for generation of the sequence are

described in References 1-3. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI.' Information on line availability can be found at:

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-27801-015095"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Karpen,G., Bellen,H., Rubin,G. and Spradling,A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota,
Neoptera, Badopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                      Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
                                                                                                                 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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  Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Best Local Similarity 93.6
Matches 15; Conservative
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/close_lib="Drosophila melanogaster PL strains, transposon insertion flanking sequences"
/note="Drosophila melanogaster was mutagenized by remobilization of the piggyBac vector pBac(GAL4D,EXFP) remobilization of the piggyBac vector pBac(GAL4D,EXFP) (Horn et al. 2003 Genetics 163: 647-661) (FlyBase ID Fbtp0017476) as described by Hacker et al. 2003 (Proc Natl Acad Sci USA 100: 7726). Each strain in the collection has an independent insertion of the mutator transposon and the name of each strain begins with the letters PL. Genomic DNA was prepared from samples from each PL strain, DNA segments flanking the transposon insertion sites were amplified by inverse PCR, and the inverse PCR products were sequenced as described by Bellen et al. 2004 (Genetics 167: 761-781)."
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Arabidopsis thaliana T-DNA flanking sequence GK-521H07-020048,
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
Elanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                     piggyBAC.
The piggyBAC insertion position is 47 in the 50 bases. This
insertion position refers to the first base of the 4 base target
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Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 50;
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/organism="Zea mays"
/mol type="genomic DNA"
/cultivar="mised background w23/A188/B73/K55"
/db xref="taxon:457"
/tissue type="leaf"
/dev_stage="leaf"
/dev_stage="leaf"
/docst="dult"
/lab_host="bult0"
/lote="organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon pBlueScript backbone); Site 1: BamHi bite 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web site 'www.radb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. NA was extracted from leaf strips, double digested using BamHi and BglII, and ligated to form circular plasmids.
DH108 cells were transformed and then screened on LB
                                                                                                                                                                                          1119073002.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic G722753.1 G1:37757925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Faxi 650 725 8221
Faxi 650 725 8221
Faxis babbc@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
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c06535-5prime Exelixis piggyBac PB insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of piggyBac,
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84.2%; Pred. No. 1.4e+05;
iive 0; Mismatches 3;
  0; Mismatches
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Location/Qualifiers
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Best Local Similarity 84.2
Local 16; Conservative
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     16; Conservative
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CG722753
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                                                                     Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone tise?. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MT for Plant Breeding Research in the context of the GABI-Kat project GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz.koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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Danio rerio genomic clone DKEY-63F21, genomic survey sequence.
AL981876
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Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GK-521H07-020048"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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  4 (bases 1 to 33)
Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.4e+05;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-63F21"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huckle, E. and Hunt, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TTTGGGGTTTTGGGGTTTT 20
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84.2%;
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Direct Submission
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DR63F21T/c
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REPERENCE AUTHORS JOURNAL PUBMED

COMMENT

TITLE

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/ Organisme "Zea mays"
/ wol type="genomic DNA"
/ wol type="genomic DNA"
/ cultivat="mixed background W23/A188/B73/K55"
/ db xrefe="taxon:4577"
/ tissue_type="leaf"
/ tissue_type="leaf"
/ dev stage="adult"
/ dab_host="bl119" - RescueMu Grid AA"
/ done lib="1119 - RescueMu Grid AA"
/ clone lib="1119 - RescueMu Grid AA"
/ clone lib="1119 - RescueMu Grid AA"
/ clone lib="adult"
/ steel li BamHl; site_2: BglII;
/ RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips; double digested using
BamHl and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL940076 31 bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-244B11-014397,
                                                                                                                                                                                                                                                                                                                                      Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Unpublished (2001)
Ocontact: Walbot V
Department of Biological Sciences
Stanford University
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 50)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 650 723 2227
Fax: 650 725 8221
Bamil: walbot@stranford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 50;
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84.2%; Pred. No. 1.5e+05;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 California Ave, Palo Alto, CA 94304,
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Class: transposon-tagged.
Location/Qualifiers
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                       CG729919 GI:37772091
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Matches 16; Conservative
survey sequence.
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                                                                                                                           Zea mays
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AL940076/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="texton.722"
/dlore_lib="texton.722"
/clone_lib="Texton.722"
/clone_lib="Texton.722"
/clone_lib="Texton.722"
/clone_lib="Texton.722"
/clone_lib="Textor.pygbac PB (GenBank accession number AV515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37oC water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viabality, and used for recovery of flanking genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                                                                     Thibbault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francise-Lang, H.L., Singh, C.M., Cheung, A., Erickson, C., Fisher, W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Sunder, C., Kopczynski, C., Duyk, G., Winberg, M., Shao, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J. A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          piggyBac element.
The piggyBac insertion position is 47 in the 50 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
                                                                                                                                                  Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 50)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: Rhoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
                                                                                                                           Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Roger A Hoskins
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   genomic survey sequence.
                                                           CZ470781.1 GI:62964794
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RESULT 20 CG729919 LOCUS DEFINITION

Query Match

Matches

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Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Mawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ774479 10kb plasmid UUGCIM library Mus musculus genomic
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%; Score 13.8; DB 8; Length 46; 88.2%; Pred. No. 2.1e+05; ive 0; Mismatches 2; Indels
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="GDB:3781127"
/db_xref="taxon:9606"
/clone="IMAGE:230031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
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AZ774479.1 GI:12899972
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                                                                                                               and Marra, M.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone f26h11. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA trangment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
                                                                                                                                                    An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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yu55d08.sl Soares fetal liver spleen INFLS Homo sapiens CDNA clone
IMAGE:230031 3' similar to SP:JC2012 JC2012 RIBOSOMAL PROTEIN 17K -
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/db_xref="taxon:3702"
/clone="GK-244B11-014397"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
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Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
  identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                           High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
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88.2%; Pred. No. 2.1e+05;
ive 0; Mismatches 2; Indels (
                                                                                                             Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K.
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                                               Bioinformatics 19 (11), 1441-1442 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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IMAGE:1627271 3' Similar to TR:033563 Q33563 EATRO 164 KINETOPLAST
;contains L1.t1 L1 repetitive element ;, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb plasmid UUGCIM library"
/note="Wector: PWD42Tv; Purified genomic DNA from
musculus C57BL/6J (male) was obtained from the Jackson
                     Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
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                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0004 row: A column: 05
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC2M0004A05"
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1 (bases 1 to 37)
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                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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/mol_type="mrkNa"
/db_xxef="mrkNa"
/db_xxef="mrkNa"
/db_xxef="mrkNa"
/db_xxef="mrkNa"
/clone="INAGE:162721"
/lab_bost="DA108"
/clone lib="soares NFL T GBC_S1"
/clone lib="soares"
/clone lib="soa
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1. (bases 1 to 7)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1352 Std Brror: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                Unpublished (1997)
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                                                                                                         Tumor Gene Index
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Gaps

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M0367G03F Mouse 10kb plasmid UUGCIM linear GSS 13-DEC-2000 clone UUGCIM0367G03 F, genomic survey sequence. AZ579518.1 GI:11693947 GSS.
                                                                                                                                                                                                                                                                                                             CF295607 39 bp mRNA linear EST 14-AUG-2003 30DGS--05-K02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--05-K02, mRNA
       by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enhartocidaes; Oryzaa.

(Dases 1 to 39)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yoongli, KyeongQi, KyeongQi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps

    .39
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
                                                                                                    Score 13.6; DB 2;
Pred. No. 2.5e+05;
0; Mismatches 4;
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                                                                                                      68.0%;
                                                                                                                                            16; Conservative
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Best Local Similarity
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Best Local Si
Matches 16
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CF295607/c
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AZ579518/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 04-OCT-2000
                                                                                                                                                                                         /tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DHIOB"
/lab_host="DHIOB"
/clone_lib="NHIOB"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E 1 (bases 1 to 38)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.lnli.gov

Plate: LLCM818 row: n column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE974781 38 bp mRNA linear EST 04-OCT-20
601680831R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951175 3',
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80.0%; Pred. No. 2.5e+05;
ive 0; Mismatches 4;
Insert Length: 1210 Std Brror: 0.00 Seg primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2140844"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
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BE974781
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Best Local Similarity
Matches 16; Conserv
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BE974781
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ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Zuechtungsforsching, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g10360. Details on the protocols used for generation of the sequence are described in References 1.3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mgo.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                             An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC16 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA
                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:3702"
/dlone="GK-7470.470.4638"
/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                  Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                                                                                                                Bioinformatics 19 (11), 1441-1442 (2003)
12874060
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                       Arabidopsis thaliana (thale cress)
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Matches 16; Conserv
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalez (gil 4732114 | gb | AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana T-DNA flanking sequence GK-747F04-024638, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone_lib="Mouse_lokb plasmid_UGCIM library" /note="Tvector: PMP42nv; Purified genomic_DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse_DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wiright, D., Weises, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: G column: 03
Seg primer: CGTTGTPAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0367G03"
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  musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
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Best Local Similarity
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DEFINITION

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RESULT 29 BX946019

Matches

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source
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AZ634906/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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/lab host="xx10-Gold"
/lab host="xx10-Gold"
/clool lib="dm-clood"
/root cons. The mRNA was isolated from entire roots
of 8 day old "williams' seedlings which were propagated on paper towels with (stilled water. Stratagene's cons. Synthesis Kit (catalog #200401) was used to synthesize the cons. First- strand synthesis was performed with 5-methyl GCDNA. First- strand synthesis was performed with 5-methyl GCAPA, hence the ligated CDNA is hemmethylated.
Stratagene's first-strand synthesis primer was used [GAAGAGAGAGAGAACACACTCCCAG(T)-18]. After second-strand synthesis, the CDNA ends were 'Polished' with clone Ptu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and pincylory raced. The Alon Stew Within the Iliburgian synthesis primer was restricted by digestion with Xho! all Xhol sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 50bp cutoff, using GibcoBK Life Technologies' CDNA Size Fractionation column. The column eluent was then ligated into Stratagone's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and Xho!, and phosphorylated). Both the white and blue colonnes appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n=15) have been sequenced, and possess putative CDNA inserts. This library was constructed by Dr. Paul Kelm & Vigginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Kelm), 520-523-1373 (Virginia H. Coryell), Fax: 520-523-7500, email: paul. Keim@nau.edu,
                                                                                                                                                                                                                                                                                                    Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
relone is listed in the 'Other ESTs on clone' field. Trace
considered overall poor quality Possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
4163; email: info@biogeneticservices.com)
                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1004-468"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Williams"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: -40RP from Gibco
High quality sequence stop: 1
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AI442438.1 GI:4296179
                                                                     Glycine max (soybean)
                                                                                                                                                                                                                                                                                  (bases 1 to 43)
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                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                              REFERENCE
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VERSION
KEYWORDS
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FEATURES

COMMENT

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/sex="Male"
//lab host="B. Coli strain XL10-Gold, Tl-resistant, F-"
//lab host="B. Coli strain XL10-Gold, Tl-resistant, F-"
//clone lib="Mouse 10kb plasmid UUGCIM library"
//note="Wedtor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
liaboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with Ta DNA polymerase and Ta
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil H732114 [gb] AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Really, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                       AZ634906 13-DEC-200 A3 bp DNA linear GSS 13-DEC-200 DN490P20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0490P20 R, genomic survey sequence.
                                                                                   Gaps
                                                                                   ;
0
                 Length 43;
                                                                               Indels
          68.0%; Score 13.6; DB 1;
80.0%; Pred. No. 2.5e+05;
iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 0490 row: P column: 20
Seq primer: CACACAGAAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                             1 TITIGGGGTTITGGGGTTIT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ634906.1 GI:11757096
GSS.
Query Match
Best Local Similarity 80.09
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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Gaps

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Oryza sativa (japonica cultivar-group)

Enkaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Enkaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 44)

SKim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lu (published (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongIn, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                              CF300934 11-AUG-2003 1LEAF--05-J13.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J13, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ476389 44 bp DNA linear GSS 04-OCT-2000 1M0295E09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0295E09 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:33947"
/clone="7LBAF--05-J13"
/clone="7LBAF--05-J13"
/tlssue trype="leaf"
/dev stage="7 days after germination"
/lab_nost="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Bukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryotas, Metazoa; Chordata; Ciares; Rodentia;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 44)
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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0; Mismatches
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/cultivar="Nackdong"
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CF300934.1 GI:33672695
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                                                               1 TTTTGGGGTTTTGGGGTTTT
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   16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENARYOTA; Matazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Bacdyperygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophildae; Drosophila.

I (bases 1 to 43)
I (bas
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db xref="taxon:722"
/clone_lib="Exelixis P element XP insertions"
/clone_lib="Exelixis P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hosped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 29-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster genomic Sequence recovered from 3' end of P element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The P element insertion position is 1 in the 43 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence recovery method was inverse PCR. Sequence orientation is forward strand relative to 5' end of {\bf P}
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                        CZ472331 43 bp DNA linear GSS 2:
d01604-3prime Exelixis P element XP insertions Drosophila
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                                                                      Length 43;
                                                                                                                                          4; Indels
                                                                      Score 13.6; DB 9;
Pred. No. 2.5e+05;
                                                                                                                                      0; Mismatches
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Nat. Genet. 36 (3), 283-287 (2004)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CZ472331.1 GI:62966344
                                                                      68.0%;
80.0%;
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Acyrthosiphon pisum (pea aphid)
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/cultivar="yr2"
/db_xref="taxon:7029"
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Location/Qualifiers
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Contact: D. Tagu
INRA Rennes
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Best Local Similarity 80.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of puble [4732114]gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Oryza sativa (japonica cultívar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Nu. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus G78L/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0295 row: E column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 44.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0295E09"
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                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
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CF298361/c
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/ wol type="mrNA"

/mol type="mrNA"
/cultivar="Nackdong"
/db xref="taxon 1994"
/clone="7LEAF-01-L10"
/fissue type="leaf"
/dev stage="7. days after germination"
/lab host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped with oligoribonuclectides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (Bases I to 45)
Hunter,W., Martinez-Torres,D., Rabbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
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APHL-2DN XXI-A6 APHL3SD ACYTCHOSiphon pisum cDNA clone ApHL3SDXXIA6
                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yogin, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
1 (bases 1 to 45)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                       UMR Bi03P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

    .45
    /organism="Acyrthosiphon pisum"
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ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ793049 46 bp DNA linear GSS 16-FEB-2001
2M0045M14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0045M14 R, genomic survey sequence.
                                                                                                /note—Typerory DDNR-LIB; Site_1: SfiIA; Site_2: SfiIB; Sample name: ApHL3SD; Plant growth place: INRA-Rennes, UMR BiO3P; PS 35.37, 356.31 Le Rheu cedex, France: Soil conditions: peat; Sowing date: 20/03/2003; Harvesting date: 10/04/2003; Stress date: no stress; Description: applies incollated on one-week old vicia faba germinations under non sterile conditions.; experimental condition: short photoperiod (12-hr light/12-hr dark at 18 c)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42Ivy, Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                /dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: M column: 14
Seg primer: CACAAAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/clone="UUGC2M0045M14"
                                                                         lib="ApHL3SD"
tissue type="head"
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Conservative
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TITLE

SOURCE

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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 47)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Dlasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ786064 16-FEB-200 2M0030G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic conne UUGC2M0030G22 R, genomic survey sequence.
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/clone lib="Mouse lokb plasmid UUGCN library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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University of Utah Genome Center
University of Utah
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Mus musculus
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Plate: 0030 row: G c
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Fax: 801 585 7177
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ub54h01.s1 Soares mammary gland NWLMG Mus musculus cDNA clone IMAGE:1381585 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(1) CHAIN PRECURSOR (HUMAN); gb:X58251 Mouse COLlA2 mRNA for pro-alpha-2(1) AA959573
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Marram, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="texon:10090"
/clone="IMAGE:1381585"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
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/clone_lib="Soares mammary gland NMLWG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from mammary
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.0%; Score 13.6; DB 9; Length 47; larity 80.0%; Pred. No. 2.5e+05; Conservative 0; Mismatches 4; Indels
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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/organism="Mus musculus"
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gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinifones; Cyprinidae; Danio.

1 (bases 1 to 50)

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (27-Jah. 2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 174112. 174112
This part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene. Further details:
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                                                                                                                                                                                                                                                                                                                                                                                                             GSS 28-JAN-2003
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Danio rerio genomic clone DKEY-174112, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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80.0%; Pred. No. 2.5e+05;
ive 0; Mismatches 4;
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Location/Qualifiers
                                                                                                                                                                      68.0%; Score 13.6; DB 1;
80.0%; Pred. No. 2.5e+05;
ive 0; Mismatches 4;
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-17412"
/tissue type="Testis"
/note="Vector pIndigoBAC-536"
                                                                                                                                                                                                                                                          1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                   28 TTCAGGGGTTTTTGGTTTTT 47
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BX171071.1 GI:28002776
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                                                                                                                                                                    Query Match
Best Local Similarity 80.01
Matches 16; Conservative
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1 (bases 1 to 24)
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Best Local Similarity
Matches 16; Conserv
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TA131B05Q/c
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BX171071/c
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/clone lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BgIII;
RescueMu is a 4.9 kb, mcdiffed maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units: For more information on RescueMu, go to the web site 'http://www.murransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHi and BgIII, and ligated to form circular plasmids. DH10B calls were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/clone_lib="NCI_CGAP_Lym12"
/note="Corgan: lymph_node; Vector: pCMV-SPORT6; Site_1:
Sal; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1439312 30-MAR-199 MRNA linear EST 30-MAR-199 II. 1596-12.X1 NCI CGAP Lym12 Homo sapiens CDNA clone INAGE: 2134798 3' similar to SW.FRP2 HUMAN PO2812 SALIVARY PROLINE-RICH PROTEIN PRECURSOR ; contains MER22.b2 TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon"
/clone="IMAGE:2134798"
/tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 30;
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Pred. No. 2.9e+05;
0; Mismatches 1;
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AI439312.1 GI:4303441
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1 (bases 1 to 34)
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Best Local Similarity 93.3
Matches 14; Conservative
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                               Direct Submission

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project. Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@eanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects.

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayedetigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2916406 30 bp DNA linear GSS 08-AUG-2005 4021001C10.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot \nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    Chases 1 to 30)
    Walbot, V.

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Possible ligation site of ends cut by 2 different endonucleases.
Peverse complemented post-ligation sequence from source sequence.
Plate: 4021001 row: C column: 10
Class: transposon-tagged.
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/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_hose="BH108"
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              Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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855 California Ave, Palo Alto, CA 94304, USA
7E1: 650 723 2221
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.0%; Score 13.4; DB 11;
Best Local Similarity 93.3%; Pred. No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Trypanosoma brucei"
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/strain="TREU927"
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/clone="131b05"
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CZ916406/c
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Homo sapiens
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Best Local Similarity
Matches 14; Conserv
       AI865173
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                                                                           ORGANISM
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37 bp mRNA linear EST 21-DEC-1998 qwile03.x1 NCI_CGAP_Ut3 Home againan s.DNA clone IMAGE:1990780 3' similar to SW:PRPL HUMAN P04280 SALIVARY PROLINE-RICH PROTEIN PRECURSOR ;contains element MSR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index.
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: cgapbe-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/LLNL at:
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/lab host="noming, 2 pooled tumors"
/lab host="noming, cGAP_Ut3"
/clone=lib="NCI_CGAP_Ut3"
/note="Crgan: ulerus; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

1 (bases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                    1; Indels
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Pred. No. 3e+05;
 Pred. No. 3e+05;
0; Mismatches
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1990780"
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93.3%;
                                                                          34 GGGGTTTTTGGGTTT 20
                                                     5 GGGTTTTGGGGTTT 19
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 Similarity
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AI280814
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DEFINITION
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AI280814/c
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Sequencing Center
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/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: '
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: '
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: '
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Organ: lymph node; Vector: lymph node; Colored node; Site_1: lymph node;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidaa; Murinae; Mus.

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/db_rate="taxon:9606"
/clone="IMAGE:2411785"
/tissue_type="lymphoma, follicular mixed small and large
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1M0555122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0555122 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.

1 (bases 1 to 49)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tunor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Contact: Robert B. Weiss
University of Utah Genome Center
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AZ761211.1 GI:12869877
AI865173.1 GI:5529280
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                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAPA (gil 4732114 [gb] ARA29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiilo-Gold (Stratagene) cells and selected for ampicillin resistance."
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Enders; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
                          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                       0.00
                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0555 row: I column: 22
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0555122"
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15; Conservative
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     University of Utah
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                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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Direct Submission

Direct Submission

Submisterd (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Submisterd (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment (8) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiogen.fr).
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1M0352C18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0352C18 R, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Uniouse whole genome scaffolding with paired end reads from 10kb plasmid inserts blank (2000)
Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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ilarity 83.3%; Pred. No. 3.5e+05;
Conservative 0; Mismarchee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/mol_type="qenomic DNA"
/db_xref="taxon:3702"
/clone="576D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="T-DNA flanking sequence
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0352 row: C column: 18
Seq primer: CACAGGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ecotype="Wassilewskija"
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Location/Qualifiers
1. .37
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Li Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.

Li Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.

Direct Submission

L. Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion within the locus defined by BAC clone
F3F19. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiz-velln.mpg.de/GABI-Kat/.
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                                                                                                                                                                                                                                                      AL944738 1-100-2004 Al bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-284D09-015289,
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GR-28109-015289"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FGT) database the identification of T-DNA insertion mutants in Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyl rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
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BioTechniques 35 (6), 1164-1168 (2003)
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Matches 15; Conserv
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                                                                                     g
                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gil 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
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Plasterk and N.V.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 40)
                                                                                                                                                                                 /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGIM library"
/note="Vector: PWD4ZDv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Danio rerio genomic clone DKEY-61C20, genomic survey sequence.
BX120037
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3 US-10-131-827-1029 Sequence 10 3 US-09-406-074-4 Sequence 4, 3 US-09-406-074-3 Sequence 3, 3 US-09-438-486A-60 Sequence 60	3 US-10-131-827-5465 Sequence 54	3 US-08-851-843A-30 sequence 30 3 US-08-851-843A-60 sequence 60	3 US-08-974-549A-557 Sequence 55	3 US-08-854-050-60 Sequence 50	3 US-09-430-323-30 Sequence 30	3 US-09-430-323-60 Sequence 60	3 US-09-402-1615-35/ sequence 35	3 IIS-09-766-253-30 Segmence 30	3 IIS-09-766-253-60 Semience 60	3 US-10-054-295-30 Sequence 30	3 US-10-054-295-60 Seguence 60	3 US-09-438-486A-30 Sequence 30	3 US-10-131-827-4217 Sequence 42	3 US-10-131-827-7605 Sequence 76	3 US-08-879-457-2 Sequence 2,	3 US-08-675-119-2 Sequence 2,	3 US-08-851-843A-43 Sequence 43	3 US-US-BSI-843A-45 Sequence 45	3 US=VS=3/4=349A=113 SEQUENCE II.	3 US-08-854-050-43 Sequence 43	3 US-U8-854-U5U-45 Sequence 45	3 US=09=430-323-43 Sequence 43	3 US-09-430-323-45 Sequence 45	3 US-09-467-932-2	3 US-09-402-181B-113 Sequence 11	3 US-09-721-456-113 Sequence 11	3 US-09-766-253-43 Sequence 43	3 US-09-766-253-45 Sequence 45	3 US-10-054-295-43 Sequence 43	3 US-10-054-295-45 Sequence 45	3 US-09-438-486A-43 Sequence 43	3 US-09-438-486A-45 Sequence 45,	3 US-I0-I3I-827-5325 Sequence 532	3 03-03-433-714C-101 364uence 10:	3 IIS-08-781-986A-2244 Semience 22	2 IIS-08-128-011-4 Semience 4.	2 US-08-403-888A-142 Sequence 143	2 US-08-149-096A-7 Sequence 7,	6 PCT-US92-10792-4 Sequence 4,	3 US-09-422-978-842 Sequence 842	3 US-09-422-978-2476 Sequence 247	2 US-08-227-180B-26 Sequence 26,	3 US-09-318-138-49 Seguence 49	2 US-08-186-229-6 Sequence 6,	2 US-08-470-124-6 Sequence 6,	2 US-08-207-901-29 Sequence 29,	3 US-09-422-978-9236 Sequence 923	3 US-09-780-049-86 Sequence 86,	6 PCT-US92-10792-46 Sequence 46,	6 PCI-0592-10/92-4/ Sequence 4/,	6 FC1-0392-10/92-48 Sequence 48,	6 PCT-US92-10792-51 Sequence 31,	3 US-09-422-978-8417 Semience 841	3 US-09-672-126B-4 Semience 4.	6 PCT-US92-10792-34 Semience 34.	6 PCT-110792-10792-35	6 PCT-11S92-10792-38 Semience 38	3 TTC-09-206-808-8	3 US-U9-206-898-8 Sequence 8,	3 US-09-870-122A-8 Sequence 8,	6 PCT-US93-08329-3 Sequence 3,	3 US-10-131-827-5127 Sequence 512	3 US-09-422-978-8042 Sequence 804	3 US-10-002-623-718 Sequence 718
3 US-10-131-827-1029 Sequence 10 3 US-09-406-074-4 Sequence 4, 3 US-09-406-074-3 Sequence 3, 3 US-09-438-486A-60 Sequence 60	3 US-10-131-827-5465 Sequence 54	3 US-08-851-843A-30 sequence 30 3 US-08-851-843A-60 sequence 60	3 US-08-974-549A-557 Sequence 55	3 US-08-854-050-60 Sequence 50	3 US-09-430-323-30 Sequence 30	3 US-09-430-323-60 Sequence 60	3 US-09-402-1615-35/ sequence 35	3 IIS-09-766-253-30 Segmence 30	3 IIS-09-766-253-60 Semience 60	3 US-10-054-295-30 Sequence 30	3 US-10-054-295-60 Seguence 60	3 US-09-438-486A-30 Sequence 30	3 US-10-131-827-4217 Sequence 42	3 US-10-131-827-7605 Sequence 76	3 US-08-879-457-2 Sequence 2,	3 US-08-675-119-2 Sequence 2,	3 US-08-851-843A-43 Sequence 43	3 US-US-BSI-843A-45 Sequence 45	3 US=VS=3/4=349A=113 SEQUENCE II.	3 US-08-854-050-43 Sequence 43	3 US-U8-854-U5U-45 Sequence 45	3 US=09=430-323-43 Sequence 43	3 US-09-430-323-45 Sequence 45	3 US-09-467-932-2	3 US-09-402-181B-113 Sequence 11	3 US-09-721-456-113 Sequence 11	3 US-09-766-253-43 Sequence 43	3 US-09-766-253-45 Sequence 45	3 US-10-054-295-43 Sequence 43	3 US-10-054-295-45 Sequence 45	3 US-09-438-486A-43 Sequence 43	3 US-09-438-486A-45 Sequence 45,	3 US-I0-I3I-827-5325 Sequence 532	3 03-03-433-714C-101 364uence 10:	3 IIS-08-781-986A-2244 Semience 22	2 IIS-08-128-011-4 Semience 4.	2 US-08-403-888A-142 Sequence 143	2 US-08-149-096A-7 Sequence 7,	6 PCT-US92-10792-4 Sequence 4,	3 US-09-422-978-842 Sequence 842	3 US-09-422-978-2476 Sequence 247	2 US-08-227-180B-26 Sequence 26,	3 US-09-318-138-49 Seguence 49	2 US-08-186-229-6 Sequence 6,	2 US-08-470-124-6 Sequence 6,	2 US-08-207-901-29 Sequence 29,	3 US-09-422-978-9236 Sequence 923	3 US-09-780-049-86 Sequence 86,	6 PCT-US92-10792-46 Sequence 46,	6 PCI-0592-10/92-4/ Sequence 4/,	6 FC1-0392-10/92-48 Sequence 48,	6 PCT-US92-10792-51 Sequence 31,	3 US-09-422-978-8417 Semience 841	3 US-09-672-126B-4 Semience 4.	6 PCT-US92-10792-34 Semience 34.	6 PCT-110792-10792-35	6 PCT-11S92-10792-38 Semience 38	3 TTC-09-206-808-8	3 US-U9-206-898-8 Sequence 8,	3 US-09-870-122A-8 Sequence 8,	6 PCT-US93-08329-3 Sequence 3,	3 US-10-131-827-5127 Sequence 512	3 US-09-422-978-8042 Sequence 804	3 US-10-002-623-718 Sequence 718
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US-10-131-827-1029 Sequence 10 US-09-406-074-4 Sequence 4, US-09-406-074-3 Sequence 3, US-09-438-486A-60 Sequence 50	4.4 72.0 50 3 US-10-131-827-5465 Sequence 54	4.2 /1.0 26 3 US-08-851-843A-60 sequence 30	4.2 71.0 26 3 US-08-974-549A-557 Sequence 55	4.2 71.0 26 3 US-08-854-050-50 Sequence 50	4.2 71.0 26 3 US-09-430-323-30 Sequence 30	4.2 71.0 26 3 US-09-430-323-60 Sequence 60	4.2 71.0 20 3 US-09-402-1616-55/ Sequence 55	4.2 71.0 26 3 US-09-766-253-30 Semience 30	4.2 71.0 26 3 IIS-09-766-253-60 Semience 60	4.2 71.0 26 3 US-10-054-295-30 Sequence 30	4.2 71.0 26 3 US-10-054-295-60 Seguence 60	4.2 71.0 26 3 US-09-438-486A-30 Sequence 30	4.2 71.0 50 3 US-10-131-827-4217 Sequence 42.	4.2 71.0 50 3 US-10-131-827-7605 Sequence 76	4 70.0 15 3 US-08-879-457-2 Sequence 2,	4 70.0 15 3 US-08-675-119-2 Sequence 2,	4 70.0 15 3 US-08-851-843A-43 Sequence 43	4 /0.0 ID 3 US-US-85I-843A-45 Sequence 45	4 /0.0 ID 3 US=08-3/4-349A-IIS SEQUENCE II.	4 70.0 15 3 US-08-854-050-43 Sequence 43	4 /0.0 L5 3 US-US-854-U5U-45 Sequence 45	4 /0.0 IS 3 US-US-430-323-43 Sequence 43	4 /0.0 Is 3 US-09-430-323-45 Sequence 45	4 /0.0 L5 3 US-09-46/-932-2 Sequence 2,	4 70.0 15 3 US-09-402-1818-113 Sequence 11	70.0 15 3 US-09-721-456-113 Sequence 11.	4 70.0 15 3 US-09-766-253-43 Sequence 43	4 /0.0 IS 3 US-09-766-253-45 Sequence 45	4 70.0 L5 3 US-10-054-295-43 Sequence 43	4 70.0 15 3 US-10-054-295-45 Sequence 45,	4 70.0 15 3 US-09-438-486A-43 Sequence 43	4 70.0 15 3 US-09-438-486A-45 Sequence 45,	14 /0.0 50 3 US-IO-I3I-8Z/-53Z5 Sequence 533	3 8 69 0 50 3 118-08-955-1715-2044 Gemienne 202	69.0 50 3 IIS-08-781-986A-2244 Semience 22	3.6 68.0 21 2 HS-08-128-011-4 Semience 4	3.6 68.0 21 2 US-08-403-888A-142 Sequence 14	3.6 68.0 26 2 US-08-149-096A-7 Sequence 7,	3.6 68.0 32 6 PCT-US92-10792-4 Sequence 4,	3.6 68.0 47 3 US-09-422-978-842 Sequence 842	3.6 68.0 47 3 US-09-422-978-2476 Seguence 247	3.4 67.0 20 2 US-08-227-180B-26 Seguence 26,	3.4 67.0 32 3 US-09-318-138-49 Seguence 49	3.2 66.0 30 2 US-08-186-229-6 Sequence 6,	3.2 66.0 30 2 US-08-470-124-6 Sequence 6,	3.2 66.0 50 2 US-08-207-901-29 Sequence 29,	2.8 64.0 18 3 US-09-422-978-9236 Sequence 923	2.8 64.0 20 3 US-09-780-049-86 Sequence 86,	2.8 64.0 20 6 PCT-US92-10792-46 Sequence 46,	2.8 64.0 20 6 PCI-US9Z-IO/9Z-4/ Sequence 4/,	2.0 04.0 20 0 FCI-US9Z-IO/SZ-48 Sequence 48,	2.8 64.0 20 6 PCT-IIS92-10792-52 Semience 51,	2.8 64.0 21 3 US-09-422-978-8417 Semience 841	2.8 64.0 24 3 US-09-672-126B-4 Semience 4.	2.8 64.0 26 6 PCT-US92-10792-34 Segmence 34.	2.8 64.0 26 6 PCT-11892-10792-35 Semionre 35	2.8 64.0 26 6 PCT-11592-10792-38 Semience 38	2.0 03.0 20 0 FCI - 0532 - 10/32 - 30 054461105 30,	2.8 64.0 31 3 US-US-898-8 Sequence 8,	2.8 64.0 31 3 US-09-870-122A-8 Sequence 8,	2.8 64.0 31 6 PCT-US93-08329-3 Sequence 3,	2.8 64.0 50 3 US-10-131-827-5127 Sequence 512	2.6 63.0 21 3 US-09-422-978-8042 Sequence 804	2.6 63.0 23 3 US-10-002-623-718 Sequence 718

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STREET: One Liberty Place - 46th Floor CITY: Philadelphia
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Best Local Similarity
Matches 20; Conserval
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Patent No. 5952490
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
TITLE OF INVENTION: Sequence
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingura. Toachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew Lib
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STRIE: California
COUNTRY: United Strie
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COUNTRY: U.S.A.
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,888A
FILING DATE: 12-JUN-1995
CLASSIFICATION: 435
FRICK APPLICATION BATA:
APPLICATION NUMBER: 09/954,185
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REFERRENCE/DOCKET NUMBER: 1515-1229
TELEFONMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 121:
LENGTH: 39
INFORMATION CALCHING: 121:
LENGTH: 39
INFORMATION CALCHING: 121:
LENGTH: 39
INFORMATION CALCHING: 31916
SEQUENCE CHARACTERISTICS:
LENGTH: 39
TTYPE: mucleic acid
STRANDEDNESS: single
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Length 44;
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: -
1..44

LOCATION: 1..44

CHER INFORMATION: /note= "hairpin primer"
US-08-974-5498-568
                                          CURSEITCATION DATA:
CURSIFICATION DATA:
CURSIFICATION DATA:
CLASSIFICATION DATA:
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 19-NOV-1997
FILING DATE: 01-OCT-1996
FRICK APPLICATION DATA:
FILING DATE: 18-APR-1997
FRICK APPLICATION DATA:
FILING DATE: 18-APR-1997
FRICK APPLICATION DATA:
FILING DATE: 18-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
FRICK APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
FRICK APPLICATION DATA:
FILING DATE: 14-AUG-1997
FRICK APPLICATION DATA:
FILING DATE: 11-AUG-1997
FRICK APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FRICK APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FRICK APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FREERENCE/DOCKET NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FREERENCE/DOCKET NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FREERENCE/DOCKET NUMBER: MO PCT/US97/17618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       015389-002610US
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APPLICANT: Cech. Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 566
SEQUENCE CHARACTERISTICS:
                        CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-854-050-42
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APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen
APPLICANT: Chapman, Karen
APPLICANT: Chapman, Karen
APPLICANT: Mariey, Calvin B.
APPLICANT: Andrews, William H.
ADPLESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 20; DB 3; Length 44; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        015389-002930US
                                                                                                                                                                                                                                                             PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: AA hase Dairs
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US-08-974-549A-568
; Sequence 568, Application US/08974549A
; Patent No. 6166178
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 rrrrccccrrrrccccrrrr 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-851-843A-42
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Sequence 568 Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: UNMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: OL-OCT-1966
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REFERENCE/COCKET NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 20; DB 3; Length 44; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                           Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 9th Floor
                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECTULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TITIGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 57¢
TELEPAX: (415) 576-C
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-402-181B-568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-CT-1996
CLASSIFICATION S36
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-CCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-CCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-CCT-1996
TELECOMMUNICATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
                           APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States of America
ZIP: 94101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-430-323-42
; Sequence 42, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.;
; Lingmer, Joachim; Nakamura, Toru
; Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TITIGGGGTTTTGGGGTTTT 20
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Matches 20; Conservative
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MEDIUM TYPE: FLOPPY GISK
MEDIUM TYPE: FLOPPY GISK
GONTWARE: Patentin Release #1.0, Version #1.30
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CIASSIFCATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,312
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
                             Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 3; Length 44; llarity 100.0%; Pred. No. 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..44
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPIO, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTTTGGGGTTTTGGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 568
                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-721-456-568
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100.0%; Score 20; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <unknown>
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..44
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: -curknown>
PRIOR APPLICATION: -curknown>
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,553
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 10-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     015389-002620US
                                                                                         STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOAPPY disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 568, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-402-181B-568
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Gaps

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GENERAL INFORMATION:
APPLICANT: CECH, THOMAS R.
APPLICANT: LINGABER, JOACHIM
APPLICANT: LINGARER, JOACHIM
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: MAKAMURA, TORU
APPLICANT: MAKIN, GENGG B.
APPLICANT: MAKIN, GENGG B.
APPLICANT: MORIN, GENGG B.
APPLICANT: TITLE OF INVENTION: TELOMERASE VALLIAM H.
TITLE OF INVENTION: TELOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: US/09/438,486A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 20; DB 3; Length 44; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFANT: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTHARE: PATENTIN Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION NUMBER: US/10/054,295
FILING DATE: CLASSIFICATION NUMBER: US/10/054,295
FILING DATE: CLASSIFICATION NUMBER: US/10/054,050
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/10/08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/10/08/44,419
FILING DATE: 10-CCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 42, Application US/09438486A Patent No. 6927285
                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-438-486A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: 08 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELECHOMUNICATION INFORMATION:

TELECHOME: (415) 576-0200
                                                                                                                                                                                                                            Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVERTION: No. 6808880el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: /desc_= DDNA:
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-766-253-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
                                                     ; Sequence 42, Application US/09766253; Patent No. 6808880; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rrrreegerrrreegerrrr 44
                                                                                                                             APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOPOLOGY: linear
          RESULT 8
US-09-766-253-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gragg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SUCHENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/951,312
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/951,312
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
PRIOR APPLICATION NUMBER: US 08/911,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcadero Center, El STREET: El S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 567, Application US/08974549A Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TITIGGGTTTTGGGGTTTT 20
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-974-549A-567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 20; DB 3; Length 44; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/851,843A FILING DATE: 06-MAY-1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapmen, Toru
APPLICANT: Morin, Greeg B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randclph T.
REGISTRATION NUMBER: 36,4229
REPRENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/851,843
PRIOR FILING DATE: 1997-05-06
PRIOR PELING DATE: 1997-05-06
PRIOR PILING DATE: 1997-04-25
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 223
SOFTWARE: PATCHIN Ver. 3.2
SEQ ID NO 42
LENGTH: 44
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-AFR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-08-851-843A-41
Sequence 41, Application US/08851843A
Patent No. 6093809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cech, 7
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRNI APPLICATION DATE:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <u >CURRON</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Gregg B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
    PILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGBH: NEORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/854,050
  US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-854-050-41
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Sequence 41, Application US/08854050

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNEATOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend and Townsend and Crew LLP
              PRINCATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
ATORNEY AGENT: NFORMATION:
AMARE: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPAK: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two Embarcadero Center, 8th Floor
San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 TTTTGGGTTTTGGGGTTTT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 20; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-974-549A-567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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Lingner, Joachim
Nakamura, Toru
Chamura, Toru
Chamura, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSOFTWARE: Patentin Release #1.0, Version #1.30
CURSOFTWARE: 22-No. 6617110-2000
CLIASSIFICATION OFF: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLIASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 3; Length 46; 100.0%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CATTE: California COUNTRY: USA
                                                                                              ATTOLICATION NOWBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

ATOREST ATOREST O1-OCT-1997

ATOREST/AGENT INFORMATION:
NAME: Ausenbus, Scott L.
REFERENCE/DOCKET NUMBER: 015389-002620US

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs

TYPE: nucleic acid
STREE CHARACTERISTICS:
LENGTH: 46 base pairs

TYPE: nucleic acid
STREE CHARACTERISTICS:
LENGTH: 46 base pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,
                                   FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 567, Application US/09721456 Patent No. 6617110 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TITIGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-402-181B-567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
US-09-721-456-567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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STREET: Two Embarcadero Center, Eighth Floor
STRIE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: BAPTIC COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: «Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Month of the Market Mar
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Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                    NAME: Apple, Randoh T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/86,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/724,643
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DESCRIPTION: //desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-430-323-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 567, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-402-181B-567
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Gaps

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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
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APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
PAPLICATION NUMBER: US 08/846,017
PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: United States of America
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 20; Conservative
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US-10-054-295-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-766-253-41
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Lingner, Joachim
Nakamira, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                PILING DATE: 18-APR-1997

PILING DATE: 25-APR-1997

PILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: S0-002610US

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELEPHONE: (415) 576-0300

TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..46

GTHER INFORMATION: /note= "hairpin primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-09-721-456-567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prec. No. 100.0%; Prec. No. Mismatches
    US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41, Application US/09766253 Patent No. 6808880 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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US-09-766-253-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851,843A

FILING DATE: 06-MAY-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/86,017

RIGHTON APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION:

PRIOR APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION:

PRIOR APPLICATION NUMBER: US 08/724,643

FILING DATE: 10-OCT-1996

CLASSIFICATION:

APPLICATION NUMBER: US 08/724,643

FILING DATE: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                      ALUNESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                 APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               015389-002930US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
US-08-851-843A-40
; Sequence 40, Application US/08851843A
; Patent No. 6093809
                                                                           Sequence 37, Application US/08851843A Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTGGGGTTTT 20
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TELECOMPUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELETAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94111
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                                                         US-08-851-843A-37
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APPLICANT: CECH, THOMAS R.

APPLICANT: LINGNER, JOACHIM
APPLICANT: LINGNER, JOACHIM
APPLICANT: CHAPMAN, KAREN B.

APPLICANT: CHAPMAN, KAREN B.

APPLICANT: CHAPMAN, KAREN B.

APPLICANT: MORIN, GREGG B.

APPLICANT: ANDREWS, MILLIAM H.

TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE VARIANTS

TITLE OF INVENTION: GENE 1990-11-12

FILE REFERENCE: 018/062 1990-11-12

CURRENT APPLICATION NUMBER: 08/846,017

PRIOR APPLICATION NUMBER: 08/846,017

PRIOR FILING DATE: 1997-04-18

PRIOR FILING DATE: 1997-04-18

PRIOR FILING DATE: 1997-04-18

PRIOR FILING DATE: 1997-04-18

PRIOR FILING DATE: 1996-10-01

NUMBER OF SEQ ID NOS: 223

SOFTWARE: PARCHILIN VET: 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels
FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INCOMMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/09438486A
Patent No. 6927285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 ririrgegerrirgegerrir 46
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                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
US-09-438-486A-41
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LENGTH: 46
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Gaps

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Length 48;
                                                             APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE SS:
ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                    COMPUTER TEADABLE FORM:
MEDIUW TYPE: USA

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 10-NOV-1997
CLASSIFICATION NUMBER: US/08/974,549A
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: US/08/44,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US/08/844,419
PRIOR APPLICATION NUMBER: US/08/846,017
PRIOR APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US/08/851,843
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US/08/912,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: US-AUG-1997
ATTONENEY/AGMATION:
APPLICATION NUMBER: WO PCT/US97/17618
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: US-AUG-1997
ATTONEY/AGMATION:
AND AND AUG-1997
ATTONEY/AGMATION:
AND AND AUG-1997
ATTONEY/AGMATION:
AND AND AUG-1997
                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REELERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1..48
; OTHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam PC-COMBATISH
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 0-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Marin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and STEET: Two Person
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 22
US-08-974-549A-564
; Sequence 564, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim; APPLICANT: Lingner, Joachim; APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 ririrécédiririécédirir 48
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TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-851-843A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcaders Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 0-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 0-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
FILING DATE: 01-OCT-1996
CLASSIFICATION: S36
FILING DATE: 01-OCT-1996
  ;
                                                                                                                                                                                                                               Sequence 37, Application US/08854050
Fatent No. 6261836
GENERAL INFORMATION:
APPLICANT: Lingmer, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
ITILE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/ACENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 37:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                      1 TTTTGGGGTTTTTGGGGTTTT 20
                                                                                                       29 rrrrssscrrrrssscrrrr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                          RESULT 23
US-08-854-050-37
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Matches
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Query Match 100.0%; Score 20; DB 3; Length 48; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTRY: UNITED SCALES C. CONTRY: UNITED SCALES C. CONTRY: UNITED SCALES C. CONTRY: CONTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
PILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION SAGO SAGO SAGO STELMS APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 20-002196
CLASSIFICATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHRACTERISTICS:
FRANTHH 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Townsend and Townsend and Crew LLP
T: Two Embarcadero Center, 8th Floor
San Francisco
California
XY: United States of America
                                                                                                                                    APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, 225
CORRESPONDENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                              US-08-854-050-40
; Sequence 40, Application US/08854050
; Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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STRANDEDNESS: sing
                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-854-050-40
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RESULT 24
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Gaps ; 0

Conservative

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ZIF: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <a href="https://documer.com/">Unknown></a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 3; Length 48; Pred. No. 7;
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                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                               STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                           Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 08/654,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 564, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
                               Sequence 40.5. Application US/09430323;
Patent No. 6309867;
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTTTGGGGTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 27
US-09-402-181B-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-430-323-40
                 US-09-430-323-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPENATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
APPLICATION NUMBER: US/09/430,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                           APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 0-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                         Sequence 37, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTTTGGGGTTTTGGGGTTTT 20
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TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 20; Conserv
                                                                                                                RESULT 25
US-09-430-323-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-430-323-37
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0; Gaps

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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregs B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 1..48
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                         Sequence 564, Application US/09721456 Patent No. 6617110 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 564: SEQUENCE CHARACTERISTICS:
                                                                JS-09-721-456-564
                                     RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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0
                                                                                   Chapman, Karen B.

Morin, Gregg B.

Harly, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: USA
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: CURRENT COUNTRY
COUNTRY APPLICATION: AUMROND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 20; DB 3; Length 48; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 
CLASSIFICATION: 
CLASSIFICATION: 
CLASSIFICATION: 
CLASSIFICATION OFATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 11-AUG-1997
APPLICATION NUMBER: US 08/915,503
AUG DATE: 11-AUG-1997
AUG DATE: 11-AUG DATE: 11-AUG-1997
AUG DATE: 11-AUG-1997
AUG DATE: 11-AUG DATE: 11-AUG-1997
AUG DATE: 11-AUG DATE: 11-A
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REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcadero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 TTTTGGGGTTTTGGGGTTTT 48
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-03(
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
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COMPUTE: United States of America
CUNTRY: United States of America
CUNTRY: April
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTES: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIPICATION: AUNTROWN>
PRIOR APPLICATION: AUNTROWN>
PRIOR APPLICATION NUMBER: US/08/46,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US/08/443
FILING DATE: 01-OCT-1996
ATTORREY/AGENT INFORMATION:
ANDERSY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 20; DB 3; Length 48; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Joachim
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880e1 Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATIONAL APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
FERERENCE TOWNER: 015389-002920US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) DESCRIPTION: //desc = "DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 40: US-09-766-253-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                  JS-09-766-253-40
Sequence 40, Application US/09766253
Patent No. 6808880
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 37, Application US/10054295; Patent No. 6921664; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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                                                                                         Gaps
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                                            100.0%; Score 20; DB 3; Length 48; 100.0%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: CCC, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, 8th Floor
                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-0an-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                         Sequence 37, Application US/09766253 Patent No. 6808880 GENERAL INFORMATION:
                                                                                                                                    1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                              29 rrrrcccrrrrcccrrrr 48
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INFORMATION FOR SEQ ID NO: 37:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                          Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
US-09-721-456-564
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US-09-766-253-37
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APPLICANT: CECH, THOMAS R.
APPLICANT: LINGMER, JOACHIM
APPLICANT: LINGMER, JOACHIM
APPLICANT: NAKAMURA, TORU
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: MORIN, GREGG B.
APPLICANT: HARLEY, CALVIN
APPLICANT: ANDREWS, WILLIAM H.
APPLICANT: ANDREWS, WILLIAM H.
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND TITLE OF INVENTION: TELOMERASE VARIANTS
FILE REPERENCE: 018/062
                                                                                                                                     CORPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/8854,050
FILING DATE: CURROWN-
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
ATTORNEY/AGENT INFORMATION:
AND ADDITION NUMBER: US 08/724,643
FILING DATE: US-DATA-1996
ATTORNEY/AGENT INFORMATION:
AND ADDITIONS ADDITIONS AND ADDITIONS AND ADDITIONS AND ADDITIONS AND ADDITIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION INVEST: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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100.0%; Pred. No. 7;
iive 0; Mismatches 0
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CURRENT FILING DATE: 1999-11-12
PRIOR PELLICATION NUMBER: 08/651,843
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-04-25
PRIOR PELLING DATE: 1997-04-25
PRIOR PELLING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR PELLING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR PILING DATE: 1997-04-18
                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/09438486A Patent No. 6927285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                              COMPUTER READABLE FORM:
           STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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US-09-438-486A-37
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
UNMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»

APPLICATION NUMBER: 08 08/846,017
FILING DATE: 25-APF-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APF-1997
APPLICATION NUMBER: US 08/724,643
APTICATION DUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                           STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 rrrrccccrrrrccccrrrr 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                          ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-054-295-37
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US-10-054-295-40
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Gaps

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APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                        94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-40
                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-uy-ab-aba-qu
is Sequence 40, Application US/09438486A
; Batent No. 692728
; GENERAL INFORMATION:
; APPLICANT: CECH, THOMAS R.
; APPLICANT: CHAPMAN, RARB
APPLICANT: CHAPMAN, RARB
APPLICANT: CHAPMAN, RARB
APPLICANT: HARLEY, CALVIN
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ANDREWS, WILLIAM H.
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TITLE OF INVENTION: GENE POR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TITLE OF INVENTION: GENE POR HUMAN TELOMERASE OF TITLE OF INVENTION UNDBER: US/09/438,486A
; FILE REFERENCE: 018/062
; CURRENT APLICATION NUMBER: 08/81,843
; PRIOR FILING DATE: 1997-05-06
; PRIOR FILING DATE: 1997-06-06
; PRIOR FILING DATE: 1997-04-18
; PRIOR FILING DATE: 1997-04-18
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 223
; SOFFWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                              DB 3; Length 48;
                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                              Query Match 100.0%; Score 20; DE Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/08851843A
; Sequence 39, Application US/08851843A
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Chapman, Karen B.
; APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
     NUMBER OF SEQ ID NOS: 223
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 37
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
US-09-438-486A-40
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US-08-851-843A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 40
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                 FEATURE:
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Local Similarity 100.0%; Pred. No. 7.1;
les 20; Conservative 0; Mismatches A. T. 1.
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APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Morain, Greegg B.
APPLICANT: Morain, Greegg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, 721
CORRESPONDENCES: 727
CORRESPONDENCES ADDRESS:
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/74,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
NUMBER: MENDORMATION:
NUMBER: APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 566, Application US/08974549A Patent No. 6166178 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTTTGGGGTTTTGGGGTTTT 20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER:
COMPUTER: TEM PC COMPUTER:
COMPUTER: PACHION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION: SAS
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapmar, Toru
APPLICANT: Mortin, Gregg B.
APPLICANT: Mortin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor STREET: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                      Sequence 39, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAK: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                       RESULT 37
US-08-854-050-39
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                                                            CITY: San Firancisco
CITY: San Firancisco
COMPUTE: California
COUNTER: California
COMPUTE: BADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-CDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
CLASSIFICATION NUMBER: US 08/44,419
FILING DATE: 19-NOV-1997
RELOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-COT-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 11-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-CCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-CCT-1997
PRIOR APPLICATION NUMBER: 36,429
PLEECOMMUNICATION INPROMERE: 01-2389-002610US
TELECOMMUNICATION INPROMERE: 01-2389-002610US
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: -

LOCATION: 1..50

LOCATION: 1..50

GTHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-566
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 566
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                       Gaps
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100.0%; Score 20; DB 3; Length 50; 100.0%; Pred. No. 7.1;
                      Indels
                       Mismatches
                                              1 TTTTGGGGTTTTGGGGTTTT 20
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0
                                    Gaps
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                                                           1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                 Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      ZIE: 94111-3834

COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENTION DATA:
    APPLICATION NUMBER: US/09/402,181B
    FILING DATE: 29-Sep-1997
    CLASSIFICATION: <underween
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                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /note= "hairpin primer" SEQUENCE DESCRIPTION: SEQ ID NO: 566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: cursor-1997
CLASSIFICATION: curknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-0CT-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ausenhus, Scott L. REGISTRATION NUMBER: 42,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 Trrreeserriresestrir 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELBFAX: (415) 576-0.
INFORMATION FOR SEQ ID NO: 566
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                            Chapman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-402-181B-566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: vunknown.
PRIOR APPLICATION NUMBER: US/05/430,323
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                   APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
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PAILOR AFFLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APF-1997
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLGGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 39
US-09-402-181B-566
; Sequence 566, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
                                            Sequence 39, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TITIGGGTTTIGGGGTTTT 20
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415)
                          US-09-430-323-39
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Gaps

22

US-09-721-456-566

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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION NUMBER: US/09/721,456
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,549A
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-NOY-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-NER-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/913,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                                                                                            APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION: 1..50
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 015389-002610US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
RESULT 40
US-09-721-456-566
; Sequence 566, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
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                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA
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                                              Gaps
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100.0%; Score 20; DB 3; Length 50; larity 100.0%; Pred. No. 7.1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 3; Length 50; 100.0%; Pred. No. 7.1; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
                                                                                                                                                                                                                                                                                                                                                                                                        Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Can-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECTULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                      RESULT 41
US-09-766-253-39
; Sequence 39, Application US/09766253
; Patent No. 60888880
; PATENT NO. 6088880
; PATENTAL THOCNAMICN:
; APPLICANT: Cech, Thomas R.
Lingner, Joachim, Nakamura, Toru Chapman, Karen B.
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                     31 rrrreecerrrreecerrrr 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-C
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-766-253-39
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APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Arich, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/08851843A Patent No. 6093809 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Nakamura, Toru APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two bulkers
CITY: San Francisco
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-851-843A-39/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
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                                                                                                                                                                                                                                                                                                                                                                   CUNTRY: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 08/844,419
FILING DATE: L8-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: IBM-RPR-1997
ATTORNEY/AGRATINNER: US 08/724,643
FILING DATE: IBM-RPR-1997
ATTORNEY/AGRATINNER: US 08/724,643
FILING DATE: IBM-RPR-1996
ATTORNEY/AGRATINNER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 3; Length 50; 100.0%; Pred. No. 7.1; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              Crew LLP
                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                           Morin, Gregg B Harley, Calvin Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid

BESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-054-295-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                Sequence 39, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
US-10-054-295-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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Sequence 39, Application US/09438486A Patent No. 6927285 GENERAL INFORMATION: APPLICANT: CECH, THOMAS R. APPLICANT: LINGNER, JOACHIM

RESULT 43 US-09-438-486A-39

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, OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-09-438-486A-39
APPLICANT: NAKAMURA, TORU
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: HARLEY, CALVIN
TILLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TITLE OF INVENTION: TELOMERASE VARIANTS
TITLE OF INVENTION: TELOMERASE VARIANTS
TITLE OF INVENTION: TELOMERASE VARIANTS
TITLE OF INVENTION TELOMERASE VARIANTS
TITLE OF INVENTION: TELOMERASE VARIANTS
TITLE OF INVENTION: TELOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR PILING DATE: 1997-04-18
PRIOR PELING DATE: 1997-04-18
PRIOR PELICATION NUMBER: 08/44,419
PRIOR PILING DATE: 1997-04-18
PRIOR PELING DATE: 1997-04-18
PRIOR PELING DATE: 1997-04-18
SEQ TO NOS: 223
SOFTWARE: PATENTING VARIER: 08/344,419
PRIOR FILING DATE: 1996-110-01
SOFTWARE: PATENTING DATE: 1996-110-01
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APPLICATION NUMBER: US/08/851,843A
FTI.ING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Namura, Toru
APPLICANT: Namura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Addrews, William H.
ITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: TWO Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..50
OTHER INFORMATION: /note= "hairpin primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                 PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
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CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 566:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTGGGGTT 18
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 46
US-08-854-050-39/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Calliornia
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-Base #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFTATION NUMBER: US/08/974,549A
FILING DATE: 01-NOV-1997
FILING DATE: 01-OCT-1996
PRIOR APPLICATION UNMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor
San Francisco
FILING DATE: 18-APR-1997
CLASSIFICATION:
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TENGTH: 50 base pairs
TERGY ANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTGGGGTT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-851-843A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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Sequence 566, Application US/09402181B

Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingnar, Joachim
Nakamura, Toru

Chapman, Karen B.

Morin, Greeg B.

Harley, Calvin B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834

COMPUTER READABLE POORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
       APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIEFCATION: CUNKNOWN-
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/851,050
FILING DATE: 09-MX-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MX-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
50;
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FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 576-0200
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100.0%; Pr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTTTGGGGTTTTGGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.0
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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Pred. No. 50;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                     CLASSIFICATION: 5.0.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFRAK: (415) 576-0200
TELEFRAK: (415) 576-0300
TELEFRAK: (415) 576-0300
TELEFRAK: (415) 576-0300
TELEFRAK: CAPRACTERISTICS:
LENGTH: 5.1.2.2.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Scor.
100.0%; Pred. No. J...
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STATE: California
COUNTRY: United States of America
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
CLASSIFICATION NUMBER: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
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Best Local Similarity 100.0
...dhes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 47
US-09-430-323-39/c
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Length 50;
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PatentIn Release #1.0, Version #1.30
          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NO. 6617110-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/09/74,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/91,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
REPERRENES/POCKET NUMBER: 86,429
REPERRENES/POCKET NUMBER: 86,429
REPERRENES/POCKET NUMBER: 86,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "hairpin primer" SEQUENCE DESCRIPTION: SEQ ID NO: 566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews, William H.
TITLE OF INVENTION: NO. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%; Score 18; DB 3; 100.0%; Pred. No. 50;
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Patent No. 6808880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS
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OTHER INFORMATION:
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MOLECULE TYPE: DNA
FRATURE:
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Matches 18; Conserv
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
RADRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 3; Length 50;
Pred. No. 50;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                     FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
             FILING DATE: 01-OCT-1996
PPDLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 566:
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Patent No. 6617110
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
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LENGTH: 50 base pairs
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STRANDEDNESS: single
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US-09-721-456-566/c
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Gaps

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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Ploor
CITY: Sal Francisco
STATE: California
COMPUTRY: United States of America
2IP: 94111
COMPUTRE RADABLE PORM:
MEDIUW TYPE: Floppy disk
COMPUTRE: REDABLE PORM:
MEDIUW TYPE: Floppy disk
COMPUTRE: REDABLE PORM:
MEDIUW TYPE: Ploppy disk
COMPUTRE: BAPC Compatible
COMPUTRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: 108/09/766,253
FILING DATE: 19-20-2001
FRIOR APPLICATION NUMBER: 108/09/766,253
FILING DATE: 1997-04-25
FILING DATE: 1997-04-26
FILING DATE: 1997-04-25
FILING DATE: 1997-04-26
FILING DATE: 1997-04-25
FILING DATE: 1997-04-26
FILING DATE: 1997-04-25
FILING DATE
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Search completed: February 15, 2006, 21:14:09 Job time : 48.9587 secs

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Seguence:

Title: Perfect

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 February 16, 2006, 01:43:22; Search time 290.248 Seconds (without alignments) 569.815 Million cell updates/sec
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US-10-877-124-568
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Maximum Match 100%
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seq length: 50
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Sequence 30, Appl Sequence 60, Appl Sequence 557, App Sequence 557, App Sequence 557, App	Sequence 337, App Sequence 99, Appl Sequence 117, App	Sequence 4217, Ap Sequence 7605, Ap Sequence 43, Appl	Sequence 45, Appl	Sequence 43, Appl Sequence 45, Appl	Sequence 43, Appl	Sequence 45, Appl Sequence 43, Appl	Sequence 45, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 45, Appl	Sequence 113, App Sequence 113, App	Sequence 113, App	Seguence 113, App Seguence 66 Appl	Sequence 5325, Ap	Sequence 1981, Ap	Sequence 32, Appl Sequence 11, Appl	Sequence 48, Appl	Sequence 257773,	Sequence 2244, Ap	Seguence 2244, Ap Seguence 371, App	Sequence 2154, Ap	Sequence 474680, Sequence 692527.	Sequence 102555,	Sequence 433201, Sequence 35, Appl	1 41	25	2 2	Seguence 295, App Seguence 305, App	8	3 5	CAC	7	CIC	¥ _	- 77	_``	3 4	2	, co	¥.	<u>4</u> , π	00	equence 50,	Sequence 50, Appl Sequence 123, App	equence 106
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US-10-053-758-37 US-10-053-758-40 US-10-054-295-37 US-10-054-295-40 US-10-054-611-37 US-10-054-611-47	US-10-325-810-564 US-10-877-124-564	US-10-8//-UZZ-564 US-10-877-146-564 US-10-131-827-5734	US-09-843-676-61	US-U9-766-253-61 US-09-438-486-61	US-10-053-758-61	US-10-054-295-61	US-10-325-810-114	US-10-877-124-114 US-10-877-022-114	US-10-877-146-114	US-11-166-990-39	US-10-843-88/-1033 US-10-973-783-1416	US-10-956-157-129722	US-11-049-446-60 US-10-085-906-51	US-10-131-827-1029	US-10-708-204-67	US-108-204-1/90 US-09-888-326-735	US-09-776-479-692	US-US-1/6-4/9-694 US-09-776-479-883	US-09-776-479-692	US-09-776-479-694 US-09-776-479-883	US-10-112-653-665	US-10-112-653-667 US-10-112-653-854	US-10-017-995-692	US-10-017-995-694 US-10-017-995-883	US-10-163-862-4	US-10-140-013-32 US-10-314-578-692	US-10-314-578-694	US-10-314-578-883 US-10-309-775A-6	US-10-831-778-692	US-10-831-778-893	US-10-163-862-3	US-10-973-783-662	US-10-845-667-1250	US-10-845-867-1480 US-10-131-827-5465	US-10-719-956-215749	US-10-719-956-215750 TR-10-719-900-519045	US-10-719-900-910968	US-11-036-317-624650	US-09-843-676-50 US-09-843-676-60	US-09-766-253-30	US-09-766-253-60 US-09-438-486-30	US-09-438-486-60	US-10-053-758-30	US-10-054-758-60 US-10-054-295-30	US-10-054-295-60
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Sequence 164159,
Sequence 235930,
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Sequence 95877, A
Sequence 103736,
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                            653453,
161728,
912559,
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US-10-719-956-1070
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US-10-843-527-95877
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US-10-473-126-692
US-10-473-126-692
US-10-473-126-1035
US-10-473-126-1036
US-10-473-126-1036
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Sequence 73, Application US/09776479
Publication No. US20030087848A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
RESULT 1
US-09-776-479-73
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; Publication No. US20030050268A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; TITLE REFERENCE: C01039/70060(AMS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR PILING DATE: 2001-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
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US-09-776-479-73
is Sequence 73, Application US/09776479
is Sequence 73, Application US/09776479
is Publication No. US2004067902A9
igeneral information:
http://doi.org/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.10
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FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
FRIOR APPLICATION NUMBER: US 60/179,991
FRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-776-479-73
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) OTHER INFORMATION: Synthetic Sequence US-10-314-578-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 20; Conservative
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Sequence 73, Application US/10017995

Publication No. US20030055014A1

GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.

TITLE OF INVORMATION:
CURRENT APPLICATION NUMBER: US/10/017,995

CURRENT PELL 20137/7025 (HCL/MAT)

CURRENT PELLOTON NUMBER: US/10/017,995

CURRENT PELLOTON NUMBER: US/10/017,995

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 73

LENGTH: 20
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Publication No. US20030212026A1
GENERAL INFORMATION:
APPLICANT: Schetter, Christian
APPLICANT: Schetter, Christian
APPLICANT: Object, Oxog
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US 60/156,113
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR PLING DATE: 1909-09-27
PRIOR PLING DATE: 1909-09-27
PRIOR PLING DATE: 1909-09-27
PRIOR PLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
                                                                                                                                                                                                            100.0%; Score 20; DB 5; I ilarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0;
                                                                                                                      ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-67
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                    TYPE: DNA ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 20; Conserva
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US-10-314-578-73
                   SEQ ID NO 67
LENGTH: 20
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LENGTH: 20
                                                                                                                   FEATURE:
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APPLICANT: Bates, Paula J
APPLICANT: Trent, John O
APPLICANT: Trent, John O
APPLICANT: Trent, John O
APPLICANT: Xi, Xiaohua
TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT
TITLE OF INVENTION: DISEASES
FILE REPERENCE: 9799910-
CURRENT APPLICATION NUMBER: US/10/118,854
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 28
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## SPELICANT: Bratzler, Robert L.

## APPLICANT: Pouron, Vaves

## TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the ITILE OF INVENTION: Treatment of Asthma and Allergy

## TITLE OF INVENTION: Treatment of Asthma and Allergy

## CURRENT APPLICATION NUMBER: US/10/831,778

## PRIOR PILING DATE: 2000-02-03

## NUMBER OF SEQ ID NOS: 1093

## SEG ID NO 73

## SEG ID NO 73

## SEG ID NO 73
     Length 20;
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Query Match
100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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Pred. No. 1.2e+02;
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COTHER INFORMATION: synthetic oligonucleotide
US-10-118-854-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Best Local Similarity
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Sequence 29, Application US/10961479

Sequence 29, Application US/20050187176A1

Publication No. US20050187176A1

GENERAL INFORMATION:

APPLICANT: BATES, PAULA J.

APPLICANT: BARVE, SHIRISH S.

TITLE OF INVENITION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO TITLE OF INVENITION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO TITLE OF INVENITION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO CURRENT PEPLICATION NUMBER: US/10/961,479

CURRENT FILING DATE: 2004-10-08

PRIOR PILING DATE: 2003-10-10

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 29

LENGTH 28

LENGTH 28
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US-10-961-479-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetically generated oligonucleotide
US-10-690-984-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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100.0%; Score 20; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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100.0%; Score 20; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                           US-10-690-984-11

US-10-690-984-11

Sequence 11, Application US/10690984

Publication No. US20050090671A1

GENERAL INFORMATION:
APPLICANT: Chang, Ta-Chau
APPLICANT: Chang, Cheng-Chung
APPLICANT: Wu, Jin-Yi
TITLE OF INVENTION: QUARRULEX STABILIZER
FILE REFERENCE: 08919-112001
CURRENT PAPLICATION NUMBER: US/10/690,984
CURRENT PILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 13

SEQ ID NO 11

LENGTH: 28

LENGTH: 28
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; Patent No. US20020164786Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TITIGGGGTTTTGGGGTTTT 20
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5 TTTTGGGGTTTTGGGGTTTT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                       APPLICANT: Bates, Paula J
APPLICANT: Mi, Yingchang
TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 09799910-0034
CURRENT APPLICATION NUMBER: US/10/607,455
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/392,143
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 28
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US-10-683-480-28

is Sequence 28, Application US/10683480

j Sequence 28, Application US/10683480

j Publication No. US20050053607A1

j GENERAL INFORMATION:
 j APPLICANT: BATES, PAULA J.

j APPLICANT: TRENT, JOHN O.

j APPLICANT: TRENT, JOHN O.

j APPLICANT: TRENT, JOHN O.

j TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS OF

TITLE OF INVENTION: MALIGNANT DISEASES

j TITLE OF INVENTION: MALIGNANT DISEASES

j FILE REPRENCE: LOUG-1012-CIP-US

CURRENT FILING DATE: 2003-10-09

j PRIOR PRELICATION NUMBER: 10/118,854

pRIOR FILING DATE: 2002-04-08

j NUMBER OF SEQ ID NOS: 38

j SOFTWARE: PatentIn Ver. 3.2
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     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: synthetic oligonucleotide US-10-607-455-28
  0; Mismatches
                                                                                                                                                                        RESULT 8
US-10-607-455-28
'Sequence 28, Application US/10607455
'Publication No. US20040132049A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTTGGGGTTTT 20
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                                                      1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
     20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-683-480-28
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LENGTH: 28
     Matches
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Gaps

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Gaps

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COUNTER PREABABLE FORM:

MEDIUM TYPER: Floppy disk

CCMPUTER: IBM PC compatible

CCMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253

FILING DATE: 19-7an-2001

FILING DATE: 19-7an-2001

FILING DATE: 1997-04-25

APPLICATION NUMBER: 08/846,017

FILING DATE: 1997-04-25

APPLICATION NUMBER: 08/846,017

FILING DATE: 1997-04-25

APPLICATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

TELEPHONE: (415) 576-0200

MENDRAMIN STOR STO. 11 NO. 42.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 3; Length 44; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/09438486
| Publication No. US20030009019A1
| GENERAL INFORMATION |
| APPLICANT: Cech, Thomas R. |
| APPLICANT: Lingner, Joachim |
| APPLICANT: Maxamura, Toru |
| APPLICANT: Morin, Greeg B. |
| APPLICANT: Morin, Greeg B. |
| APPLICANT: Andrews, William H. |
| TITLE OF INVENTION: No. US20030009019A1e1 Telomerase |
| UWMBER OF SEQUENCES: 223 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Townsend and Townsend and Crew LLP |
| STREET: Two Embarcadero Center, 8th Floor
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                             STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
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COMPUTER READABLE FORM:
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STATE: California
COUNTRY: United Stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-438-486-42
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                                                                                                                                                                                                                                                                                                                                                           STATE: CALIDOTHIA
COUNTY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BAPC COMPATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
ATTORNAY AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 3; Length 44; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                       Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36, 429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ); SEQUENCE DESCRIPTION: //desc = "DNA"; SEQUENCE DESCRIPTION: SEQ ID NO: 42: US-09-843-676-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
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Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TITIGGGGTTTTGGGGGTTTT 20
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                         Cech, Thomas R.
Lingner, Joachim
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative C
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                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
     GENERAL INFORMATION:
APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-766-253-42
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Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFRENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 20; DB 5; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/81,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California COUNTRY: United States of America
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APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    );

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-053-758-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 42, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
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COMPUTER READABLE FORM:
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
MEDIUM TYPE: Floppy disk
COMDUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION S36
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: U-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: RANGOLID T:
APPLICATION NUMBER: US 08/724,643
FILING DATE: NAMBER: US 08/724,643
FILING DATE: NAMBER: US 08/724,643
FILING DATE: U-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: U-OCT-1996
TELEPONIUNICATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELEPONIUNICATION NUMBER: 36,429
TELEPAX: (415) 576-0300
INPORMATION POR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH - 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/10053758
Publication No. US20030032075A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recentricecertry 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-053-758-42
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Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPRY disk

MEDIUM TYPE: RIOPRY disk

MEDIUM TYPE: RIOPRY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: AUNROWN-

PRIOR APPLICATION: AUNROWN-

PRIOR APPLICATION NUMBER: US/09/402,181

FILING DATE: 20-Sep-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: S5-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: US-APR-1997

APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CATE: California COUNTRY: USA
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/ACENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 5; I
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECTULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEG ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 568, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                        LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.8
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
US-10-325-810-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-054-611-42
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US-10-054-611-42
Sequence 42, Application US/10054611
Sequence 42, Application US/10059787Alel Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS: 325
SEREET: TWO EMBARCAGERO Center, 8th Floor
STREET: TWO Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 5; Length 44; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MERR: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                      FILING DATE: CURROWNS
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
NAME: APPLIC
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAR: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 20; Conservative
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Gaps
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100.0%; Score 20; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..44
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORREY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                    FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-MG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AG-1997
APPLICATION NUMBER: WO PCT/US97/17618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                               US 08/846,017
                               FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 568:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 TTTTGGGGTTTTGGGGTTTT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-877-022-568
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Publication No. US20040242529A1

Publication No. US20040242529A1

GENERAL INFORMATION:
Lingmer, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: USA

COMPUTER: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 24-Jun-2004
CLASSIFICATION: <underweenzage
Universal CATION: <underweenzage
UNIVERSAL CATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..44
; CTHER INFORMATION: /note= "hairpin primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 568:
US-10-325-810-568
                                                                                                                                                                                                                                                                                                  NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION:
TELEPHONE: (415) 576-0200
TELEFAR: (415) 576-0300
INFORMATION FOR SEQ ID NO: 568:
SEQUENCE CHARACTERISTICS:
                                                                                            FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ririregegiririegegirir 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
US-10-877-124-568
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                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
                     STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..44

GTHER INFORMATION: /note= "hairpin primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 568:
US-10-877-146-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 8; L
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATA:
PAPLICATION NUMBER: US/09/432,503
APPLICATION NUMBER: 06/974,549
APPLICATION NUMBER: 06/974,549
APPLICATION NUMBER: 06/974,549
FILING DATE: 4Uhrnown
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <UNKNOWN>
  and Townsend
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TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTTTGGGGTTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 568
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserva
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US-09-843-676-41
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Publication No. US20050013825A1
GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 8; Length 44; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-0CT-1997
APPLICATION NUMBER: W0 PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INPORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFIRENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUTCATION INPORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..44
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-NOv-1999
APPLICATION NUMBER: US/974,549
FILING DATE: cUnknown>
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/86,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/81,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Unn-2004
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 568:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TITIGGGGTTTTGGGGTTTT 20
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
US-10-877-146-568
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Gaps

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STAKEE: California
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATA:
APPLICATION NUMBER: US 08/46,017
FILING DATE: 1997-04-25
FILING DATE: 197-04-25
FILING DATE: O1-OCT-1996
ATTORNEY/AGENT INPORMATION:
WARNEY CALLOR OF COMPATION:
WANNEY CALLOR OF COMPATION:
WANNEY CALLOR OF CAL
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| Sequence 41, Application US/09438486
| Publication No. US20030009019A1
| GENERAL INFORMATION:
| APPLICANT: Cech, Thomas R. APPLICANT: Lingmer, Joachim APPLICANT: Chapman, Karen B. APPLICANT: Maxmura, Toru APPLICANT: Maximin, Gregg B. APPLICANT: Andrews, William H. TITLE OF INVENTION: No. US20030009019A1e1 Telomerase: ITLE OF INVENTION: No. US20030009019A1e1 Telomerase: NUMBER OF SEQUENCES: 223
| CORRESPONDENCE ADDRESS:
                         TITLE OF INVENTION: No. US20020187471A1el Telomerase NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 3; I
100.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 94111-3834 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    );
SEQUENCE DESCRIPTION: /desc = "DNA";
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-766-253-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTTTGGGGTTTTTGGGGTTTT
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Best Local Similarity 100.
Matches 20; Conservative
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100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                         APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 2c-Apr-2001
CLASSIPICATION: 556
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: Twomsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPL:
RAGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 94111
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SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
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Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
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LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-843-676-41
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US-09-766-253-41
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 5; Length 46
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0; Indels
                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PctentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: IB-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APF-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toachim
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 26
US-10-054-295-41
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| Sequence 41, Application US/20030032075A1
| GENERAL INFORMATION: Lingner, Joachim Nakamura, Toru Chapman, Karen B. Morin, Gregg B. Harley, Calvin Andrews, William H.

TITLE OF INVENTION: No. US20030032075A1e1 Telomerase NUMBER OF SEQUENCES: 225
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 0.-OCT-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 36,429
FILING DATE: 0.-OCT-1996
CLASSIFICATION S36
PRIOR APPLICATION NUMBER: 015389-002931US
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 015389-002931US
FILING DATE: 01-OCT-1996
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: GLASSIFISTICS:
CLASSIFICATION NUMBER: 015389-002931US
TELEPAX: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPAX: (415) 676-0200
TELEPAX: (
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COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 riricecerrirecerrir 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-438-486-41
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Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: 433
CORRESPONDENCES: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STRAME: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 5; 1
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-5ep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                          APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

BESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-054-611-41
                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 567, Application US/10325810 Publication No. US20030204069A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 28
US-10-325-810-567
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 5; L 100.0%; Pred. No. 1.2e+02;
                                                                                    FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
  DATE: 18-Jan-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 46 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 20; Conservative
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US-10-054-611-41
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Gaps

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APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTIONS: 727

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                  APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: NO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , LOCATION: 1..46
; OTHER INFORMATION: /note= "hairpin primer"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 1.2e+02;
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           08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 567, Application US/10877022; Publication No. US20040247613A1; GENERAL INFORMATION:
        APPLICATION NUMBER: US 0 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO: 567: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 TITIGGGGTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-877-022-567
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin B.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STARE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Un-2004
CLASSIFCATION: <URNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 6; Length 46; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: 1..46
LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                                                                                                                                    NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REGISTRATION NUMBER: 42,271
REPERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFARM: (415) 576-0300
INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 Dase pairs
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO 08/915,503
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-NOV-1999
APPLICATION NUMBER: 08/974,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 567, Application US/10877124 Publication No. US20040242529A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 ririrgegiriringegiriri 46
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-877-124-567
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                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                          Townsend and Crew LLP
Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer";
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-10-877-146-567
                                                                                                                                                                                                                                                                                    APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/99/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: US/99/4,549
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-AFR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-AFR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 25-AFR-1997
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-CCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 20; DB 8; 1
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09843676
Patent No. US20020164786A1
                          ADDRESSEE: Townsend and STREET: Two Embarcadero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                         CITY: San Francisco
STATE: California
COUNTRY: USA
  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA
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US-09-843-676-37
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Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Jun-2004
CLASSIPICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: - ..46
LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 8; 1 100.0%; Pred. No. 1.2e+02;
                                                                                                                                           PRIOR APPLICATION DATE:
APPLICATION UNMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: CURNOWN
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/854,050
RILING DARE: 09-MAX-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 31
US-10-877-146-567
Sequence 567, Application US/10877146
Publication No. US20050013825A1
GENERAL INFORMATION:
JAMPHINGRAT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTTTGGGGTTTTGGGGTTTT 20
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INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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us-09-669-187a-73.szlm50.rnpbm

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COMPUTER IS TOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CASSIFICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION NUMBER: 015000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 48;
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 3; Length 48
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
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Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09766253 Publication No. US20020187471A1 GENERAL INFORMATION: Geol, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTGGGGTTTT 20
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Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 34
US-09-766-253-37
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                     APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 01-OCT-1996
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APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
Lingner, Joachim Nakamura, Toru Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-843-676-40
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Length 48;
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APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
ATTLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECHOMMUNICATION INFORMATION:
TELECHOMES (415) 576-0300
TELECHONE: (415) 576-0300
TELECHONE: (415) 576-0300
TELECHONE: (415) 676-0300
TELECHONE: (415) 676-0300
TELECHONE: (415) 676-0300
TELECHONE: (415) 676-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE SUBDIRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
STREET: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 20; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/09438486; Publication No. US20030009019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: other n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-766-253-40
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US-09-438-486-37
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Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRNT APPLICATION DATE: 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 3; Length 48; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 35
US-09-766-253-40
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                   FILING DATE: 01-00T-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APDIe, Randolph T.
RECISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTET READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,758

FILING DATE: 18-Jan-2002

CLASSFICATION: 536

PRIOR APPLICATION NUMBER: US/08/654,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 01-OCT-1996
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PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
VITORNEY/ACTION: 536
VITORNEY/ACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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US-10-053-758-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Callvin
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
APPLICANT: ANGREWS, William H.
APPLICANT: ANGREWS, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWALEN SISTEM: PC-DUS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486 FILING DATE: 12-NOV-1999 CLASSIFICATION NUMBER: US 08/851,843 APPLICATION NUMBER: US 08/851,843 FILING DATE: 6-MAY-1997 CLASSIFICATION DATA: PRICK APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 CLASSIFICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 CLASSIFICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 CLASSIFICATION: 250 CLASSIFICATION: 2
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                                               CLASSIFICATION 536
PRIOR APPLICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
TELEPAC CHARACTERISTICS:
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
DESCRIPTION: /desc = "DNA"
US-09-438-486-37
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US-09-438-486-40
Sequence 40, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTGGGGTTTT 20
                         18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
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Best Local Similarity
Matches 20; Conserv
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Andrews, William H.
TITLE OF INVENTION: No. US20030044953Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor TTTY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 20; DB 5; Sest Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: 4Uhchown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 11-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America
                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKAL INFUGENTION:
APPLICANT: Cech, Thomas R.
Lingmer, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/10054295 Publication No. US20030044953A1 GENERAL INFORMATION:
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                                                                LENGTH: 48 base pairs
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TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 37:
                   INFORMATION FOR SEQ ID NO: 40
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                US-10-053-758-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-10-054-295-37
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TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
            REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 5; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                              LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California COUNTRY: United States of America
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FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
US-10-053-758-40
i Sequence 40, Application US/10053758
i Publication No. US20030032075A1
i GENERAL INFORMATION:
i APPLICANT: Cech, Thomas R.
i Information:
i Nakamura, Toru Chapman, Karen B.
Morin, Gragg B.
Harley, Calvin Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triregegiririegegirir 48
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
100.0%;
                                                                                                              TELEFAX: (415) 576-0
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                      US-10-053-758-37
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Gaps

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 48;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 5; L
100.0%; Pred No. 1.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1986
ATTORNEY/AGENT INFORMATION:
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

BESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-054-611-37
                                                                                                                                                                                                   Sequence 37, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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Chapman, Karen B.
Morin, Gregg B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-(1) INFORMATION FOR SEQ ID NO: 37
  20; Conservative
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Matches 20; Conservative
                                                                                                                                                                                   US-10-054-611-37
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  Matches
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                                                                                                                                                             Gaps
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                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews, William H.

TITLE OF INVENTION: No. US20030044953Alel Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
RADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIF: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
                                                                                                           Query Match
100.0%; Score 20; DB 5; 3
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 5; I
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-0an-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: CURROWN:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-054-295-40
                   DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
other nucleic acid
                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                            . Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
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Best Local Similarity
                                                              US-10-054-295-37
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US-10-054-295-40
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Gaps

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ZIP: 94111-3814

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFYCATION NUMBER: US/08/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 19-APR-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 11-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 11-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                  Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 20; DB 6; Length 48; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ייחבא אחנדים "hairpin primer" seq ID NO: 564:
US-10-325-810-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTTTGGGGTTTTGGGGTTTT 20
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                         Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
Nakamura, Toru
                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..48
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 20; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: -Unknown-
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 564, Application US/10325810
Publication No. US;0030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                              Sequence 40, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-325-810-564
                            US-10-054-611-40
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US-10-877-124-564
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                                                                                                                                 APPLICANT: Cech, Thomas R.

APPLICANT: Cingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION: 1..48
CUTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1997
APPLICATION WUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 0.2.Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: 4.UnKnown>
APPLICATION NUMBER: 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 2-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
                                                           Sequence 564, Application US/10877124; Publication No. US20040242529A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 564: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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US-10-877-022-564

| Sequence 564, Application US/10877022
| Publication No. US20040247613A1
| GENERAL INFORMATION:
| APPLICANT: Cech, Thomas R. Lingmer, Joachim Nakamura, Toru Chapman, Raren B. Morin, Gregg B. Harley, Calvin B. Andrews, William H. TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
  Length 48;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Jun-2004
CLASSIFICATION NUMBER: US/10/877,022
FILING DATE: CALMANOM
APPLICATION NUMBER: US/09/432,503
FILING DATE: CALMANOM
APPLICATION NUMBER: US/08/44,419
FILING DATE: CALMANOM
APPLICATION NUMBER: US/08/844,419
FILING DATE: S-APR-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WS/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WS/0PCT/US/97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WS/0PCT/US/97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WS/0PCT/US/97/17618
FILING DATE: 01-OCT-1997
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
  100.0%; Score 20; DB 8;
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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                                                                                                         1 TITIGGGGTTTTGGGGTTTT 20
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                                                      20; Conservative
Query Match
Best Local Similarity
Matches 20; Conserv
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TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                      ; incarion: 1..48; OTHER INFORMATION: /note= "hairpin primer"; SEQUENCE DESCRIPTION: SEQ ID NO: 564:
               ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 8; 1
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States of America
ZIP: 94111
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RAPLICATION NUMBER: US/09/843,676
FLING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
FILING DATE: 01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTTTGGGGTTTTTGGGGTTTT
                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-843-676-39
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Harley, Calvin B.
Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                        Score 20; DB 8; Length 48; Pred. No. 1.2e+02; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <UNKNOWn>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                  NAME/KEY:
LOCATION: 1..48
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: AUNKNOWN
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/915,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM FYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 564, Application US/10877146 Publication No. US20050013825A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                      1 TITIGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                        Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
    LENGTH: 48 base pairs
                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Hum
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                      MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                US-10-877-022-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 47
US-10-877-146-564
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                       US-09-438-486-39
, Sequence 39, Application US/09438486
; Publication No. US2003009019A1
; GENERAL INFORMATION:
                                                                                                                                                                                   1 TTTTGGGGTTTTGGGGTTTT 20
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020187471A1el Telomerase
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION NUMBER: 08/446,017
APPLICATION NUMBER: 08/446,017
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENTON NUMBER: 36,429
REFERENTON NUMBER: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 015389-002920US
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09766253 Publication No. US20020187471A1
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                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-C
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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US-09-766-253-39
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Gaps
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                                                                                                                                          Length 50;
                                                                                                                                                                                               Indels
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingmer, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1el Telomerase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATION
OPERATION
OPERATOR
OPERATOR
OPERATOR
SOFTWARE:
PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION S36
FILING DATE: 18-APR-1997
CLASSIFICATION S36
FILING DATE: 01-OCT-1996
CLASSIFICATION S36
ATTORNEY/AGENT INFORMATION:
FREERRENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION NUMBER: 015389-002931US
TELECOMMUNICATION NUMBER: 015389-002931US
TELECOMMUNICATION NUMBER: 015389-002931US
TELECOMMUNICATION NUMBER: 015389-002931US
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                    100.0%; Score 20; DB 3; I
ilarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco CITY: San Francisco STATE: California CAUNTAY: United States of America ZIP: 94111-3834
;
SEQUENCE DESCRIPTION: /desc = "DNA"
;
US-09-766-253-39
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; DESCRIPTION: /desc = "DNA"
US-09-438-486-39
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	Gaps
	0
Length 50;	Indels
Score 20; DB 3; Pred. No. 1.2e+02;	; Mismatches 0;
100.08;	tive 0
ilarity	20; Conservative
ch 1 Sim	20;
Query Match Best Local Similarity	Matches

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Search completed: February 16, 2006, 02:34:00 Job time: 294.248 secs

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Sequence:

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Searched:

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Sequence 465690,
Sequence 185950,
Sequence 185950,
Sequence 467314,
Sequence 665, App
Sequence 665, App
Sequence 67, App
Sequence 67, App
Sequence 67, App
Sequence 67, App
                                                         Sequence 565951,
Sequence 6025, A
Sequence 626220,
Sequence 62621,
Sequence 114338,
Sequence 13815,
Sequence 138215,
Sequence 626295,
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1 7 US-10-310-914A-238162 Sequence 2 7 US-10-310-914A-238201 Sequence 2 7 US-10-310-914A-628235 Sequence 2 7 US-10-310-914A-628236 Sequence	4.4 72.0 22 7 US-10-310-914A-626237 Sequence	4.4 72.0 23 7 US-10-310-914A-238202 Sequence	4.4 72.0 24 7 US-10-310-914A-565981 Sequence 4.4 72.0 25 7 US-10-310-914A-238163 Sequence	4.4 72.0 26 7 US-10-310-914A-138182 Sequence	4.2 71.0 19 7 US-10-310-914A-455340 Sequence	4.2 71.0 20 7 US-10-310-914A-208723 Sequence	4.2 71.0 20 7 US-10-310-914A-328480 Sequence	4.2 71.0 20 7 US-10-310-914A-621470 Sequence	4.2 71.0 20 7 US-10-310-914A-935090 Sequence	4.2 71.0 20 7 US-10-310-914A-1222900 Sequence	4.2 71.0 20 7 US-10-310-914A-1222903 Sequence	4.2 71.0 21 7 US-10-310-914A-111276 Sequence	4.2 /1.0 21 / US-10-310-914A-322150 Sequence 4.2 71.0 21 7 US-10-310-914A-328481 Sequence	4.2 71.0 21 7 US-10-310-914A-328482 Sequence	4.2 71.0 21 7 US-10-310-914A-348738 Sequence	4.2 71.0 21 7 US-10-310-914A-540890 Sequence	4.2 71.0 21 7 US-10-310-914A-621471 Sequence	4.2 71.0 21 7 US-10-310-914A-845458 Sequence	4.2 71.0 21 7 US-10-310-914A-845471 Sequence	4.2 /1.0 /2 / US-1U-31U-914A-844/4 Sequence	4.2 71.0 22 7 US-10-310-914A-445665 Sequence	4.2 71.0 22 7 US-10-310-914A-465262 Sequence	4.2 71.0 22 7 US-10-310-914A-549696 Sequence	4.2 71.0 22 7 US-10-310-914A-621472 Sequence	4.2 71.0 22 7 US-10-310-914A-845459 Sequence	4.2 71.0 23 7 US-10-310-914A-208735 Sequence	4.2 71.0 23 7 US-10-310-914A-208749 Sequence	4.2 71.0 23 7 US-10-310-914A-322142 Sequence	4.2 71.0 23 7 US-10-310-914A-322176 Sequence	4.2 71.0 23 7 US-10-310-914A-465292 Sequence	4.2 71.0 23 7 US-10-310-914A-467819 Sequence	4.2 71.0 23 7 US-10-310-914A-467906 Sequence	4.2 71.0 23 7 US-10-310-914A-845463 Sequence	4.2 71.0 23 7 US-10-310-914A-1035982 Sequence	4.2 71.0 24 7 US-10-310-914A-111296 Sequence	4.2 71.0 24 7 US-10-310-914A-348737 Sequence	4.2 71.0 24 7 US-10-310-914A-431969 Sequence	4.2 71.0 24 7 US-10-310-914A-465293 Sequence	4.2 71.0 24 7 US-10-310-914A-465676 Sequence	4.2 /1.0 24 / US-10-310-914A-490698 Sequence	4.2 71.0 24 7 US-10-310-914A-540871 Sequence	4.2 71.0 24 7 US-10-310-914A-621491 Sequence	4.2 71.0 24 7 US-10-310-914A-621493 Sequence	4.2 71.0 24 7 US-10-310-914A-1059987 Sequence	4.2 71.0 24 7 US-10-310-914A-1177640 Sequence	4.2 71.0 25 7 US-10-310-914A-111266 Sequence	4.2 71.0 25 7 US-10-310-914A-208725 Sequence	4.2 /1.0 25 / US-10-310-914A-490843 Sequence	4.2 71.0 25 7 US-10-310-914A-540891 Sequence	4.2 71.0 25 7 US-10-310-914A-621517 Sequence	4.2 71.0 25 7 US-10-310-914A-1107886 Sequence	4.2 71.0 25 7 US-10-310-914A-1222945 Sequence	4.2 /I.O 25 II US-II-IZI-049-55550/ Sequence 55550/,	4.2 /1.0 25 11 US-11-136-52/-15519 Sequence 15512, .	11:00 TT C2 07:10 TT C2 07:1 TT C3 07:10 T

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Sequence 596008, Application US/10310914A
Publication No. US/2006003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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| Publication No. US20060003322A1
| Publication No. US2006000332A1
| Publication No. US2006000332A1
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| TITLE OF INVENTION: uses thereof
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-67
                    FILE REPERENCE: C1039.700600301
CURRENT APPLICATION NUMBER: US/11/12,654
CURRENT FILING DATE: 2005-05-12
FRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
LENGTH: 20
  TITLE OF INVENTION: INFLAMMATORY DISEASES
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Best Local Similarity 90...
-hes 18; Conservative
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US-10-310-914A-596008
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Sequence 1056,
Sequence 1100961,
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Sequence 150268,
Sequence 150268,
Sequence 150271,
Sequence 15038,
Sequence 15038,
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Sequence 150272,
Sequence 714555,
Sequence 749740,
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Sequence 429786,
Sequence 522413,
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Sequence 429793,
Sequence 455404,
Sequence 622062,
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Sequence 714554,
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Sequence 7
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Sequence 9
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US-10-310-914A-429807

US-10-310-914A-727253

US-10-310-914A-727253

US-10-310-914A-727253

US-10-310-914A-347390

US-10-310-914A-543246

US-10-310-914A-5432346

US-10-310-914A-562535

US-10-310-914A-562535

US-10-310-914A-714531

US-10-310-914A-714531

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US-10-310-914A-7182520

US-10-310-914A-1182520

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US-10-310-914A-592413

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US-10-310-914A-562181

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Sequence 67, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC RESULT 1 US-11-127-654-67

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Sequence 138179, Application US/10310914A

Sequence 138179, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOOTWARE: Patentin version 3.3

SEQ ID NO 138179
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich. Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CFUSOI
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 138168
LENGTH: 21
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94.4%; Pred. No. 1.7e+02;
ive 0; Mismatches 1;
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Pred. No. 1.7e+02;
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Best Local Similarity 94.4
Matches 17; Conservative
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Best Local Similarity 94.4
Matches 17; Conservative
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US-10-310-914A-138179/c
                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138168
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ORGANISM: Human
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Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

CURRENT PELING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARKE: PatentIn version 3.3

SEQ ID NO 596011
                                                                                                                                                                                                                            RESULT 4

US-10-914A-596068/C

US-10-310-914A-596068/C

US-10-310-914A-596068 Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200. CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILE NOS: 1388402

SOSTWARE: PATENTIN version 3.3
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                                                               Length 24;
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Pred. No. 1.2e+02;
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                                                                                                  2; Indels
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                                                              Score 16.8; DB 7;
Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
0; Mismatches 2;
                                                  84.0%; scc.
90.0%; Pred. No. ...
0; Mismatches
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US-10-310-914A-138168/c
; Sequence 138168, Application US/10310914A
                                                                                                                                       1 TTTTGGGGTTTTGGGGTTTT 20
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90.0%;
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90.0%;
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Best Local Similarity 90.09
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Best Local Similarity 90.0
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Best Local Similarity 90.0
Matches 18; Conservative
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US-10-310-914A-596011/c
       ; ORGANISM: Human
US-10-310-914A-185978
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ORGANISM: Human
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ORGANISM: Human
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LENGTH: 25
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APPLICANT: Bentwich, Isaac
APPLICANT: Biler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION VNDHER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 138196
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 227183, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 227183
LENGTH: 24
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Publication No. US20060003322A1
FURDRATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 138229
LENGTH: 25
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Pred. No. 1.7e+02;
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94.4%; Pred. No. 1...
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94.4%;
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Best Local Similarity 94.4
Matches 17; Conservative
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US-10-310-914A-227183/c
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  GENERAL INFORMATION:
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; ORGANISM: Human
US-10-310-914A-138229
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                                                                                                                                                                                                                                                                                       ORGANISM: Human
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ORGANISM: Human
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: USes thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                           Length 22;
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                                                                                       1; Indels
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                                         Query Match
82.0%; Score 16.4; DB 7;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1;
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Pred. No. 1.7e+02;
0; Mismatches 1;
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US-10-310-914A-138196/c
; Sequence 138196, Application US/10310914A
; Publication No. US20060003322A1
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Best Local Similarity 94.4%;
Matches 17; Conservative (
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Best Local Similarity 94.4%;
Matches 17; Conservative (
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US-10-310-914A-138228/c
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US-10-310-914A-138180/c
US-10-310-914A-138179
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LENGTH: 22
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LENGTH: 23
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Sequence 271479, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000332A1
Publication No. US2006000332A1
Publication No. US2006000332A1
Publication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
TITLE OF INVENTION: uses 10202-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 271479
LENGTH: 21
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TITLE OP INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING OF A STRAIN DISPOSED ON AN ITILE OF INVENTION: ABSORBENT CARRIER FILE OF INVENTION: ABSORBENT CARRIER FILE REPRESENCE: 023131.41500

FILE REPRESENCE: 023131.41500

CURRENT APPLICATION NUMBER: US/11/170,693

CURRENT FILING DATE: 2005-06-29

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2001-09-04

PRIOR FILING DATE: 2005-03-08

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 39

LENGTH: 20
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Pred. No. 3e+02;
0; Mismatches 2; Indels
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US-10-310-914A-1342346/c
; Sequence 1342346, Application US/10310914A
; Publication No. US20060003322A1
; PUBLICATION:
; APPLICANT: Bentwich, Isaac
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(20)

CTHER INFORMATION: Forward Primer
US-11-170-693-39
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mus sp.
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ORGANISM: Human
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICATION WIGHER:
APPLICATION WIGHER:
INSTANCE: 06087, 0200. CPUS01
CURRENT APPLICATION WIGHER:
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 138236
LENGTH: 26
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         82.0%; Score 16.4; DB 7; Length 25; 94.4%; Pred. No. 1.8e+02;
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                                                 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%; Score 16.4; DB 7;
94.4%; Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
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                                                 0; Mismatches
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                                                                                      3 TIGGGGTTTIGGGGTTTT 20
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94.4%;
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Best Local Similarity 94.4°
                                                 17; Conservative
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Matches 17; Conservative
           Query Match
Best Local Similarity
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US-10-310-914A-138236/c
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US-11-170-693-39/c
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                                                 Matches
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Sequence 114323, Application US/10310914A
| Publication V. US2006000332A1
| General INFORMATION: US2006000332A1
| GENERAL INFORMATION: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| TITLE REFERENCE: 06087.0200.CPUS01
| TITLE REFERENCE: 06087.0200.CPUS01
| CURRENT APPLICATION WUMBER: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: ParentIn version 3.3
| SEQ ID NO 1143293
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Publication No. US20060003322A1

GENERAL INFORMATION.

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION WUBBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 844567

LENGTH: 24
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
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89.5%; Pred. No. 3.1e+02;
iive 0; Mismatches 2;
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      2 TTTGGGGTTTTGGGGTTTT 20
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Best Local Similarity 36.8
Matches 7; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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US-10-310-914A-1143293/c
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US-10-310-914A-271527/c
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US-10-310-914A-844567
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION:
Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
STATLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 626126
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                             Length 22;
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89.5%; Pred. No. 3.1e+02;
iive 0; Mismatches 2;
FILE REFERENCE: 06087.0200.CPUS01
CURRENT PAPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1342346
LENGTH: 22
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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US-10-310-914A-626125/c
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                                                                                                                                                                                                            TYPE: RNA
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US-10-310-914A-565951/C

US-10-310-914A-565951, Application US/10310914A

Sequence 565951, Application US/10310914A

Sequence 565951, Application US/10310914A

FULLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: USes thereof

TITLE OF INVENTION: USes thereof

FILE REFERENCE: 06087-0200. CFUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 565951

LENGTH: 27
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US-10-310-914A-626220/c
US-10-310-914A-626220/c
Sequence 626220, Application US/10310914A
Sequence 626220, Application No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
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; Publication No. US20060024715A1
; General No. US20060024715A1
; General INFORMATION:
; APPLICANT: Affymetrix. Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REPERENCE: 3690.1
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR PILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 60025
; LENGTH: 50
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Pred. No. 3.3e+02;
0; Mismatches 2;
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Pred. No. 3.1e+02;
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1 UUUUGGAUUUCGGGGUUU 19
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Human
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US-11-175-859-60025
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Sequence 271489/C

Sequence 271489, Application US/10310914A

Sequence 271489, Application US/10310914A

Publication No. US20060003322A1

Publication No. US20060003322A1

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PATENTIN version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 644566, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                                                                        Score 15.8; DB 7;
Pred. No. 3.1e+02;
0; Mismatches 2;
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  CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 271527
LENGTH: 25
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36.8%;
                                                                                                                                                                                                                           Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 30.0.
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Best Local Similarity 8>...
Local 17; Conservative
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US-10-310-914A-844568
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                                                                                                                                                            ORGANISM: Human
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LENGTH: 26
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Sequence 626141, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
GENERAL GENERAL GENERAL
TITLE OF INVENTION:
USES THEREOFY
TITLE OF INVENTION:
USES THEREOFY
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 626141
LENGTH: 20
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Publication No. US20060003322A1
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT FAPLICATION UNDER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 138178
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
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Pred. No. 4.4e+02;
0; Mismatches 1; Indels
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Pred. No. 4.4e+02;
0; Mismatches 1;
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                               19 TGGGGTTTTGGGGGTTT 3
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 94.1%;
Matches 16; Conservative
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US-10-310-914A-138178
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich. Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USes thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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| Publication No. US20060003322A1
| Publication No. US2006000332A1
| GENERAL INPORMATION:
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| FILE REFERENCE: 06087.0200.CPUS01
| CURRENT APPLICATION UNGBER: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 114338
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77.0%; Score 15.4; DB 7; Length 19;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.0%; Score 15.4; DB 7; Length 19; 94.1%; Pred. No. 4.4e+02; ive 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
               CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 626220
LENGTH. 10
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Best Local Similarity 94.1
Matches 16; Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
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US-10-310-914A-1143338/c
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US-10-310-914A-626221/c
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; ORGANISM: Human
US-10-310-914A-1143338
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US-10-310-914A-626221
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LENGTH: 19
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4 TGGGGTTTTGGGGTTTT 20

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Sequence 1143370, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1143370
LENGTH: 25
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APPLICANT: Hakonason, Hakon

APPLICANT: Halapi, Eva

APPLICANT: Halapi, Eva

TITLE OF INVENTION: METHODS OF DIAGNOSIS AND TREATMENT FOR

TITLE OF INVENTION: ASSCIATION

FILE REFERENCE: 2345.2044-003

CURRENT APPLICATION NUMBER: US/11/043,752

CURRENT APPLICATION NUMBER: US/11/043,752

CURRENT FILING DATE: 2005-01-26

PRIOR PILING DATE: 2004-07-14

PRIOR FILING DATE: 2004-07-14

PRIOR FILING DATE: 2004-07-14

PRIOR FILING DATE: 2004-04-05

NUMBER OF SEQ ID NOS: 4326

SOFTWARE: FastSEQ for Windows Version 4.0

LEADTH: 20

LEADTH: 20
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85.0%; Pred. No. 5.3e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.0%; Score 15.4; DB 7; 94.1%; Pred. No. 4.5e+02;
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Publication No. US20060014165A1
GENERAL INFORMATION:
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Matches 16; Conservative
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   24 TGGGGTTTTGGGGGTTT
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                 RESULT 36
US-10-310-914A-1143370/c
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US-10-310-914A-84509/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Human
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US-10-310-914A-626295/C
US-10-310-914A-626295/C

; Sequence 626295, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOPTWARE: Patentin version 3.3
; SEQ IDN 06 526295
. LENGTH: 25
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL G
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                                                                                                                                                                                                                                                                                                        77.0%; Score 15.4; DB 7; Length 25; 94.1%; Pred. No. 4.5e+02; ive 0; Mismatches 1; Indels
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CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 138235
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TGGGGTTTTGGGGTTTT 20
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 94.1
Matches 16; Conservative
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US-10-310-914A-626296/c
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US-10-310-914A-675377, Application US/10310914A

Sequence 675377, Application US/10310914A

Sequence 675377, Application US/10310914A

Publication No. US2060003322A1

GRNERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses 105/10/310,914A

CURRENT APPLICATION WUMBER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 675377

LENGTH: 21

LENGTH: 21
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, 1800
TITLE OF INVENTION: Uses thereof
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Pred. No. 5.3e+02;
0; Mismatches 3;
Score 15.2; DB 7;
Pred. No. 5.3e+02;
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Pred. No. 5.3e+02;
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0; Mismatches 3
                                         0; Mismatches
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US-10-310-914A-238142/c
; Sequence 238142, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                   1 TITIGGGTTTTGGGGTTTT 20
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0%;
Matches 17; Conservative
Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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US-10-310-914A-1222901
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US-10-314A-622070/C

US-10-310-914A-622070/C

US-10-310-914A-622070, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200. CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PARENTIN version 3.3
          APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE DETERRANCE: 06607.0200.CPUSOI
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: Patentin version 3.3
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Pred. No. 5.3e+02;
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85.0%; Pred. No. 5.3e+02;
iive 0; Mismatches 3;
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85.0%; Pred. No. 5...
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Best Local Similarity 85.0
Matches 17; Conservative
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Matches 17; Conservative
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CRGANISM: Human
US-10-310-914A-622070
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                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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LENGTH: 21
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% Sequence 282917/c
% Sequence 282917/c
% Sequence 282917, Application US/10310914A
% Publication No. US20060003322A1
% Fublication No. US2006000332A1
% GENBEAL INRORATION:
% APPLICANT: Shiler, Kvuzat
% APPLICANT: Shiler, Kvuzat
% APPLICANT: Shiler, Kvuzat
% APPLICANT: Bandwinch, Isaac
% APPLICANT: Shiler, Kvuzat
% APPLICANTON: uses thereof
% FILE REFERENCE: 06087.0200.CPUS01
% CURRENT APPLICATION UNBER: US/10/310,914A
% CURRENT FILING DATE: 2002-12-06
% NUMBER OF SEQ ID NOS: 1388402
% SOFTWARE: Patentin version 3.3
% SOFTWARE: Patentin version 3.3
% SEQ ID NO 282917
LENGTH: 23
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: USES thereof
TITLE OF INVENTION: USES thereof
CURRENT APPLICATION UNMERS: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 465697
LENGTH: 23
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                                                3; Indels
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76.0%; Score 15.2; DB 7;
85.0%; Pred. No. 5.4e+02;
:ive 0; Mismatches 3;
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Pred. No. 5.4e+02;
0; Mismatches 3;
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                                                                                         1 TITIGGGGTTTTGGGGTTTT 20
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85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
    Query Match 76.0
Best Local Similarity 85.0
Matches 17; Conservative
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US-10-310-914A-465697/c
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; ORGANISM: Human
US-10-310-914A-465697
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ORGANISM: Human
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US-10-314A-465689/c

US-10-310-914A-465689/c

US-10-310-914A-465689/c

Sequence 465689, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 465689
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Sequence 122898, Application US/10310914A

Sequence 122898, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bantwich, Isaac
APPLICANT: Bailer, Kuzat
APPLICANT: Bilier, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.cPUS01
CURRENT APPLICATION UNDER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SOFTWARE: LENGTH: 22
                         APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Baioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                     Length 22;
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Pred. No. 5.4e+02;
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85.0%; Pred. No. so.
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Best Local Similarity 85.03
Matches 17; Conservative
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Matches 17; Conservative
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                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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RESULT 49
US-10-310-914A-651609/C
US-10-310-914A-651609/C
Sequence 651609, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000332A1
Publication No. US2006000332A1
PAPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USES thereof
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200. CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SSEQ ID NO 651609
LENGTH: 23
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Baloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Baloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 501657
LENGTH: 23
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US-10-914A-675445/c
US-10-910-94A-675445/c

i Sequence 675445, Application US/10310914A

i Sequence 67545, Application US/10310914A

i GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

i APPLICANT: Shiler, Kuzat

TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
CURRENT PELLACATE: 06097.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PAECHIL OF VERSION 3.3
SOFTWARE: PAECHIL OF VERSION 3.3
LENGTH: 23
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76.0%; Score 15.2; DB 7; Length 23;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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Best Local Similarity
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; ORGANISM: Human
US-10-310-914A-501657
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Query Match

Gaps ö Best Local Similarity 85.0%; Pred. No. 5.4e+02; Matches 17; Conservative 0; Mismatches 3; Indels Search completed: February 16, 2006, 02:52:56 Job time : 188.446 secs 1 TTTTGGGGTTTTGGGGTTTT 20 ð В

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us-09-669-187a-80.szlm50.rge

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VERSION AX103888.1 GI:13920085 KEYWORDS SOURCE SOURCE SYnthetic construct ORGANISM synthetic construct ORGANISM synthetic construct other sequences; artificial sequences.  AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C. TATTLE TAUTHORS Immunostimulatory nucleic acids JOURNAL Patent: WO 0122972-A 80 05-APR-2001; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical GmbH (DE) GmbH (DE) FRATURES I. 19 FRATURES I. 19 // Coganism="synthetic construct" // Mol type="unassigned DNA" // Mol type="unassigned DNA"	Oxigin  Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 1.38+02;  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 GGGGTGACGTTCAGGGGG 19  Db 1 GGGGTGACGTTCAGGGGG 19	AX355419 Sequence 4 AX355419 AX355419.1 Synthetic	ORGANISM synthetic construct  Other sequences, artificial sequences.  REFERENCE 1 AUTHORS Weiner, G. and Hartmann, G. TITLE Methods for enhancing antibody-induced cell lysis and treating cancer JOURNAL Patent: WO 0197843-A 447 27-DEC-2001; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) FEATURES Location/Qualifiers source 119		cal Similarity 100.0%; i 19; Conservative 0; 1 GGGTGACGTTCAGGGGGG 1	RESULT 3 AX546941 LOCUS LOCUS DEFINITION Sequence 80 from Patent WO02053141. ACCESSION AX546941 VERSION AX546941.1 GI:25812085 KEYWORDS SOURCE SOURCE ORGANISM Synthetic construct ORGANISM synthetic construct other sequences; artificial sequences.
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synthetic construct synthetic construct other sequences; artificial sequences.

REFERENCE

AX103888 19 bp Sequence 80 from Patent WO0122972. AX103888

RESULT 1
AX103888
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PAT 01-MAR-2003
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02051141-A 82 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
                                                                                              Query Match 91.6%; Score 17.4; DB 6; I Best Local Similarity 94.7%; Pred. No. 8e+02; Matches 18; Conservative 0; Mismatches 1;
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94.7%; Pred. No. 8e+02;
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Patent: US 6008200-A 1 28-DEC-1999;
Location/Qualifiers
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AX546943
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Immunostimulatory nucleic acids
Breant: WO 0122972-A 82 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DB)
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100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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ilarity 94.7%; Pred. No. 8e+02;
Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="Synthetic Sequence"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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/mol_type="unassigned DNA"

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Bratzler, R. L.
Inhibition of angiogenesis by nucleic
Patent: WO 02053141-A 80 11-UUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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Sequence 448 from Patent W00197843.
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Sequence 82 from Patent WO0122972.
AX103890
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AX355420
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 224 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
Vectors and methods for immunization or therapeutic protocols Patent: US 6821957-A 63 23-NOV-2004; University of Iowa Research Foundation; Iowa City, IA Location/Qualifiers
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74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels
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Immunomodulatory oligonucleotides
Parent: EP 1167377-A 1 02-JAN-2002;
THE UNIVERSITY OF IOWA RESEARCH FOUNDATION
Location/Qualifiers
                                                                                                                                                                                                       74.7%; Score 14.2; DB 6;
84.2%; Pred. No. 3.2e+04;
iive 0; Mismatches 3;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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    forganism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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other sequences; artificial sequences.
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Sequence 224 from Patent W00122972.
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Sequence 1 from Patent EP1167377.
AX342378
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 84.2
Matches 16; Conservative
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Unclassified.
1 (bases 1 to 20)
1 (bases 1 to 20)
Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
Vectors and methods for immunization or therapeutic protocols
Patent: US 6339068-A 63 15-JAN-2002;
Location/Qualifiers
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Unclassified.
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Krieg,A.M., Davis,H.L., Wu,T. and Joachim,S.
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Pred. No. 3.2e+04;
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/wol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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AR607454
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Sequence 63 from patent US 6339068.
AR182891
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Sequence 1 from patent US 6194388
AR135030 GI:14123935
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    GGGTCAACGTTCAGGGGGG 20
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AR135030
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
                                                                                                                                    Methods for enhancing antibody-induced cell lysis and treating
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 224 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
                                                                                                                                                                  Patent: WO 0197843-A 449 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Synthetic Sequence"
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Sequence 18 from patent US 6566500.
AR337615
AR337615.1 GI:33724001
 Seguence 449 from Patent WO0197843.
                                                                                                                       Weiner, G. and Hartmann, G.
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AX355421.1 GI:18620089
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AR337615/c
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Patent: BP 1167379-A 1 02-JAN-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Patent: BP 1167379-A 1 02-JAN-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Pred. No. 3.2e+04;
0; Mismatches 3;
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    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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/db_xref="taxon:32630"
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other sequences; artificial sequences.
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Sequence 1 from Patent EP1167379.
AX342405
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Seguence 1 from Patent EP1167378.
AX342438
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Best Local Similarity 84.2%;
Matches 16; Conservative
84.2%;
 Best Local Similarity 84.2
Matches 16; Conservative
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PAT 05-OCT-2002
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                             Query Match 70.5%; Score 13.4; DB 6; Length 30; Best Local Similarity 93.3%; Pred. No. 7.9e+04; Matches 14; Conservative 0; Mismatches 1; Indels
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Patent: WO 02052044-A 6462 04-JUL-2002;
Riken (JP)
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Patent: WO 02052044-A 313 04-JUL-2002;
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Sequence 6462 from Patent W002052044.
AX520264 GI:23570800
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/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="cysMR"
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the generation or modification of metabolic pathways
Patent: WO 2004076659-A 21 10-SBP-2004;
Metabolic Explorer (FR)
Location/Qualifiers
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Zink, O.
                                                                                                                                                                                                                                                             Gaps
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            Vitetta, E.S., Ghetie, V.F., Smallshaw, J. and Baluna, R.G. Vitetta, E.S., Ghetie, V.F., Smallshaw, J. and Baluna, R.G. Compositions and methods for modifying toxic effects of proteinaceous compounds
Patent: US 656500-A 18 20-MAY-2003;
Board of Regents, The University of Texas System; Austin, TX Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 22)
Ulanovsky,L. and Raja,M.C.
Nucleic acid amplification using modular branched primers
Patent: US 6197556-A 5 06-MAR-2001;
Location/Qualifiers
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 21 from Patent WO2004076659.
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 5 from patent US 6197556.
AR137717.1 GI:14479226
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/organism="unknown"
/mol_type="genomic DNA"
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CQ874726.1 GI:52747896
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/db xref="taxon:33630"
/noFe="Syntheric oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
                                                                                                         Weiner, G. and Hartmann, G. Methods for enhancing antibody-induced cell lysis and treating
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83.3%; Pred. No. 1e+05;
iive 0; Mismatches 3; Indels
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Patent: WO 0197843-A 423 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol type="unassigned DNA"
DA xref="taxon:32630"
/note="Synthetic oligonucleotide
phosphorodithioate backbone"
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83.3%; Pred. No. 1e+05;
iive 0; Mismatches 3;
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Sequence 521 from Patent WO02053141.
AX547382
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AX355395.1 GI:18620063
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 524 05-APR-2001,
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
                                                                                                                                                                                                                                                  Krieg,A.M., Schetter,C. and Vollmer,J.C.
Immunostimulacory nucleic acids
Patent: WO 0122972-A 521 05-ABR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
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|db_xref="taxon:32630"

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/db_xref="taxon:32630"
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Sequence 521 from Patent WO0122972.
AX104329
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Sequence 524 from Patent WO0122972.
AX104332. GI:13920529
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PAT 25-NOV-2003
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83.3%; Pred. No. 1e+05;
live 0; Mismatches 3; Indels
                                                                                                                               Length 32;
1. .32
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="bescription of artificial sequence: Oligonucleotide"
                                                                                                                                                                                                                                                                                                                  linear
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Novel anti-IGF-IR antibodies and uses thereof
Patent: WO 03059551-A 97 24-JUL-2003;
PIERRE FABRE MEDICAMENT (FR)
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/organism="synthetic construct"
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/db_xref="texon:32630"
/note="Oligonucleotide"
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Humanization of antibodies
Patent: WO 2005042743-A 463 12-MAY-2005;
                                                                                                                             Score 13.2; DB 6
Pred. No. 1e+05;
0; Mismatches
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CS087335
CS087335.1 GI:66712784
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other sequences; artificial sequences.
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Sequence 97 from Patent WO03059951.
AX805700
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                                                                                                                               ch 69.5%;
1 Similarity 83.3%;
15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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Best Local Similarity
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Location/Qualifiers
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                                         Inhibition of angiogenesis by nucleic acids Inhibition of angiogenesis by nucleic acids Patent: WO 02053141-A 521 11-JUL-2002; Coley Pharmaceutical Group, Inc. (US)
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/db_xref="texon:32630"
/note="Synthetic Sequence"
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other sequences; artificial sequences.
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Sequence 97 from Patent WO2005058967.
CS121639
                  other sequences; artificial sequences
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Sequence 524 from Patent WO02053141.
AXS47385
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CS121639
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Patent: WO 02008453-A 180 31-JAN-2002;
Phase-1 Molecular Toxicology (US)
Location/Qualifiers
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/noTe="Primers"
                                                                                                                                                            Dall-Acqua,W., Damschroder,M. and Wu,H.
Humanization of antibodies
Patent: WO 2005042743-A 505 12-MAY-2005;
Medimmune, Inc. (US)
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             CSO87377 47 bp DNA Sequence 505 from Patent WO2005042743.
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CQ827797.1 GI:49456213
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                                                               CS087377.1 GI:66712826
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                  Indels
 Pred. No. 9.9e+04;
0; Mismatches 3;
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Humanization of antibodies
Patent: WO 2005042743-A 466 12-MAY-2005;
Medimmune, Inc. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="Primers"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primers"
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Humanization of antibodies
Patent: WO 2005042743-A 504 12-MAY-2005;
MedImmune, Inc. (US)
Location/Qualifiers
                                                                                                                                                           Sequence 466 from Patent WO2005042743.
CS087338
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Disease risk estimating method using sequence polymorphisms in
specific region of chromosome 19
Patent: WO 200403229-A 57 08-3M-2004;
Aarhus University (DK); Arbejdamilj Instituttet (National
Institute of Occupational Health) (DK)
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Method for purifying Keratinocyte growth factors
Patent: EP 133,981-A 26 13-AUG-2003;
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                                                              ch 67.4%; Score 12.8; DB 6; 1 Similarity 87.5%; Pred. No. 1.6e+05; 14; Conservative 0; Mismatches 2;
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/noTe="Probe"
/db_xref="taxon:9606"
/note="CD90 antisense primer"
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synthetic construct
other sequences; artificial sequences.
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Sequence 57 from Patent WO2004003229.
CQ760615.
CQ760615.1 GI:44904118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 26 from Patent EP1334981.
AX814043
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                                                                                                                                4 GTGACGTTCAGGGGGG 19
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Kamboj,R. and Nutt,S.
Glutamate receptor (or EAA receptor) polynucleotides and their uses
Patent: US 6136544-A 29 24-0CT-2000;
Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Compositions comprising muscle progenitor cells and uses thereof
Patent: WO 2004012503-A 47 12-FEB-2004;
Tigenix N.V. (BE)
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                                                                                                                            /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
                         Dawn,C.
Replication protein
Patent: WO 2004051269-A 20 17-JUN-2004;
Yorkshire Cancer Research (GB)
Location/Qualifiers
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 other sequences; artificial sequences
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AR135661
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    .20
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"

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Matches 14; Conservative
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1 (bases 1 to 32)
Koziel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V.,
Wright,M.S., Launis,K.L., Rothstein,S.J., Bowman,C.G., Dawson,J.L.,
Dunder,E.M., Pace,G.M. and Suttie,J.L.
Synthetic DNA sequence having enhanced insecticidal activity in
maize
              PAT 29-SEP-1999
                                                                                                                                            Cases 1 to 32)
Koziel, M.G., Desai, N.M., Lewis, K.S., Warren, G.W., Evola, S.V.,
Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L., Bowman, C.G.,
Dawson, J.L., Dunder, E.M., Pacc, G.M. and Suttie, J.L.
Synthetic DNA sequence having enhanced activity in maize
Patent: Location/Qualifiers
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    .32
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/mol_type="unassigned DNA"

    .32
/organism="unknown"
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       32 bp
Sequence 43 from patent US 5859336.
AR029533
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Sequence 43 from patent US 6075185.
AR098486
AR098486.1 GI:12807743
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                               Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.
Disease risk estimating method using sequence polymorphisms in a specific region of chromosome 19
aptent: WO 2004,003229-A 139 08-JAN-2004;
Aarhus University (DK); Arbejdsmilj Instituttet (National Institute of Occupational Health) (DK)
Location/Qualifiers
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Human single nucleotide polymorphisms
Patent: wO 0166800-A 1698 13-SEP-2001;
WHITEHERAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probe"
                                                                                                          Sequence 139 from Patent WO2004003229. CQ760697
                                                                                                                                                                                                                                   other sequences; artificial sequences.
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Sequence 1698 from Patent WO0166800.
AX249619
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/db_xref="taxon:9606"

    .31
    /organism="Homo sapiens"

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CQ760697.1 GI:44904200
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AX249619/c
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PAT 06-JUL-2002

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                                                            Length 32;
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Detection of genetic polymorphisms
Patent: WO 02052044-A 822 04-JUL-2002;
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1.6e+05;
ches 2;
                                                                                                                            67.4%; Score 12.8; DB 6;
llarity 87.5%; Pred. No. 1.6e+05;
Conservative 0; Mismatches 2;
 1. .32
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="primer P5(a)"
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/mol type="unassigned DNA"
/mol type="unassigned"
/note="primer P5(a)"
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Sequence 822 from Patent WO02052044.
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Patent: BP 1213356-A 43 12-JUN-2002;
Syngenta Participations AG (CH)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX453908
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Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W., Pevola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L., Rothstein, S.J., Bowman, C.G., Dawson, J.L., Dunder, E.M., Pace, G.M. and Suttie, J.L., Synthetic JNA sequence having enhanced insecticidal activity in maize
Patent: US 5625136-A 43, 29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W., Evola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L. and Rothstein, S.J.
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Transgenic maize seed and method for controlling insect pests Patent: US 6720488-4 31 31-APR-2004;
Syngenta Investment Corporation; Wilmington, DE
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Pred. No. 1.6e+05;
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Location/Qualifiers
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Patent: EP 1209237-A 43 29-MAY-2002;
Syngenta Participations AG (CH)
Location/Qualifiers
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Sequence 43 from Patent EP1209237.
AX441412
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87.5%;
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AX441412/c
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PAT 05-OCT-2002

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Search completed: February 15, 2006, 18:55:32 Job time: 469.843 secs
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                                                                                                                                                                                                                                                                                                                                   Planomicrobium okeanokoites
Planomicrobium okeanokoites
Planomicrobium okeanokoites
Bacteria; Firmicutes; Bacillales; Planococcaceae; Planomicrobium.
1 (bases 1 to 50)
Sugisaki, H. and Kanazawa, S.
New restriction endonucleases from Flavobacterium okeanokoites
(FokI) and Micrococcus luteus (MluI)
Gene 16 (1-3), 73-78 (1981)
6282705
Original source text: Fokeanokoites DNA, clone pAO43.
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Planomicrobium okeanokoites
Bacteria; Firmicutes; Bacillales; Planococcaceae; Planomicrobium.
1 (bases I to 50)
Sugisaki,H. and Kanazawa,S.
New restriction endonucleases from Flavobacterium okeanokoites
(FokI) and Micrococcus luteus (MluI)
Gene 16 (1-3), 73-78 (1981)
6282705
Original source text: Fookeanokoites DNA, clone pAO43.
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Flavobacterium okeanokoites Fokl cleavage site F2/F7.
M18006.1 GI:148700
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Flavobacterium okeanokoites FokI cleavage site F7/F1.
M18007 M10381
M18007.1 GI:148701
                             ch 67.4%; Score 12.8; DB 6; Length 41; 1 Similarity 77.8%; Pred. No. 1.6e+05; 14; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.4%; Score 12.8; DB 1; Length 50; Best Local Similarity 87.5%; Pred. No. 1.6e+05; Matches 14; Conservative 0; Mismatches 2; Indels
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/organism="Planomicrobium okeanokoites"
/mol_type="genomic DNA"
/db_xref="taxon:244"
26 bp_upstream of FokI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .50 / Corganism="Planomicrobium okeanokoites" / Organism="Planomicrobium okeanokoites" / / Mol_LYpe="genomic DNA" / / db xref="taxon:244" / db vpstream of Fokl site.
                                                                                                             1 GGGGTGACGTTCAGGGGG 18
                                                                                                                                   29 GGGGTGACKAGCTGGGGG 12
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Best Local Similarity
                                                                                                                                                                                                       RESULT 49
FVBFOKIB/c
LOCUS
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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FVBFOKIC
LOCUS
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COMMENT
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COMMENT
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TITLE
                                                                       Matches
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ORIGIN
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4 GTGACGTTCAGGGGGG 19

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Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; tungal infection; cancer; asthma; infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.

Immunostimulatory nucleic acid #71.

(first entry)

12-JUN-2001

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Adc12469 Human sec
Add036024 Human sec
Add03606 Human sec
Add34658 Human sec
Add5341 Human sec
Add5341 Human sec
Add5341 Human sec
Add57303 Human sec
Ade73038 Human sec
Ade73038 Human sec
Ade73403 Human sec
Ade73403 Human sec
Add673404 Human sec
Add673402 Human sec
Add73402 Human sec
Add73403 Human sec
Add673478 Human sec
Add6854 Human sec
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Add6855 Human sec
Add6865 Human sec
Add6866 Human sec
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Add60137 Human sec
Add60054 Human sec
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AAX52415
AAC58429
ADC78545
AAF72573
AAC97459
ADC12469
ADD05024
ADD04030
                         ADI38120
ACA59081
ACA58478
ADJ26388
                                          ADE79303
ADE79727
ADE73403
                                                      ADE73938
ADE99492
ADE98611
ADE99038
ADG40508
ADF73902
                                                                                    ADG92321
ADG92748
                                                                                             ADH20537
ADH07392
                                                                                                         ADH06965
ADI18707
                                                                                                                 ADH97486
ADI65854
ADH60597
ADJ99654
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ADE99238
ADG40708
ADG92521
ADG92948
ADH20737
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ADI18907
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ADJ26588
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ADH60137
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ADI66054
                                                                                                      ADH59937
                                                                                                                                   ADL08847
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Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.

Krieg AM, Schetter C, Vollmer J;

WPI; 2001-273485/28

(IOWA ) UNIV IOWA RES FOUND. (COLE-) COLEY PHARM GMBH.

99US-0156113P

25-SEP-1999;

25-SEP-2000; 2000WO-US026383

WO200122972-A2.

Synthetic.

05-APR-2001

27-SEP-1999; 99US-0156135P. 23-AUG-2000; 2000US-0227436P.

Disclosure; Page 40; 338pp; English.

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulate and immunostimulate and immunostimulates. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, rampylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi to a Thi immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 4; Length 19; 100.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibitory oligonucleotide #80.
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Best Local Similarity 100.
Matches 19; Conservative
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ABS77596
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Gaps ö

ALIGNMENTS

AAF98955 standard; DNA; 19 BP AAF98955

AAF98955; SXXX

RESULT 1

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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, breat cancer, connect, cervical cancer, colon and rectum cancer, connective tissue cancer, cesophageal cancer, elon and rectum cancer, connective tissue cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
                                                                                                                                                               cancer, such as basal cell carcinoma, comprises
                                                                                                                                                                                  Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory, antiinflammatory, dermatological; antipsoriatic; antiulcer; gene therapy, vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 6; Length 19; 100.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
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0
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                                                                                                                                                                                                                                                                                                 Disclosure; Page 208; 312pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunostimulatory nucleic acid #74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the invention
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  22-JUN-2000; 2000US-0213346P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2002; 2002US-00112653.
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                                             (IOWA ) UNIV IOWA RES FOUND
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                                                                                            Hartmann G;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                       developing cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                               Weiner G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 administering at least one antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted anglogenesis. The method is useful for inhibiting anglogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, myocardial anglogenesis, plaque neovascularisation, telanglectasia, haemophiliac joints, anglofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is an antianglogenic nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 6; Length 19; 100.0%; Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 21; 276pp; English
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                                                                                                                                                                                                                                                                                                                                              (COLE-) COLEY PHARM GROUP INC
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                                                                                                                                                                                                                                                       14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                                    14-DEC-2000; 2000US-025534P
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention
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                                                                                                                                                                                                                                                                                                                                                                                            Bratzler RL;
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                                                                                                                    Synthetic
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19; Conservative
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                                                                                                                                                                                                                                                                                                             25-NOV-2004
                                                                                                                                                                                                                                                                 Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G mucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responative subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                 The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermetitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colltis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
 eczema
                                                                                                                                                                                                                             Gaps
        allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
Treating non-allergic inflammatory diseases, such as psoriasis,
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                    DB 9; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 9; Length 19; 100.0%; Pred. No. 18;
                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                              Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                     100.0%; Score 19; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fouron Y;
                                             Disclosure; Page 10; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid #71
                                                                                                                                                                                                                                                     1 GGGTGACGTTCAGGGGG 19
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                                                                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                             19; Conservative
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(PETE/) PETERSEN D
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                                                                                                                                                                                                                 Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                              ADB36457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; baccerial infection; viral infection.
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Pred. No. 18;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allergic response suppressor oligonucleotide #80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, SEQ ID NO 80; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of an immunostimulatory nucleic acid.
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                                                                  1 GGGGTGACGTTCAGGGGGG 19
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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02-FEB-2001; 2001US-00776479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-833006/82.
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject nucleic acids, and instructions for administering them to a subject useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
                 diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                               14-DEC-2000; 2000US-0255534P.
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Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Bratzler RL;
                                                                                                                                                                                                                      11-JUL-2002
                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (pyrich) for thymidine (T) rich. The method is used to vaccinate subjects against tumnou antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, hemophilus, campylobacter, clostridium, Escherichia coll and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a finz to a Thl immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                            Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                      infectious disease; allergy; immune deficiency; phosphorothioate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.6%; Score 17.4; DB 4; Length 19; 94.7%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
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                                                                                            Immunostimulatory nucleic acid #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vollmer J;
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-273485/28
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                                                                                                                                                                                                                          Synthetic.
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                       AAF98957;
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ABS77598
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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                        The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                           Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                             91.6%; Score 17.4; DB 9; Length 19; 94.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                    Disclosure; Page 10; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid #73.
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PETERSEN D M.
FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-657977/62.
                  WPI; 2003-521815/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB36459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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(FOUR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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셤
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                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, brain and central nervous system (CNS) cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, colon and rectum cancer, larynx cancer, larynx cancer, larynx cancer, larynx cancer, pancreatic cancer, prostate cancer, hadden'n's lymphoma, melanoma, mayeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                            Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic cortact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; crohn's disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.6%; Score 17.4; DB 6; Length 19; 94.7%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 209; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory nucleic acid #76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΒP
                     22-JUN-2001; 2001WO-US020154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGTGTCGTTCAGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2002; 2002US-00112653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2001; 2001US-0279642P.
                                                               22-JUN-2000; 2000US-0213346P
                                                                                                          (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACD99390 standard; DNA; 19
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                                                                                                                                                       Hartmann G;
                                                                                                                                                                                                 WPI; 2002-154611/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRIEG A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003050268-A1.
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                                                                                                                                                         Weiner G,
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Best Loca Matches

RESULT 10

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Gaps

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Indels

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Ligand binding; restriction enzyme; nucleic acid determination; pharmaceutical; BamHI; ss.
                                                                                                                                                                                                                                                                                                                                                                                               Modulating polynucleotide ligand binding site affinity using determination of the flanking duplex sequences.
                                                                                                    Polynucleotide sequence including binding site for BamHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 40; 62pp; English.
                          AAZ95948 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                     (TMTE-) IM TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                            Lane MJ, Benight AS,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-116369/10.
                                                                                                                                                                                                                                                     04-JUN-1999;
                                                                                                                                                                                                 WO9963077-A2
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                                                                             10-APR-2000
                                                                                                                                                                                                                           09-DEC-1999.
                                                                                                                                                                        Synthetic.
                                                   AAZ95948;
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RESULT 13
            AAZ95948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and acopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose
                                        Gaps
                                                                                                                                                                                                                                                                ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.6%; Score 17.4; DB 13; Length 19; 94.7%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels (
             Length 19;
                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          Allergic response suppressor oligonucleotide #82.
            Score 17.4; DB 9;
Pred. No. 1.1e+02;
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 82; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petersen DM, Fouron Y;
                                                                  GGGGTGACGTTCAGGGGGG 19
                                                                                           cecerercerreaceces 19
                                                                                                                                                           BP.
             91.68;
                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-2004; 2004US-00831778
                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000; 2000US-0179991P.
02-FEB-2001; 2001US-00776479.
                                                                                                                                                           ADU89398 standard; DNA; 19
                                                                                                                                                                                                                10-FEB-2005 (first entry)
             Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-833006/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PETE/) PETERSEN !
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                             US2004235774-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bratzler RL,
                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-2004.
                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                      ADU89398;
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Faldasz BD;

99WO-US012516. 98US-0087905P. 99US-00324672.

(first entry)

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The invention provides a method for determining the sequence of polymucleotide flanking regions that modulate ligand binding characteristics of an adjacent binding site. The method comprises: (1) providing a number of different binding site. The method comprises: (1) providing a number of different duplex polymucleotides, each having the sequence flanking the binding site, (ii) exposing the duplex to a ligand selective for the binding site; (iii) isolating duplexes which bind or not bind the ligand, and (iv) determining the nucleotide composition of the flanking duplex sequence by sequencing the duplex sequence adjacent to the binding site. The invention is used to modulate the ligand-binding characteristics of any nucleotide sequence. The invention is less costly and more efficient than prior art techniques that moderate ligand binding using small molecule pharmaceuticals. Sequences AAS95762-296170 represent polymucleotide sequences including the binding site for the restriction enzyme BamHI and used in the course of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory oligodeoxyribonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.8%; Score 14.4; DB 3; Length 40; 93.8%; Pred. No. 3.1e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40 BP; 9 A; 9 C; 15 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunostimulatory; oligodeoxyribonucleotide; ODN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
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Matches 15; Conservative
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Gaps

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1 GGGGTGACGTTCAGGGGGG 19 GGGGTGTCGTTCAGGGGGG 19 us-09-669-187a-80.szlm50.rng

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method for enhancing the immunostimulatory effect of an antigen encoded by nucleic acid contained in a nucleic acid construct. The method in involves determining the CpG-N and CpG-S motifs present in the construct, removing neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG (CpG-S) motifs in the construct, thereby producing a nucleic acid construct having enhanced immunostimulatory efficacy. The method can be used for immunisation against viral antigens, e.g. from hepatitis B virus (HBV), bacterial antigens or an antigen derived from a parasite. They can also be used for expression of a therapeutic polypeptide, e.g. growth factors, tumour suppressors, cytokines, apoptotic proteins, interferons, hormones, clotting factors, ligands and receptors. (Updated on 20-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B cell; stimulant; immune response; B cell activation; cancer; vaccine; immunostimulatory molecule; infection; therapy; 88.
                                                                                                                                                                                                                                                                                                                                                                             Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for enhancing the immunostimulatory effect of an antigen or enhancing the expression of a therapeutic polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 2; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
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/*tag= a
/note= "phosphorothioate backbone"
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"phosphorothioate backbone"
                                                                                                                                                                                                       (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
(IOWA ) UNIV IOWA RES FOUND.
(QIAG-) QIAGEN GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 64; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                               Schorr J,
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                                                                                                 98WO-US010408
                                                                                                                                           97US-0047209P
97US-0047233P
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Best Local Similarity 84.2%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                             Davis HL, Krieg AM,
                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059712/05
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                   WO9852581-A1.
                                                                                                     20-MAY-1998;
                                                                                                                                             20-MAY-1997;
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                                                           26-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs) of the invention. The ODNs contain at least one unmethylated CpG dinucleotide, and have the formula: $\int \text{NICGX2N2} 3', \text{where at least one nucleotide separates consecutive CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2 does not contain a CCGG tetramer or moreleotide separates consecutive CpGs, X1 and X2 are selected from CpT, GpG, GpA, ApT and ApA, X3and X4 are selected from TpT or CpT, N is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2 does not contain a CCGG terramer or more than one CCG or CGG trimer. The ODNs activate lymphocytes in a subject and redirect a subject is immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other cells to produce Th1 cytokines, including IL-12, IFW-gamma and GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder, autoimmune diseases, in desensitisation therapy, as an artificial adjuvant during antibody generation in a mammal such as a mouse or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                       New immunostimulatory nucleic acid molecules - which contain at least one unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
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                        disease;
                      Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease; desensitisation therapy; artificial adjuvant; antibody generation; ss
unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 25; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGTCAACGTTCAGGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV74249 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CpG-N motif SOS-ODN 1981 DNA.
                                                                                                                                                                                                           97WO-US019791
                                                                                                                                                                                                                                                     96US-00738652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                             (IOWA ) UNIV IOWA RES FOUND.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                          Kline JN;
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-272127/24.
                                                                                                                                                                                                             30-0CT-1997;
                                                                                                                                                                                                                                                        30-OCT-1996;
                                                                                                                         WO9818810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2003
15-MAR-1999
                                                                                                                                                                   07-MAY-1998
                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                            Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV74249;
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Gaps

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WO200122972-A2.
                                                       07-FEB-1995;
         US6194388-B1
                                27-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF99097;
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                        This sequence represents a B cell stimulatory oligonucleotide. The invention relates to compositions comprising an oligonucleotide (I) with unmethylated guantine and cytosine nucleotides and an antigen in a carrier. The oligonucleotides can be administered to a subject in a composition with an antigen in a carrier to enhance an immune response by and can be used to tract, prevent or ameliorate an immune system and can be used to tract, prevent or ameliorate an immune system deficiency e.g. cancer or a viral, fungal, bacterial or parasitic infection. They can also be administered as a vaccine adjuvant to stimulate the response of a host to a vaccine. The compositions can be used to treat humans or vertebrate animals including dogs, cats, sheep pigs, cows, goats, chickens, mice and monkeys. Preceding chemotherapy with the immunostimulatory oligonucleotides should be useful for
                                                                                                                                                  Immunostimulatory oligonucleotides which enhance B cell activation useful for treating an immune system deficiency e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligodeoxyribonucleotide, ODN; cytosine-guanine dinucleotide; CpG; immunostimulatory; therapy; immune system deficiency; tumour; cancer; antibacterial; antiparasitic; fungicide; antiviral; cytostatic; leukaemia; systemic lupus erythematosus; sepsis; autoimmune disease; immunoinhibitory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                  increasing the responsiveness of malignant cells to subsequent chemotherapy. The 8-40 nucleotide size of the oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 74.7%; Score 14.2; DB 3; Length 20; Best Local Similarity 84.2%; Pred. No. 3.7e+03; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunostimulatory oligodeoxyribonucleotide (ODN) 1585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/mod_base= OTHER
                                                                                                                                                                                       Claim 10; Col 10; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                         facilitates uptake into cells
                                 95US-00386063
                                                        94US-00276358
                                                                               (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD02961 standard; DNA; 20
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                                                                                                                           WPI; 2000-086224/07.
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                                 07-FEB-1995;
                                                        15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2001
           28-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                      Krieg AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 17
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The present invention relates to immunomodulatory oligodeoxyribonuclectides (ODMs) containing methylated or unmethylated represents a compositions having unmethylated CpG dinuclectides. Immunostimulatory ODN compositions having unmethylated CpG dinuclectides are useful for activating lymphocytes and for treating, preventing or ameliorating an immune system deficiency e.g. tumour or cancer or viral, fungal, bacterial or parasitic infection and leukaemia. Neural ODN that contains a methylated CpG dinuclectides are useful for treating diseases such as systemic lupus erythematosus, sepsis and autoimmune diseases. Immunoinhibitory ODN Gontaining CpG dinuclectides that are not in the stimulatory motif and activity. The present sequence is an immunostimulatory
                                                                                                                                                                                                                                                                                                                                                               Immunostimulatory composition useful for stimulating immune response in a subject, comprises antigen and immunostimulatory nucleic acid comprising oligonucleotides having unmethylated cytosine-guanine dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-parasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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immunostimulatory, tumour, viral infection, bacterial infection,
fungal infection, parasitic infection; cancer, asthma,
infectious disease, allergy, immune deficiency, phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                         Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity. The present sequence is ar oligodeoxyribonucleotide (ODN) 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Col 10; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGTGACGTTCAGGGGGG 19
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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95US-00386063.
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                                                                94US-00276358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                             (IOWA ) UNIV IOWA RES FOU
(COLE-) COLEY PHARM GROUP
                                                                                                                                                                                                                                     Krieg AM, Klinman D,
                                                                                                                                                                                                                                                                                                      WPI; 2001-217934/22
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lession, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                        Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                           Claim 2; Page 23; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid of the invention
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                                                                                                                                                                                                                                                                                                                         response. The method comprises administering an immunostimulatory uncleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                      Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                          present invention relates to a method for stimulating an immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.7%; Score 14.2; DB 4; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present seguence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         Claim 101; Page 42; 338pp; English.
                                                                                           Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGGG 19
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                   UNIV IOWA RES FOUND.
COLEY PHARM GMBH.
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                                                                                           Schetter C,
                                                                                                                                       WPI; 2001-273485/28
                                                                                             Krieg AM,
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                   (IOWA )
(COLE-)
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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder
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                                       Gaps
                                       ö
                                                                                                                                                                                                                                                                                                                                                             cell lysis; cancer; immunostimulatory; CD20;
Score 14.2; DB 6; Length 20; Pred. No. 3.7e+03;
                                     Indels
                                                                                                                                                                                                                                                                                                                      Immunostimulatory nucleic acid SEQ ID NO: 449.
                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              angiogenesis; metastasis; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 209; 312pp; English.
                                                                          1 GGGGTGACGTTCAGGGGGG 19
                                                                                                             2 ecerreacerraces
                                                                                                                                                                                                          BP
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 74.7%;
84.2%;
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                                                                                                                                                                                                        ABL39045 standard; DNA; 20
                                                                                                                                                                                                                                                                                   (first entry)
                 Local Similarity 84.2 es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiner G, Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                             Antibody-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200197843-A2.
                                                                                                                                                                                                                                                                                   16-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-2001
                                                                                                                                                                                                                                              ABL39045;
Query Match
                                     Matches
                                                                                                                                                                     RESULT 20
                                                                                                                                                                                           ABL39045
                                                                                                                                                                                                            Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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Angiogenesis inhibitory oligonucleotide #224.

(first entry)

13-DEC-2002

ABS77740;

(COLE-) COLEY PHARM GROUP INC. 14-DEC-2000; 2000US-0255534P. 14-DEC-2001; 2001WO-US048458

WO200253141-A2.

Synthetic

11-JUL-2002

WPI; 2002-566690/60

Bratzler RL;

20 BP

ABS77740 standard; DNA;

RESULT 19

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13-AUG-2003
                                                                             25-SEP-2003
                                                                                                                                                                                                                        13-MAR-2003.
                                                                                                                                                                              Synthetic.
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Matches
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                         ACD99530
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cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, cosphageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, laver cancer, lung cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rishodynyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to treating a subject infected with HIV comprising administering a CpG nucleic acid (e.g. an adjuvant type CpG obligonucleotide, an immunostimularory CpG oligonucleotide or a B cell stimulatory CpG oligonucleotide). The CpG are used as gene therapy vaccines to treat a subject infected with HIV. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating a subject infected with HIV by administering a CpG nucleic acid.
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0
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                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                       B-cell stimulatory, CpG containing oligonucleotide #1.
                                                                                                              Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                  Score 14.2; DB 6;
Pred. No. 3.7e+03;
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-cell stimulatory CpG oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 10; 22pp; English.
                                                                                        exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGTCAACGTTCAGGGGGG 20
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                                                                                                                                                                              1 GGGGTGACGTTCAGGGGG 19
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                                                                                                                                                                                                                                                         ВЪ.
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95US-00386063.
99US-00415142.
                                                                                                                                   74.7%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2001; 2001US-00931583
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                                                                                                                                                                                                                                                        ACD91359 standard; DNA; 20
                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 84.2
Marches 16; Conservative
                                                                                                                                              Local Similarity 84.2
es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krieg AM, Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-512356/48
                                                                                                                                                                                                                                                                                                                                                                                                  US2003050263-A1.
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07-FEB-1995;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                   22-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                               ACD91359;
                                                                                                                                   Query Match
                                                                                                                                                                                                                                              RESULT 21
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Immunostimulatory oligonucleotide; unmethylated CpG dinucleotide; immunoinhibitory oligonucleotide; cellular transcripton factor; viral activity; lymphocyte activation; B cell; natural killer cell; NK; immune system deficiency; viral infection; immune disease; SLE;
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                                                                                                                                                                                                                                                                                                   Immunostimulatory, antiinflammatory, dermatological; antipsoriatic; antiuloer; gene therapy, vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating non-allergic inflammatory diseases, such as psoriasis, ecze allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymphocyte (B cell) activating oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y match 74.7%; Score 14.2; DB 9; Local Similarity 84.2%; Pred. No. 3.7e+03; hes 16; Conservative 0; Mismatches 7
                                                                                                                                                                                                                               Immunostimulatory nucleic acid #216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14; 229pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 degricaccirrrededes 20
BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2002; 2002US-00112653.
ACD99530 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA62324 standard; DNA; 20
                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BERG D J.
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systemic lupus erythematosus; sepsis; viral infection; immunosuppressive; immunostimulating; immunomodulating; antibacterial; antiinflammatory; dermatological; virucide; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma which comprises administering to a subject a poly G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                   Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of treating or preventing allergy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitogenic oligonucleotide ODN1585 used in B-cell stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.2; DB 9; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lymphocyte; B cell; natural killer cell; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
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/mod_base= OTHER
/note= "Phosphorothioate backbone"
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                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 8; 221pp; English.
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/mod_base= OTHER
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                                                                                    02-FEB-2001; 2001US-00776479
                                                                                                                                03-FEB-2000; 2000US-0179991P
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Best Local Similarity 84.2%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                              Bratzler RL, Petersen DM,
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                                                                                                                                                                         BRATZLER R L.
PETERSEN D M.
                                                                                                                                                                                                                                                                                                          WPI; 2003-657977/62.
                                                                                                                                                                                            (PETE/) PETERSEN I
(FOUR/) FOURON Y.
US2003087848-A1
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modified_base
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                                           08-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic lupus erythematosus (SLE), sepsis, or cancer. The coligonucleotides are safe to use since they do not initiate an immune reaction when administered to a subject in vivo. ACAG2324-ACAG2352 represent the immunomodulatory oligonucleotides of the invention. Note: The present sequence given as SEQ ID No:1 in the Sequence listing differs from that given on page 6 (ACAG2351) and page 17 (ACAG2352) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel immunostimulatory oligonucleotide comprising 2-100 nucleotides and containing at least one unmethylated CpG dinucleotide, useful for activating a subject's B cells or natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to immunostimulatory oligonucleotides containing at least one unmethylated CpG dinucleotide, and immunoinhibitory oligonucleotides which are capable of interfering with the activity of viral or cellular transcription factors. The immunostimulatory oligonucleotides are useful for activating a subject's lymphocytes (B cells or natural Killer (NK) cells). They are useful for treating, preventing or ameliorating an immune system deficiency. The immunoinhibitory oligonucleotides are useful for treating or preventing viral infection in a subject. They are also useful for treating or your immunoinhibitory oligonucleotides are also useful for treating or immune over immune of the composition which may be used for vaccinating a subject. The composition which may be used for treating an immune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
systemic lupus erythematosus; sepsis; cancer; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                    immunostimulant; dermatological; antiinflammatory; cytostatic; antibacterial; virucide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.7%; Score 14.2; DB 9; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13; 19pp; English.
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                                                                                                                                                                                                                   99US-00415142
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                                                                                                                                                                                                                                                                                                          (KRIE/) KRIEG A M.
                                                                                                                              US2003026782-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification
                                                                                                                                                                                                                08-OCT-1999;
                                                                                                                                                                                                                                                              07-FEB-1995;
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                                                                                    Synthetic.
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Matches

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Gaps

21-OCT-2003; 2003US-00690495.

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                                                                                                                                                                                     The present invention provides oligonucleotides comprising unmethylated CpG dinucleotides. The invention is useful to activate lymphocytes specifically to activate B cells and natural killer cells, for treating diseases associated with an immune system activation such as systemic lupus erythematosus, sepsis and viral infections. The invention is useful
                                                                                                                                                                                                                                                     agent. The
                                                                                                                                                                                                                                         as an immunosuppressive, immunostimulating, immunomodulating, antibacterial, antiinflammatory, dermatological and virucidal agent. The present sequence is a mitogenic oligonucleotide used in the stimulation of B-cells. This sequence is used in the invention.
                                                                                                                        New immunomodulatory oligonucleotides containing at least one unmethylated CpG dinucleotide, useful for treating diseases including systemic lupus erythematosus and sepsis.
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                   74.7%; Score 14.2; DB 12; Length 20; 84.2%; Pred. No. 3.7e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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/note= "Phophorothioate linkage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B-cell stimulatory CpG oligonucleotide ODN1585.
                                        US DEPT HEALTH & HUMAN SERVICES. COLEY PHARM GROUP INC. CPG IMMUNOPHARMACEUTICALS INC.
                                                                                  Krieg AM, Klinman D, Steinberg AD;
                                                                                                                                                                    Claim 5; SEQ ID NO 1; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      '*tag= b
'note= "CpG island"
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/*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               base= OTHER
                                                                                                                                                                                                                                                                                                                                                             1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                             GGGTCAACGTTCAGGGGGG 20
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  95US-00386063.
           99US-00415142.
                                 IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ36558 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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/*tag= c
                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense gene therapy
                                                                                                       WPI; 2004-356245/33.
                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004143112-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
modified_base
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  07-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-2004
             08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ36558;
                                                                                                                                                                                                                                                                                                                     Query Match
                                         (USSH )
(COLE-)
(CPGI-)
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 26
ADQ36558
                                                                                                                                                                                                                                                                                                                                         Matches
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The invention relates to a new oligonucleotide which: (a) comprises about

2-100 nucleotides and containing at least one unmethylated CpG

2-100 nucleotides and containing at least one unmethylated CpG

dinucleotide, or (b) is capable of interfering with the activity of viral

or cellular transcription factors and containing a consensus

immunoinhibitor CpG motif represented by the formula (I): 5'GCGXnGCG3'

where X a nucleotide and n 0-50. Also included are an oligonucleotide

delivery complex (composition comprising the oligonucleotide and a pharmaceutical carrier, activating a subject's B cells or natural killer

cells (by conteating the cells with the oligonucleotide and a subject by administering the composition in conjunction

(preventing or ameliorating) an immune system deficiency in a subject,

vaccinating a subject by administering the composition in conjunction

with a vaccine, treating a disease associated with an immune system

activation in a subject (by administering the composition in conjunction

with a vaccine, treating a disease associated with an immune system

cor in conjunction with a pharmaceutical carrier), an improved

cor in conjunction with a pharmaceutical carrier), an improved

cor in conjunction with a pharmaceutical carrier), an improved

cor in conjunction of diagnoses using oligonucleotide probes comprising

method for in vivo diagnoses using oligonucleotide probes comprising

coligonucleotide is useful for treating or preventing or ameliorating an

conjugonucleotide is useful for treating, preventing or ameliorating an

compositions comprising the oligonucleotide are useful for activating a

compositions comprising the oligonucleotide are useful for treating or

conjugonucleotide is useful for treating, preventing or preventing or treating, preventing or

compositions comprising the oligonucleotide are useful for treating or

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conjugonucleotide is useful for treating or preventing or ameliorating 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conjunction with a vaccine to boost a subject's immune system to effect a better response from the vaccine, or for increasing the responsiveness of the malignant cells to subsequent chemotherapy. The present sequence is a B-cell stimulatory CpG oligonocleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotides containing unmethylated CpG dinucleotide, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating, preventing or ameliorating an immune system deficiency, e.g. tumor, cancer, or viral, fungal, bacterial or parasitic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID NO 1; 14pp; English.
                                                                                                                                                                                                                                                                                                                      Steinberg AD;
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94US-00276358.
95US-00386063.
99US-00415142.
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nes 16; Conservative
                                                                                                                                                                                                                                            STEINBERG A D.
                                                                                                                                                                                                                                                                                                                      Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-552597/53.
                                                                                                                                                             KRIEG A M.
KLINMAN D.
    15-JUL-1994;
                                         07-FEB-1995;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                           Krieg AM,
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(STEI/)
                                                                                                                                                                 KRIE/)
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Matches
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                                                                                                                                                                                                                                                                                                               New oligonucleotides containing unmethylated CpG dinucleotide, useful activating a subject's B cells or natural killer cells, as vaccine, or for treating, preventing or ameliorating an immune system deficiency.
                                        immune system deficiency; immune system activation; systemic lupus erythematosus; sepsis; viral infection; chemotherapy; cytostatic; virucide; fungicide, antibacterial; antiparasitic; immunosuppressive; antiinflammatory; dermatological; ss.
                             Unmethylated CpG dinucleotide; B cell; natural killer cell;
                                                                                                                                                                                                                                       (COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                       Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                        5; SEQ ID NO 1; 14pp; English
          Unmethylated CpG dinucleotide #1.
                                                                                                                                                                                    07-FEB-1995; 95US-00386063.
08-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
                                                                                                                                                       26-FEB-2004; 2004US-00789051
                                                                                                                                                                           94US-00276358
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(COLE-) COLEY PHARM GROTTP IN
                                                                                                                                                                                                                                                                       Klinman D,
                                                                                                                                                                                                                                                                                           WPI; 2004-552569/53
                                                                                                              JS2004142469-A1.
                                                                                                                                                                           15-JUL-1994;
                                                                                                                                  22-JUL-2004
                                                                                                                                                                                                                                                                       Krieg AM,
                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                          Claim
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The invention relates to oligonuclectides containing at least one unmethylated CpG dinuclectide. The invention relates to an oligonuclectide delivery complex comprising an oligonuclectide of the invention and a targeting means, a method of activating a subject's B cells or natural killer cells by contacting the cells with an immune system deficiency in a subject, waccinating a subject by administering the composition in conjunction with a vaccine, a method of treating a disease associated with an immune system activation in a tubject by administering a neutral oligonuclectide alone or in conjunction with a pharmaceutical carrier, and a method of performing antisense therapy comprising methylating CpG containing oligonuclectides are useful for treating diseases associated with immune system activation, such as systemic lupus erythematosus and sepsis. Compositions comprising systemic lupus erythematosus and sepsis. Compositions comprising colligonuclectides of the invention are useful for activating a subject's B cells or natural killer cells, for treating a subject in a minimume system deficiency or for vaccinating a subject. immunoinhibitory oligonucleotides are useful for treating or preventing a viral infection in a subject. The oligonucleotides may also be used in conjunction with a vaccine to boost a subject's immune system to effect a better response from the vaccine, or for increasing the responsiveness of This sequence represents an cells to subsequent chemotherapy. unmethylated CpG dinucleotide of malignant

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

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Gaps
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Score 14.2; DB 12; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels (
                                                        GGGGTGACGTTCAGGGGGG 19
 74.7%;
84.2%;
                             16; Conservative
  Query Match
Best Local Similarity
                               Matches
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This invention describes novel oligonucleotides capable of interfering with the activity of viral or cellular transcription factors and containing a consensus immunoinhibitory CpG mocif having the formula: 5'GCGMGCG3', where X is a nucleotide and n is 0-50 and a phosphorothicate backbone modification. The invention also describes an oligonucleotide delivery complex comprising the oligonucleotide and a targeting means e.g. a pharmaceutical carrier. The oligonucleotide and cargeting means e.g. a pharmaceutical carrier. The oligonucleotide and subject; a preventing or amellorating an immune system deficiency in a subject; vaccinating a subject; treating a disease associated with an immune system activation in a subject (systemic lupus erythematosus or sepsis); performing antisense therapy comprising methylating CpG containing oligonucleotides prior to subject; an invivo diagnoses using oligonucleotide probes companishing methylating CpG containing oligonucleotides prior to aministration to a subject; and treating or preventing a viral infection in a subject. The targeting means is selected from cholesterol, virosome, liposome, lipid, or a target cell specific binding agent. The oligonucleotides described in the invention have antinfilammatory, New oligonucleotide comprises at least one unmethylated CpG dinucleotide, useful for stimulating an immune response or for treating diseases associated with immune system activation, e.g. systemic lupus cellular transcription factor; immunoinhibitory; CpG; phosphorothioate backbone; B cell activation; matural killer cell activation; immune system deficiency; systemic lupus erythematcous; sepsis; antisense; methylation; antiinflammatory; dermatological; immunosuppressive; virucide; ss; /note= "phosphorothioate linkage" /note= "phosphorothioate linkage" B-cell stimulating oligonucleotide ODN 1585. USSH ) US SEC HEALTH AND HUMAN SERVICES Claim 5; SEQ ID NO 1; 19pp; English. Steinberg AD; Location/Qualifiers mod_base= OTHER /mod_base= OTHER ADR20014 standard; DNA; 20 BP. 94US-00276358. 95US-00386063. 99US-00415142. COLEY PHARM GROUP INC 26-FEB-2004; 2004US-00788191 21-OCT-2003; 2003US-00690495 (IOWA ) UNIV IOWA RES FOUND ส Д 16. .20 erythematosus or sepsis. /*tag= Krieg AM, Klinman D, WPI; 2004-624263/60. US2004152656-A1 Key modified_base modified base 15-JUL-1994; 07-FEB-1995; 21-OCT-2004 05-AUG-2004 Synthetic. primer. COLE-) ADR20014 

for

GGGTCAACGTTCAGGGGGG 20

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and containing at least one unmethylated CpG dinucleotide. The oligonucleotide is capable of interfering with the activity of viral or cellular transcription factors and containing a consensus immunoinhibitory CpG motif having the formula: 5'GGGXnGGG3', where X is a nucleotide and n is 0-50. Also included are an oligonucleotide delivery complex (comprising the oligonucleotide above and a targeting means), a complex (comprising the oligonucleotide above and a targeting means), a complex (comprising the oligonucleotide above and a targeting means), a complex (comprising the oligonucleotide above and a subject's natural killer cells, treating (preventing or ameliorating) and subject's natural killer cells, treating (preventing or ameliorating) and isease associated with an immune system activation in a subject, treating a clisease associated with an immune system methylating CpG containing oligonucleotides prior to administration to a subject), in vivo diagnoses using oligonucleotides prior to administration to a subject in vivo diagnoses oligonucleotides prior to administration to a subject and treating or preventing a viral infection in a subject. The oligonucleotide is useful for treating diseases associated with immune system activation including systemic lupus erythematosus or sepsis, or for treating, preventing, or systemic lupus erythematosus or sepsis, or for treating or preventing, or oligonucleotide is also useful for treating or preventing viral coligonucleotide is also useful deficiency in a subject. The invention. It is also useful de the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systemic lupus erythematosus; sepsis; tumour; cancer; viral infection; bacterial infection; fungal infection; cytostatic; virucidal; antibacterial; fungicidal; antiinflammatory; dermatological; immunosuppressive; vaccine; gene therapy; phosphorothicate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitogenic CpG oligonucleotide ODN1585 used in B-cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunomodulatory; CpG dinucleotide; immune system deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.7%; Score 14.2; DB 13; Length 20; 84.2%; Pred. No. 3.7e+03; Live 0; Mismatches 3; Indels (
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/mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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/mod_base= OTHER
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07-FEB-1995; 95US-00386063.
08-OCT-1999; 9US-00415142.
21-OCT-2003; 2003US-00690495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 84.2
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004162258-A1
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; immunostimulatory oligonucleotide; CpG dinucleotide; transcription factor; immunoinhibitory CpG motif; B cell; natural killer cell; immune system deficiency; antisense therapy; viral infection; immune response; systemic lupus erythematosus; sepsis;
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                                                                                                                                                                                                                  Gaps
dermatological, immunosuppressive and virucide activity. ADR20014-ADR20040 represent the oligonucleotides describes in the disclosure the invention.
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                                                                                                                                                           Score 14.2; DB 13; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels (
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                                                                                                                   Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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(USSH ) US SEC HEALTH AND HUMAN SERVICES.
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'note= "CpG dinucleotide'
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95US-00386063.
99US-00415142.
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84.2%;
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/mod_base=
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nes 16, Conservative
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modified_base
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08-OCT-1999;
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                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                         AD72288777

AD72288777

AD7228777

AD7221-
XXX AD8.
XXX A
                         SKGGG
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Gaps

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New oligonucleotide comprises at least one unmethylated CpG dinucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides novel oligonucleotides containing unmethylated CpG dinucleotides and therapeutic utilities based on their ability to stimulate an immune response in a subject. Oligonucleotides of the invention are useful for treating, preventing or ameliorating an immune system deficiency or a tumour, cancer, viral, bacterial or fungal infection. They are useful for treating diseases associated with immune system activation including systemic lupus erythematosus or sepsis. They are also useful as vaccines to boost subject's immune system. The invention is also useful in gene therapy. The present sequence is a CpG oligonucleotide used to stimulate B-cells. Note: This sequence is a CpG to be the same as that shown as SEQ ID NO: I in page 18 of the specification. However these sequences differ.
                                                                                                                                                                                                                                                                                                                                                               useful for treating, preventing, or ameliorating an immune system deficiency or a tumor, cancer, viral, bacterial, or fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CpG dinucleotide, gene therapy a; vaccine; cancer; viral infection; fungal infection; bacterial infection; parasitic infection; systemic lupus erythematosus; sepsis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CpG immunomodulatory oligo, ODN 1585 used in B cell stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.2; DB 13; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
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/mod_base= Phosphorothioate backbone
15. ~20
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                          (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                        Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; SEQ ID NO 1; 19pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGTCAACGTTCAGGGGGG 20
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07-FEB-1995; 95US-00386063.
08-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR88228 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004 (first entry)
                                                                                                                                                                                                                        Klinman D,
                                                                                                                                                                                                                                                                               WPI; 2004-603584/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32-SEP-2004
                                                                                                                                                                                                                           Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR88228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR88228
ID ADR8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides oligonucleotides comprising is useful immunomodulatory unmethylated CpG dinucleotide. The invention is useful for treating, preventing and ameliorating immune system deficiencies such as systemic lupus erythematosus and sepsis, tumour, cancer, viral, bacterial and fungal infections. The invention acts as an cytostatic, virucidal, antibacterial, fungicidal, antiniflammatory, dermatological and immunosuppressive agent. The invention is also useful in the production of vaccines and in gene therapy. The present sequence is a mitoganic cpG oligonucleotide used in B-cell activation. Note: This sequence is stated to be SEQ ID NO: 1 in the sequence listing. However, this sequence differs from the sequence designated as SEQ ID NO: 1 in the
                                                                                                                                                                                                                                               New oligonucleotide comprises at least one unmethylated CpG dinucleotide, useful for treating, preventing, or ameliorating an immune system deficiency or a tumor, cancer, viral, bacterial, or fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immune response; immune system deficiency; tumour; cancer;
viral infection; systemic lupus erythematosus; sepsis; vaccine;
gene therapy; bacterial infection; fungal infection; phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.7%; Score 14.2; DB 13; Length 20; 84.2%; Pred No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CpG oilgonucleotide ODN 1585 used to stimulate B-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                         (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 1; 20pp; English.
                                                                                                                                       Steinberg AD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR45002 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-00276358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                       Krieg AM, Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                              WPI; 2004-603582/58
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ADR45002
XX
AC ADR45
DY 04-NC
XX
DE CPG C
XX
NW Viral
KW 99ne
KW 99ne
KW 98.

XX
KPT modif
FT modif
FT MODIF
FT MODIF
FT MODIF
FT WODIF
F
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8

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Gaps

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unmethylated CpG

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Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose
                                                                                                                                                                                                                                                       The invention relates to immunomodulatory oligonucleotides containing an unmethylated CpG dinucleotide. The oligonucleotide of the invention is useful in preparing a composition for treating a disease associated with an immunome system activation, e.g. systemic lupus erythematosus, sepsis or viral infection. It is also useful to prepare vaccine. The present sequence is an immunomodulatory oligonucleotide used to stimulate B
                                                                                                                                                      New oligonucleotide comprising 2-100 nucleotides and containing an unmethylated CpG dinucleotide, useful in preparing a composition for treating a disease, e.g., systemic lupus erythematosus, sepsis or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 13; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allergic response suppressor oligonucleotide #224.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                       (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                  Steinberg AD;
                                                                                                                                                                                                                               Claim 5; SEQ ID NO 1; 19pp; English.
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02-FEB-2001; 2001US-00776479.
08-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
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                                                                                                                                                                                                                                                                                                                                                                                                      ch 74.7%;
1 Similarity 84.2%;
16; Conservative
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                                                                                                  Krieg AM, Klinman D,
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(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-833006/82.
                                                                                                                              WPI; 2004-667684/65.
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Best Local Similarity
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                                                                                                                                                                                                      infection.
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(FOUR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                        New immunomodulatory oligonucleotides for preventing, treating or ameliorating diseases associated with immune system deficiency or activation, e.g. cancer, viral infection, systemic lupus erythematosus or
                                                                                                                                                                                                                                                                        The present invention relates to an oligonucleotide containing at least one unmethylated CpG dinucleotide. The invention is useful in gene therapy and for preparing vaccine. The invention is also useful for preventing, treating or ameliorating diseases associated with immune system deficiency or activation such as cancer, viral, fungal, bacterial or parasitic infection, systemic lupus erythematosus or sepsis. The present sequence is a CpG immunomodulatory oligonucleotide used in B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulator; immune system; systemic lupus erythematosus; sepsis; viral infection; vaccine; B cell; virucide; phosphorothioate backbone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    74.7%; Score 14.2; DB 13; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
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/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ODN1, oligonucleotide used to stimulate B cells.
                                                         (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                    Steinberg AD,
                                                                                                                                                                                                                                                 Claim 5; SEQ ID NO 1; 19pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGACGTTCAGGGGGG 19
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    95US-00386063.
               09-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
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95US-00386063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADS17223 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                    Krieg AM, Klinman D,
                                                                                                                                              WPI; 2004-634548/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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modified_base
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07-FEB-1995;
    07-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                    stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS17223;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                         sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 33
ADS17223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Gaps

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modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV97282;
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                 ADV97282
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                                       The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, uritaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                  Immune modulation; immunity; immunogenicity; immune disorder; tumor; cancer; cytostatic; neoplasm; systemic lupus erythematosus; SLE; antiinflammatory; dermatological; immunosuppressive; sepsis; infection; viral infection; virucide; fungal infection; fungicide; bacterial infection; antibacterial; parasitic infection; antiparasitic; autoimmune disease; Theumatoid arthritis; antiarthritic; antirheumatic; multiple sclerosis; neuroprotective; antisense therapy; hybridization; antiviral vaccine; phosphorothioate; ss.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Mitogenic CpG oligonucleotide ODN1585 used in B-cell stimulation.
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                 Score 14.2; DB 13; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                               Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLEY PHARM GROUP INC.
US DEPT COMMERCE & NAT INST STANDARDS.
                     Disclosure, SEQ ID NO 224; 235pp; English.
an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/mod base= OTHER
                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                       GGGTTGACGTTTTGGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00276358.
95US-00386063.
99US-00415142.
                                                                                                                                                                                                                                                                                                                              ADW28066 standard; DNA; 20 BP
                                                                                                                                                                                                    74.7%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2004; 2004US-00847650
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                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2005 (first entry)
                                                                                                                                                                                                              Local Similarity 84.2
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16. .20
                                                                                                                                                        method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1994;
07-FEB-1995;
09-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                                                                    ADW28066;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IOWA ) (COLE-) (USDC ) (
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                        RESULT 35
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                                                                                                                      Use of an immunostimulatory oligonucleotide for boosting an immune response of a subject, or for stimulating an immune response in a subject, where increases in IFN-gamma and IL-12 expression are indicators of the immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; immune modulation; pharmaceutical; immunomodulator; cytostatic; virudide; fungicide, antibacterial; antiparastic; antiinflammatory; dermatological; immunosuppressive; antiarthritic; antirheumatic; neuroprotective; immunostimulant; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 14; Length 20; Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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/note= "unmethylated CpG dinucleotide"
15. .20
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/mod_base= phosphorothioate backbone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 1; 19pp; English
Steinberg AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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07-FEB-1995; 95US-00386063.
09-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
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Best Local Similarity 84.2%;
Matches 16; Conservative
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/*tag=
Krieg AM, Klinman D,
                                                           WPI; 2005-065257/07
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Krieg AM,
     Krieg AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel pharmaceutical composition (A) for oral administration comprising an immunostimulatory nucleic acid (1) (8-100 concloses in length) in a pharmaceutically acceptable carrier. The immunostimulatory nucleic acid is of the formula 5.X 1 X 2 CGX 3 X 4 3. (Where C and G are unmethylated). The carrier comprises an emulsion. A composition of the invention has immunomodulator, cytostatic, virucide, fungicide, antibacterial, antiparasitic, antihlammatory, dermatological, immunosuppressive, antiarthritic, antihlammatic, neuroprotective, and immunostimulant activity. A nucleic acid of the circumors, cancers or viral, fungal, bacterial or parasitic infections) or a disease (e.g. systemic lupus erythematosus, sepsis, cheumatodia erthritis and multiple sclarosis) associated with immune system activation. The nucleic acids are useful as vaccine adjuvants to stimulate a subject's response to a vaccine, and for antisense therapies or as in vivo hybridization probes. The present sequence represents an immunosiant contains and co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                          Oral composition, useful e.g. to treat/prevent/ameliorate an immune system deficiency or diseases associated with immune system activation, comprises an immunostimulatory nucleic acid in a pharmaceutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulatory oligonucleotide of the invention, ODN 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.2; DB 14; Length 20;
Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B cell-stimulating oligonucleotide - SEQ ID 1.
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                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1; 18pp; English.
                                                                                                             Steinberg AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGACGTTCAGGGGGG 19
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(IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1995; 95US-00386063.
09-0CT-1999; 99US-00415142.
16-AUG-2001; 2001US-00931583.
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84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-AUG-2003; 2003US-00649584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.2
Best Local Similarity 16.2
Best Loca
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KLINMAN D.
STEINBERG A D.
                                                                                                             Krieg AM, Klinman D,
                                                                                                                                                              WPI; 2005-080553/09.
                                                                                                                                                                                                                                                                                         acceptable carrier.
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07-FEB-1995;
09-OCT-1999;
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(STEI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immune modulation; immunotherapy; antisense therapy; hybridization; interferon-gamma; cytokine; immune deficiency; immunostimulant; immune disorder; tumor; cancer; cytostatic; neoplasm; viral infection; virucide; infection; fungicide; bacterial infection; antibacterial; parasitic infection; antiparasitic; nucleic acid vaccine; leukemia; systemic lupus erythematosus; antiinflammatory; dermatological; immunosuppressive; sepsis; autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                  Treating a subject infected with HIV comprises administering a CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.7%; Score 14.2; DB 14; Length 20; 84.2%; Pred. No. 3.7e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CpG oligonucleotide ODN 1585 used to stimulate B cells.
                                                                                                                           nucleic acid and an anti-HIV therapy to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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/note= "Phosphorothioate backbone"
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                                                                                                                                                                               Disclosure; SEQ ID NO 1; 37pp; English.
Steinberg AD;
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/note= "Phosphore
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Best Local Similarity 84.2
Matches 16, Conservative
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Klinman D,
                                                 WPI; 2005-172294/18
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modified base
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09-OCT-1999;
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(USDC ) US
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Steinberg AD;

Klinman D,

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The invention relates to a method for increasing interferon (IFN)-gamma in a subject. The method involves administering an immunostimulatory oligonucleotide/delivery complex to modulate immune response of the subject. The invention is useful for treating diseases associated with immune system deficiency e.g. tumor or cancer or viral, fungal, bacterial or parasitic infections, as vaccine, for treating leukemia, systemic lupus erythematosus, sepsis and autoimmune diseases. The present sequence is the CpG oligonucleotide used to stimulate B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified proteinaceous composition, useful for treating e.g., tumors.
                                           Use of immunostimulatory oligonucleotide delivery complex comprising oligonucleotide linked to biodegradable delivery complex for increasing interferon-gamma levels and treating diseases associated with immune system deficiency e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricin; (x) Asp(y); primer; mutant; mutagenesis; ss; vascular leak syndrome; VLS; cancer; immunotoxin; IT; cytokine; RTA; aphasia; myaglia; fatigue; hypotension; rhabdomyolysis; MAb; ribosome inactivating protein; RTP; vaccine; graft vs. host disease; GVHD; non-Hodgkin's lymphoma; Hodgkin's lymphoma; cyrostatic; immunosuppressive; myloma; tumour; monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                  74.7%; Score 14.2; DB 14; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer, D75N, used to mutate the RTA (x)Asp(y) motif.
                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baluna RG;
                                                                                                                         Disclosure; SEQ ID NO 1; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smallshaw JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 18; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-OCT-2002; 2002US-00282935
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22-SEP-2000; 2000US-00668419
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                                                                                                                                                                                                                                                                                                                                                                     16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VITETTA E S.
GHETIE V F.
SMALLSHAW J E.
              WPI; 2005-172254/18
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                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC24305;
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(BALU/)
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The invention discloses a new modified proteinaceous composition which

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Gaps

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coid mutation that alters the ability of a (x)Asp(y) sequence to induce Vascular Leak Syndrome (VLS). The present invention relates to the field of physiology and cancer biology. The invention provides immunotoxins (TTS) and cytokines, methods for producing them, which have been mutated to lack amino acid sequences which induce VLS or other side effects. Also claimed is a ricin A chain toxin (RTA) with a reduced ability to promote toxicity in a patient, where at least one amino acid flanking the toxicity in a patient, where at least one amino acid flanking the coricity in a patient is further defined as VLS, aphasia, myalgia, fatigue, hypotension or rhabdomyolysis. Its are hybrid molecules consisting of monoclomal antibodies (MABs), or other cell binding ligands, which are biochemically or genetically linked to toxins, toxin subunits or ribosome inactivating proteins (RIPs) from plants, fungi or bacteria. The modified proteinaceous composition is plants, fungi (e.g. vaccine) graft vs. host disease (GVHD), non-Hodgkin's and Hodgkin's lymphoma, myloma and some solid tumours. The sequence presented is a primer which was used to mutate the RTA (x)Asp(y)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus template-dependent DNA polymerase for preparing cDNA molecule from RNA template comprises reverse transcriptase activity in the presence of magnesium ions and absence of manganese ions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a purified thermostable template-dependent DNA polymerase from Bacillus stearchtermophilus comprising reverse transcriptase (RT) activity in the presence of magnesium ions at a concentration of 1 mM and in the substantial absence of manganese ions. The DNA polymerase is useful for preparing cDNA molecules from RNA polymerase and for amplifying a nucleic acid. The present sequence is a PCR primer for rabbit tissue factor (RTF). This sequence was used to demonstrate the activity of the DNA polymerase of the present invention
a protein having a (x) Asp(y) sequence and at least one amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbit tissue factor PCR primer #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGTGACGTTCAGGG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
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Matches 14; Conserv
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Homo sapiens
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                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                     ABZ49680/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               concoding enzymes associated with drug metabolism. The invention relates encoding enzymes associated with drug metabolism. The invention relates concoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ50807 using a variety of detection assays, including hybridisation assays, nucleic acid errays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                     Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                             /standard name= "Single nucleotide polymorphism (SNP)"
                                                             Gaps
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0
                                   72.6%; Score 13.8; DB 4; Length 30; 88.2%; Pred. No. 5.9e+03;
                                                          Indels
            Sequence 30 BP; 6 A; 5 C; 12 G; 7 T; 0 U; 0 Other;
                                                             0; Mismatches
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                                                                                                                                                                                                                                               Human SULTX3 gene polymorphic site, #313.
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                                                                                     3 GGTGACGTTCAGGGGGG 19
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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                                                                                                          13 GGCGATGTTCAGGGGGG
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                                                                                                                                                                                                                      (first entry)
                                                             Conservative
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                                                Best Local Similarity
Matches 15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid.
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variation
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ABZ43529/
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c such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients.

This would not only take the guesswork out of selecting the drug with the care the likelihood of adverse reactions, thereby increasing safety.

CC greatest therapeutic effect for a particular patient, but would also cereduce the likelihood of adverse reactions, thereby increasing safety.

CC approval processes. For example, individuals could be selected for capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more compropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of possible drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different companions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different companions a patient needs to take before finding an effective therapy
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Pred. No. 6e+03;
0; Mismatches 2; Indels
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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88.2%;
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-583571/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200252044-A2
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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates concoding enzymes and compositions for identifying individuals who have at least to methods and compositions for identifying enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphisms data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between polymorphisms (SNPs) and be used in studying the relationship between cargorizations and human diseases, conditions, and responses to that cause or exacerbate certain diseases, SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms (CC frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms (CC drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug discovery and captured for the invention are also useful in the drug discovery and approval processes. Por example, individuals could be selected for educe the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and captured partiant populations. The methods of daverse drug or drug candidates could be revived if they were matched with more appropriate partient populations. The methods of adverse land decreases in the number of adverse drug the partiant patient patient patient 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            medications a patient needs to take before finding an effective therapy
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Sequence 41 BP; 5 A; 23 C; 2 G; 11 T; 0 U; 0 Other;

72.6%; Score 13.8; DB 6; Length 41; 88.2%; Pred. No. 6e+03; ive 0; Mismatches 2; Indels 1 GGGGTGACGTTCAGGGG 17 26 dederecerrcacece 10 Query Match
Best Local Similarity 88.2.
Local Similarity 18.2.
Local 15; Conservative 8

RESULT 43

AAD07150 standard; DNA; 22 BP AAD07150

AAD07150;

06-AUG-2001 (first entry)

PCR primer PR2-379 for improving priming site 19379 specificity.

Priming site 19379; PCR; polymerase chain reaction; amplification; branched modular primer; front module; FM; back module; BM; PCR primer; proofreading; ss.

Bacteriophage lambda.

Location/Qualifiers /*tag= a /mod_base= i /*tag= b /mod base= i mutation mutation 

22-MAY-2001.

US6235889-B1

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primers used in methods for amplifying a nucleic acid segment. The branched modular primer comprises of front and back oligonucleotide modules. The front module (FM) and back module (BM) comprise of a stem segment having a sequence that is the same from module to module and an arm segment having a sequence that varies from module to module. The arm of the back and front modules are annealed to a template which contains the priming site. These modules are designed for priming sites in lambda phage DNA. The composition is useful for amplifying a nucleic acid segment, e.g. by polymerses chain reaction (FCR). The present sequence is prooffreading amplification primer FR2-379 used for improving sequence is Bacteriophage lambda reverse priming site 19379 specificity
                                                                                                                                                                                                                                                          New composition comprising front and back oligonucleotide modules, each module has a stem and an arm segment with varying or constant sequences, useful for amplifying nucleic acid segments such as in polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to compositions for branched modular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 18; 32pp; English.
                 99US-00264466.
                                                         91US-00810898.
                                                                             95US-00384699.
                                                                                                                                         (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                      WPI; 2001-366426/38.
                 08-MAR-1999;
                                                       20-DEC-1991;
                                                                                                  06-MAY-1997;
                                                                                                                                                                               Ulanovsky L;
                                                                                                                                                                                                                                                                                                                               reaction.
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BP RESULT 44 AAF74944 ID AAF7

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Gaps

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y Match 70.5%; Score 13.4; DB 4; Length 22; Local Similarity 93.3%; Pred. No. 9.1e+03; nes 14; Conservative 0; Mismatches 1; Indels

Query Match Best Loca Matches 5 TGACGTTCAGGGGGG 19

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Gaps

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AAF74944 standard; DNA; 22 AAF74944;

Bacteriophage lambda fragment PCR ampification primer SEQ ID NO:5. Bacteriophage lambda, PCR primer, amplification, genome mapping, biomedical research, clinical diagnostic, ss. (first entry) 23-MAY-2001 

Bacteriophage lambda Synthetic.

US6197556-B1

36-MAR-2001.

97US-00852001. 91US-00810898. 36-MAY-1997; 20-DEC-1991; 06-FEB-1995;

Ulanovsky L, Raja MC; (UYCH-) UNIV CHICAGO.

(A) with modified metabolic partways comprising: (a) genetic modification of a microorganism to inhibit production or consumption of a metabolite when it is grown on a defined medium, thus affecting its ability to grow; (b) growing the modified organism in the defined medium so that evolution can occur, optionally with addition of a co-substrate to allow evolution; and (c) selecting as (A) cells able to grow on the medium, optionally in presence of co-substrate. The evolved microorganisms (A), or evolved proteins (I) expressed by them, are useful in biotransformation processes, especially those involving NaDPH-dependent enzymes, particularly synthesis of amino acids (Met. Cys. Thr. Lys or Ile) but also synthesis of mucleic acids or lipids, and metabolism of sugars. (A) provide more efficient production of selected metabolism of sugars. (A) strains. This sequence represents a nucleic acid molecule used in the method of the invention.

Sequence 30 BP; 7 A; 8 C; 9 G; 6 T; 0 U; 0 Other;

relates to a method for preparing evolved microorganisms

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                                                                                                                                               The present invention describes a method for amplifying a template nucleic acid segment (1), comprising annealing (1) to a branched primer having front (FOW) and back oligonucleotide modules with arm segments complementary to a site in (1), extending the arm of FOM to form an extending RP to form second initial extension strand, and amplifying the extending RP to form second initial extension strand, and amplifying the second strand. The method can be used for amplifying nucleic acid segments, useful in genome mapping, biomedical research and clinical diagnostics. The method climinates the need for custom primer synthesis in methods to amplify nucleic acid segments. The modular combination of just a few oligonucleotides essentially minics the performance of a conventional, custom-made primer by matching a sequence of a priming site in the template. AMF74910 to AAF7499 represent coligonucleotide sequences used in the exemplification of the present invention. N.B. Any Ne given in the oligonucleotide sequences represent inosine bases
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                                   Amplifying a template nucleic acid segment, involves annealing a combination of several branched and/or covered oligonucleotide modules selected from a pre-synthesized library, to the template DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; microorganism evolution; metabolic pathway; metabolite; biotransformation; NADPH-dependent enzyme; nucleic acid metabolism; lipid metabolism; sugar metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4; DB 4; Length 22;
Pred. No. 9.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.5%; Scc...
V 93.3%; Pred. No. >...
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                                                                                                                    Disclosure; Col 18; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2003; 2003FR-00001924.
14-MAY-2003; 2003FR-00005768.
14-MAY-2003; 2003FR-00005769.
06-NOV-2003; 2003FR-00013054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TGACGTTCAGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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WPI; 2001-256370/26
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Best Local Similarity
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ADR99754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating condition associated with survivin expression or overexpression, such as breast cancer, colon cancer, lung cancer, bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises dsRNA oligomeric sequences which are targeted to the human survivin gene. The dsRNA oligomeric compounds of the invention are useful for inhibiting expression of the human survivin gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel double-stranded compound, modulating expression of human survivin,
                                                                                                                                                                                                                                                                               survivin; antisense therapy; gene silencing; cancer; cytostatic; breast tumor; colon tumor; prostate tumor; lung tumor; bladder tumor; ovary tumor; renal tumor; pancreas tumor; non-hodgkin lymphoma; hepatocellular carcinoma; ss; siRNA; short interfering RNA; RNA interference.
                               Gaps
                               0
70.5%; Score 13.4; DB 13; Length 30; 93.3%; Pred. No. 9.2e+03; ive 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                        Human survivin gene-specific siRNA sequence - SEQ ID 196.
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                                                                                                                                                 ADW46519/c
ID ADW46519 standard; RNA; 19 BP.
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13-APR-2004; 2004US-00823448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2003; 2003US-0475324P.
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                                                               1 GGGGTGACGTTCAGG 15
                                                                                   1 GGGGTGACGGTCAGG 15
                                                                                                                                                                                                                            (first entry)
                                  14; Conservative
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                        WO2005002507-A2.
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                            07-APR-2005
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                                Matches
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New evolved microorganisms with altered metabolic pathways, useful e.g. for production of amino acids, are selected as mutants able to grow on

Disclosure; SEQ ID NO 21; 113pp; French

for production defined media.

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be used in the treatment of cancer, such as: hepatocellular cancer, breast cancer, colon cancer, prostate cancer, lung cancer, bladder cancer, ovarian cancer, renal cancer, glioblastoma, pancreatic cancer and non-Hodgkin's lymphoma. The present nucleic acid represents a human survivin-specific siRNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises dsRNA oligomeric sequences which are targeted to the human survivin gene. The dsRNA oligomeric compounds of the invention are useful for inhibiting expression of the human survivin gene, and can be used in the treatment of cancer, such as: hepatocellular cancer, breast cancer, cancer, prostate cancer, lung cancer, bladder cancer, renal cancer, ploblastoma, pancreatic cancer onn-Hodgkin's lymphoma. The present nucleic acid represents a human survivin-specific siRNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel double-stranded compound, modulating expression of human survivin, useful for treating condition associated with survivin expression or overexpression, such as breast cancer, colon cancer, lung cancer, bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                            survivin; antisense therapy; gene silencing; cancer; cytostatic; breast tumor; broast tumor; brund tumor; brostate tumor; brung tumor; brund tumor; processes tumor; non-hodgkin lymphoma; hepatocellular carcinoma; ss; siRNA; short interfering RNA;
                                                                                                                                                                       Gaps
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                                                                                                                                    Score 13.2; DB 14; Length 19; Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human survivin gene-specific siRNA sequence - SEQ ID 195.
                                                                                                                                                                       3; Indels
                                                                                                    Sequence 19 BP; 4 A; 9 C; 3 G; 0 T; 3 U; 0 Other;
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                                                                                                                                                                       0; Mismatches
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                                                                                                                                      69.5%;
83.3%;
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13-APR-2004; 2004US-00823448.
                                                                                                                                                                                                         1 GGGGTGACGTTCAGGGGG
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                                                                                                                    Query Match
Best Local Similarity 83.37
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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(BLIL ) LILLY & CO ELI
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response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immuno response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophlus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                  Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infections disease; allergy; immune deficiency; phosphorothioate; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to a method for stimulating an immune
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Pred. No. 1.1e+04;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                     Immunostimulatory nucleic acid #511.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vollmer J;
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0
               2 GGGGGAACUUCAGGUGG 19
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83.3%;
1 GGGGTGACGTTCAGGGGG
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                                                                                                                 AAF99395 standard; DNA; 20
                                                                                                                                                                                    (first entry)
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(COLE-) COLEY PHARM GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-273485/28
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        WO200122972-A2.
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27-SEP-1999;
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                                                                                                                                                                                    12-JUN-2001
                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                AAF99395;
                                                                               RESULT 48
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AAF99392 RESULT

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Score 13.2; DB 14; Length 19; Pred. No. 1.1e+04; 3; Mismatches 3; Indels

Query Match 69.5%; Best Local Similarity 66.7%; Matches 12; Conservative

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Search completed: February Job time: 153.207 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response. The method comprises administering an immunostifundatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostifundatory. The response. The present sequence is one such immunostifundatory nucleic acid. The immunostifundatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. horpesviridae, retroviridae, and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is staphylococcus, preventing cancer, asthma, infectious disease, alleryy or immune deficiency. The present sequence can also be used to redirect a Thi to a Thi immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                 Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour; viral infection; bacterial infection; fungal infection; parasitic infection, cancer, asthma; infection allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to a method for stimulating an immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiogenesis inhibitory oligonucleotide #524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                         Immunostimulatory nucleic acid #508.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 101; Page 48; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                       Vollmer J;
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                                                                                                                                                                                                                                                                  99US-0156113P
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23-AUG-2000; 2000US-0227436P.
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  AAF99392 standard; DNA; 20
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(COLE-) COLEY PHARM GMBH
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                                                                                                                                                                                        WO200122972-A2.
                                                                                                                                                                                                                                                                  25-SEP-1999;
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                                                   12-JUN-2001
                                                                                                                                                                                                                 05-APR-2001
                                                                                                                                                                 Synthetic
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                          AAF99392
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administering at least one antiangiogeness; in a subject, congitishing administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, anglofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Angiogenesis inhibitor; ss, angiogenesis, solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection, neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to inhibiting angiogenesis in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 6; Length 20;
Pred. No. 1.18+04;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                  scleroderma; hypertrophic scar
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Best Local Similarity 83.3%;
Matches 15; Conservative (
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AU263853 AU2 AA986717 uc7 CF291715 14R BI669410 603	AA948503 on53c06.: BX569627 BX569627 AZ648348 1M051701:	B1544737 603242001 CX013593 io66b06.b AA922976 6X7060.s	AU10220 AU10220 AU10220 AU102320 AG204798 Pan trog1 CV93742 PWrpcm 40	AL488820 INO CALCEL AZ483233 IMO308H16 CIECACOT DELCALOS	CZ474868 d06009-5p	AI696220 tt15d10.x CZ294761 M093F02 G	R87616 ym91g02.rl BX128210 Danio rer W34290 ma99c07.rl	BH802996 1008098B1 CG732711 1119150E0 CC458057 SALK 1154	CR974331 Homo Bapi AZ358150 1M0100K20	AZ402579 1M0169121 AZ786207 2M0031004	A1708901 ass6n10.x A2348233 1M0084G04 A1331811 fb01h06.x	AI814007 wk53e02.x AI917527 to27b02.x AZ861612 2M0168P16	CZ906573 4011001E0 CZ907034 4011004H0 CV136950 EST848159	A1088848 qa12e10.X A1811024 tr03a03.X DN447106 EST942905	AZ412343 IMUIBSEIS AG197827 Pan trogl	AA871389 vq34g05.r	AGI95359 Pan trogl	AA687728 nv08c10.8	AA877825 nriih05.8 BI547757 603191921	BI668945 603294924 AA931447 om89b09.8	AA947644 oq32a05.8 AI359345 qy29h11.x	AI364448 qw38d11.x	AZ654497 1M0528N10	AZ848760 2M0149G24 BX171717 Danio rej	AZ441185 1M0232001	AA936385 0049g03.8 AI094098 qa33h02.8	BH851581 SALK 0732	AZ381877 1M0138E08	CZ258850 AH0165 Sa CL449256 CMHD-GT_4	AA743162 ny17b09.8 AI443574 sa33g10.x
61.1 35 1 AU263853 61.1 37 1 AA986717 61.1 38 6 CF291715 61.1 41 3 BI669410	1 44 4 4 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6	4444	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	22 29 21 20 6	.9 33 10 CZ47486 .9 34 10 CZ47486	.9 37 1 AI696220 .9 39 10 CZ29476	9 41 10	0.0 84 4 C	9 50 11	24 9	.9 25 1 9 25 9 31 1	ممو	.9 31 10 .9 31 10 .9 33 7	9. 9. 9. 1. 4. 1. 5. 1.	9 35 9	37 1	9 37 10	.9 38 9.	.9 40 1 .9 40 3	.9 443 1	9 43 1		.9 43 L	9 43 9	9 44 9	.9 46 1 .9 46 1	9 47 9	.9 48 5 BQ591368 .9 48 9 AZ381877	.9 48 10 .9 48 10	.9 49 1 AA743162 .9 49 1 AI443574
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5.1.7 Biocceleration Ltd.		; Search time 1263.74 Seconds (without alignments) 703.434 Million cell updates/sec			residues	chosen parameters: 179606								results predicted by chance to have a	score distribution.		Description	CR061079 Forward s	BF568357 602184546 AZ838956 2M0134D20	BX121477 Danio rer CO411608 EST841993	AG215101 Drosophil	AZ616333 1M0446A08	CC027439 3591 1 5 AZ307335 1M0008K13	AZ768418 1M0568H23	CAULZISS 108/90/.B	AZ331072 1M0056A13 BG272395 nah29f02.	AQ074235 21 pUCB P	<b>(3 4</b>	CL686485 PRI0144b CD029249 mqns012xO	AZ783946 2M0026B08 BI259582 602968347

CG671946 RR0179 H CG671946 RR0174 Ba AA972457 OP41c04.8 R08290 yf18e09.81 R2269564 SALK 0203 AL7601394 ARADidops AL7661394 ARADidops AM772664 XM020205.y H15861 ym21e03.r1 BZ37976 SALK 1132 CR396950 ARADidops AU102339 AU102339 AU102339 AU102339 AU102339 AU102339 AU102339 AU102339 AU104854 AU104853 AU104854 UM0221014 AZ652869 1M0031G16 AZ650284 1M0031G16 AZ650284 1M0031G16 AZ650284 1M0042E01 AZ650284 1M00269N10 AZ650284 1M0269N10 AZ650384 CR066818 CZ990972 4018012F0 AZ650336 OX45912.s AZ66245 1M0569N13 CZ990972 4018012F0 AZ61033 1M0435F16 CC650847 PR10116d AZ61033 1M0435F16 CC651182 PR10116d BX624507 BX624507 AZ66113 1M0544D10 AA902238 0108C09.s AA620715 LU96000.x AI6620715 LU96400.x AI6620720 BX624507 AZ66100 ZM0230E09 AJ545578 Drosophil A135550 ZM1230E02.x A73437 ZG6502.x A7343 ZG6502.x A7343 ZG6502.x	AZ659789 1M0537P19 CZ4446734 1M0283J19 AZ976182 2M0251G01 AZ877309 2M0178B10 AL482549 T. brucei AL492210 to08e02.x B1080927 602878838 AZ871856 ZM0184024 CL658108 PR10130b AL49437 Danio rer BE51178 601152951 B1551849 603190807 BG973894 602843523 AZ640839 1M0503105 AZ997025 ZM0283119 AJ53906 Azebidops AJ530142 coo70b12.s AI613303 ty35h11.x AI684861 warxists Vi CX258681 WRX352 Vi BX622712 Arabidops AV855184 AV855184
169 10.2 53.7 46 6 CB844957 1771 10.2 53.7 46 10 CG71946 1772 10.2 53.7 47 1 AA972457 1773 10.2 53.7 47 9 BZ266964 1774 10.2 53.7 47 9 BZ266964 1775 10.2 53.7 49 10 AA772664 1776 10.2 53.7 49 9 H15861 1777 10.2 53.7 49 9 H15861 1777 10.2 53.7 49 9 H15861 177 10.2 53.7 49 9 H15861 177 10.2 53.7 49 9 H15861 177 10.2 53.7 49 9 H15861 178 10.2 53.7 49 9 H15861 189 10.2 53.7 50 1 AU104853 181 10.2 53.7 50 1 AU104853 182 10 52.6 23 9 AZ654469 183 10 52.6 25 1 AA734596 194 10 52.6 25 9 AZ66027 195 10 52.6 25 1 AA452947 195 10 52.6 25 1 AA734596 197 10 52.6 25 1 AA734597 198 10 52.6 25 1 AA734597 199 10 52.6 25 1 AA734597 10 52.6 25 1 AA734597 10 52.6 25 1 AA734597 10 52.6 25 1 AA734597 202 10 52.6 29 10 CL653182 203 10 52.6 29 10 CL653182 204 10 52.6 29 10 CL653182 205 10 52.6 29 10 CL653182 207 10 52.6 29 10 CL653182 208 10 52.6 31 1 AA9910955 209 10 52.6 31 1 AA69115 209 10 52.6 31 1 AA69115 209 10 52.6 31 1 AA69115 200 10 52.6 31 1 AA69115 201 10 52.6 31 1 AA69115 202 10 52.6 31 1 AA69115 203 10 52.6 31 1 AA69115 204 10 52.6 31 1 AA5910965 205 10 52.6 31 1 AA5910965 207 10 52.6 31 1 AA5910965 208 10 52.6 31 1 AA5910965 209 10 52.6 31 1 AA5910965 200 10 52.6 31 1 AA5910965 201 10 52.6 31 1 AA5910965 201 10 52.6 31 1 AA5910965 202 10 CL65318 203 10 AZ641551 204 10 52.6 31 1 AA5910965 205 10 CL65318 207 10 52.6 31 1 AA5910965 208 10 52.6 31 1 AA5910965 209 10 52.6 31 1 AA5910965 200 10 52.6 31 1 AA5910965 201 10 52.6 31 1 AA5910965 201 10 52.6 31 1 AA5910965 202 10 CL653182 203 10 AZ641551 203 10 AZ641551 204 10 52.6 31 1 AA5910965 205 10 CL653182 207 10 52.6 31 1 AA5910965 208 10 52.6 31 1 AA5910965 209 10 AZ641451 200 10 52.6 31 1 AA5910965 200 10 52.6 31 1 AA5910965 201 10 52.6 31 1 AA5910965 202 10 CL653182 203 10 AZ641155 204 10 AZ641155 205 10 CL653182 207 10 AZ641155 208 10 AZ641155 209 10 AZ641155 200 1	100 52.6 100 52
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Unpublished	JOURNAL	AU107364 AU107364				287
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Mammalla; Eut Hominidae: Ho		AU104852 AU104852 AII104855 AII104855				282
Eukaryota; Me		AU103171 AU103171	1 AU10317			281
Homo sapiens	SOURCE	CC455581 $SALK$ $0841$ $AII103170$ $AII103170$	יע ⊷			
EST.	KEYWORDS		<b>م</b>			
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	3	CL639450 Q007E04 G	10			
	4	H44578 yp04c03.81	8 -			267
1 GGGGTGACGT	ò	AL476937 T. brucei	1			c 266
16; Conserva	Matches	BJ060786 BJ060786	47 3 BJ060786			
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Locs	FEATURES	CW990600 BA0473 Sa RX895201 Arabidons	44 10 CW990600 44 10 BX895201			
CB10 1SA, UK	COOKINA	A5323644 IMOU43LIZ CW989647 AN0924 Sa	, 01			
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Adams, D.J.,	AUTHORS	A1445618 tj08b03.x				C 247
Sciurognathi	acwadaad	AZ441689 1M0233K24 AV833021 AV833021	ο -			
Mammalia; Eu			'n			244
Mus musculus	ORGANISM	BIS49061 603197039 BIS48343 603246901	41 3 BI549061 41 3 BI598393		10	242

## ALIGNMENTS

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Forward strand read from insert in 3'HPRT insertion targeting and chromsome engineering clone MHPP308j13, genomic survey sequence. CR061079. GI:49794551 GSS; genome survey sequence, MICER. Mus musculus (house mouse)
RESULT 1
CR061079/c
LOCUS
DEFINITION
                                                                           ACCESSION
                                                                                          VERSION
KEYWORDS
SOURCE
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/totone lib="NIH MGC 42"
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/note="Organ: pancreas, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >SOUbp following 5' adaptor: GGCACGAG(G). Size-selected by Ling for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald Mr. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                     Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., nd Bradley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 bp mRNA linear EST 12-DEC-2000 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300571 5',
Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
utheria, Euarchontoglires, Glires, Rodentia,
i, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                   20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, K. http://www.sanger.ac.uk/MICER
cation/Qualifiers
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stitutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.7%; Score 14.2; DB 11; Length 50; 84.2%; Pred. No. 3.1e+04; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                              "mol_type="genomic DNA"
'db_xref="taxon:10090"
'clone="MHPP308j13"
'clone_lib="MHPP"
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bs-r@mail.nih.gov
urement: ATCC
                                                                                                                                                                                                                                                                                                                                      rganism="Mus musculus"
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Gaps

us-09-669-187a-80.szlm50.rst

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SM Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 41)

Si Humphray, S. J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Humquery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 62P9 is

part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene: Further details:

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         balla1477 41 bp DNA linear GSS 13-MAR-2003 Danio rerio genomic clone DKEY-62P9, genomic survey sequence.
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Buell, C.R., Zheng, L., Cowles, A. and Cairney, J. Sequencing of ESTs from loblolly pine embryonic libraries Contact: C. Robin Buell
Plant Genomics Group
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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35 bp mRNA linear EST 02-JUL-20
EST441993 Sequencing EST8 from loblolly pine embryos Pinus taeda
cDNA clone PIALM51 5' end, mRNA sequence.
CO411608
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                                                                                                                        Query Match
69.5%; Score 13.2; DB 9;
Best Local Similarity 83.3%; Pred. No. 9.4e+04;
Matches 15; Conservative 0; Mismatches 3;
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/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-62P9"
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Best Local Similarity
Matches 14; Conserv
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BX121477/c
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD42nry Purfited genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Jackson Laboratory Mouse)
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                                                                                                                         AZB38956 46 bp DNA linear GSS 20-FEB-2001
2M0134D20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0134D20 R, genomic survey sequence.
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(bases 1 to 46)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
(Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH_MGC Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                             Gaps
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0
                                                                                                        Length 32;
                                                                                                                                                           2; Indels
                                                                                                     Score 13.8; DB 2;
Pred. No. 4.7e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: D column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 46.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0134D20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                              3 GGTGACGTTCAGGGGGG 19
                                                                                                           72.6%;
                                                                                                                                                                                                                                                              23 gergacerrcacreges 7
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                             15; Conservative
                                                                                                           Query Match
Best Local Similarity
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(bases 1 to 44)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Pinams1"
// Abote="Pinams1"
// Lone="Pinams1"
// Lone="Pinams1"
// Lone="Pinams1"
// Lone="Description of the property of the property
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.plantphysiol.org/cgi/content/full/127/4/1556))
The Institute for Genomic Research
712 Medical Center Dr. Rockville, MD 20850, USA
Email: rbuelletigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: ATT TAG GTA ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                      /organism="Pinus taeda"
/mol_type="mRNA"
/cultivat="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                               clone="PIALM51"
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AG215101.1 GI:22762101
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Best Local Similarity
Matches 15; Conserval
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Hayashi,S.

Direct Submission
Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Developmental Biology, Laboratory for Morphogenetic Singaling;
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan (B-mail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA986325 28-MAY-1996 aRNA linear EST 28-MAY-1996 uc79d12.xl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1431863 3' similar to TR:O14742 O14742 NUCLEOLAR PROTEIN. ;
                                                                                                                                                                          Fax:81-78-301-3183)
This clone was isolated from genomic DNA flanking an insertion of the P element vector P(GaNB) of a Drosophila strain.

Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="flanking P{GaWB} transposon insertion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 44;
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Possible reversed clone: similarity on wrong strand
Seq primer: primer name ambiguous
High quality sequence stop: 1.
Location/Qualifiers
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    .44
    /organism="Drosophila melanogaster"

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                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="NP6643"
/db_xref="taxon:7227"
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/strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="64F2"
/clone="NP6643-5-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="3"
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AA986325
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Matches 14; Conserv
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Zea mays
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JOURNAL
COMMENT
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KEYWORDS
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                                                                              /clone libe-Sugano mouse kidney mkia"
/clone libe-Sugano mouse kidney mkia"
/note-Torgan: kidney, Vector: pME188-FL3; Site 1: DralII
(CACTGTGTG); Site_2: DralII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DralII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DralII sites of the pME188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMD0446A08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0446A08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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1 (bases 1 to 37)

Dunn,D., Agagai,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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/mol_type="genomic DNA"
strain="C57BL/60"
/db xref="taxon:10090"
/clone="UUGCIM0446A08"
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Location/Qualifiers
clone="IMAGE:1431863"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                        /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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Unpublished (2000)
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Best Local Similarity
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AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfa712114 [gpl]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coll XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 42)

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Tel: 650 723 2227
Fax: 650 725 8227
Fax: 650 725 8227
Fax: 650 726 8227
Fax: 650 725 8227
Fax
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3591 1 5 1 D10.1EL y 1 3591 - RescueMu Grid P Zea mays genomic, genomic survey sequence.
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="txxed" background W23/A188/B73/K55"
/db_xref="txxed" background W23/A188/B73/K55"
/tissue_type="loaf"
/dev_stage="adult"
/lab_host="DA108"
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site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi, Muroidea; Muridae; Golfres; Rodentia; Sciurognathi, Muroidea; Muridae; Murinae; Rodentia; Sciurognathi, Muroidea; Muridae; Murinae; Mus.

E. 1 (bases 1 to 45)
S. Dunn, D., Aoyagi, A., Barber, M., Bascorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Muederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ307335 45 bp DNA linear GSS 29-SEP-200
1M0008K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0008K13 R, genomic survey sequence.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
units. For more information on RescueMu, go to the web
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                                                                                                                                                                                                                                                             64.2%; Score 12.2; DB 9; Length 42; 82.4%; Pred. No. 2.9e+05; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Exror: C
Plate: 0008 row: K column: 13
Seg primer: CACACAGGAAACAGCTATGACC

    .45
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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High quality sequence stop: 45.
Location/Qualifiers
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/clone="UUGC1M0008K13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenet
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Best Local Similarity
Matches 14; Conserva
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AZ307335/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/documents
/http://www.jax.org/resources/documents/documents/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0568H23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Cone UUGCIM0568H23 F, genomic survey sequence.
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(bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Really, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0568H23"
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Insert Length: 10000 Std Erro:
Plate: 0568 row: H column: 23
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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84112, US
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AUTHORS
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KEYWORDS
SOURCE
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EST 26-SEP-2003

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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Rodentia; Butheria; Burchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E 1 (bases 1 to 41)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Sose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
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1M0056A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0056A13 R, genomic survey sequence.
                                                                                                                                                                               Xenopus laevis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                               Expression of this close in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
BJ035059
BJ035059 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL031m15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 34;
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86.7%; Pred. No. 4.5e+05;
tive 0; Mismatches 2;
                                                                                                                                                     Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                     Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://xenopus.nibb.ac.jp.
Location/Qualifiers
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Mus musculus
                                                                             BJ035059
BJ035059.1 GI:17414312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.1
Best Local Similarity 86.7
Matches 13; Conservative
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AZ331072/c
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ORGANISM
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     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/foloe="Organ: Heart; Vector: pBluescript II SK; Site 1:
EcoR; Site_2: Xhol; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VWD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CX012159 29 bp mRNA linear EST 06-DEC-2004 io57g07.bl Whole Heart Library (DOGESTS) Canis familiaris CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                              Score 11.8; DB 9; Length 19;
Pred. No. 4.3e+05;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ballay V.S., Nascimento, L.U. and McCombie, W.R. ESTs from Canis familiaris whole heart (dog) Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mccomble@cshl.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CX012159
CX012159.1 GI:56394570
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                                                                                                                                                                                                                                                                                 62.1%;
86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

RESULT 12

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CX012159

ACCESSION

VERSION KEYWORDS

Matches

ORIGIN

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FEATURES

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Gaps

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GSS 29-SEP-2000

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Rm. 308, Bi 84112, USA

RESULT 13 BJ035059

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JOURNAL
COMMENT
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                                                  FEATURES
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1 (bases 1 to 50)

NOI/NIDR-Cape http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG272395 50 bp mRNA linear EST 20-FEB-2001 nah29f02.x1 NCI_CGAP_HN21 Homo sapiens cDNA clone IMAGE:4232571 3',
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.1%; Score 11.8; DB 9; Length 41; 86.7%; Pred. No. 4.5e+05; ive 0; Mismatches 2; Indels
                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: A column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: placmid ends
High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056A13"
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                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
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rel: 801 585 5606
                         Fax: 801 585 7177
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Best Local Similarity
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KEYWORDS
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AUTHORS
TITLE
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

Est. (bases 1 to 20)

McCouch, S.R., Kochert, G., Yu, Z.H., Wang, Z.Y., Khush, G.S.,

Coffman, W.R. and Tanksley, S.D.

Molecular mapping of rice chromosomes

Lateor. Appl. Genet. 76, 815-829 (1988)

Contact: Susan R. McCouch

Cornell University

Dept. Plant Breeding, Ithaca, NY 14853-1901, USA

Tel: 607 255 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ074235 20 Etiolated Leaf Genomic Library Oryza Bativa (indica cultivar-group) genomic clone RG152, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ars-genome.cornell.edu/cgi*2Dbin/WebAce/webace?db=ricegenes&class=Marker&object=RG152 DNA Sequencing was done by the DOE Plant Research Lab, Michigan State University. Informatics was done at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                /tissue_type="nasopharyngeal carcinoma"
/lab host="DH10B"
/clone_lib="NCI_CGAP_HN21"
/note="Organ: head/neck; Vector: pAMP1; mRNA made from head/neck tumor, cDNA made by oligo-dT priming.
licetionally cloned into UDG sites Size-selected on agarose gel, average insert size 300 bp. Primary library.cDNA Library Preparation: David B. Krizman, Ph.D."
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For mapping information, additional citations and other related
information concerning this probe, please refer to the RiceGenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Computational Biology Centers, University of Minnesota. PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.1%; Score 11.8; DB 2; Length 50; 86.7%; Pred. No. 4.6e+05; Live 0; Mismatches 2; Indels
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|db_xref="taxon:39946"
|clone="RG152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Std Error: 0.00
                                                                                                                                   /organism="Homo sapiens"
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/cultivar="IR36"
                                                                                                                                                                                                                            /clone="IMAGE:4232571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACKWARD: M13 Reverse
Insert Length: 1 Std Brror: 0
Seg primer: M13 -21 dye primer
Class: RFLP probe.
Location/Qualifiers
                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
info@image.llnl.gov
Seg primer: -40UP from Gibco.
Location/Qualifiers
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AQ074235.1 GI:3435354
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1M0029L01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clone_lib="pUC8 PstI Rice Etiolated Leaf Genomic Library" hote="Vector: pUC8; Tota" leaf DNA was digested with the restriction enzyme PstI. DHS-alpha bacterial cells were then transformed with ligated plasmid. Random genomic clones were given consecutive numbers (RG4#)as they were prepared. The same numbers were then used to designate loci in the genome as detected by genetic mapping."
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Mus musculus

Mus musculus

Mus musculus

Mus musculus

Muscapola, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Burchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Mederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library." /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C5FBL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tý of Utah
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                              61.1%; Score 11.6; DB 9; Length 20; 77.8%; Pred. No. 5.4e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone UUGC1M0029L01 F, genomic survey sequence
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0029L01"
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High quality sequence stop: 25.
Location/Qualifiers
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Length: 10000 Std Errc
0029 row: L column: 01
                                                                                                                                                                                                                                                                                                                                                          1 GGGGTGACGTTCAGGGGG 18
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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84112, US
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                                                                                                                                                                                                                                                                                                       14;
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KEYWORDS
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Contact: Stephen L. Johnson
Washington University School of Medicine
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: Zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contect:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@vesgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 28)

S clark, Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoc, M., Theising, B., Allen, M., Schurk, R.,

Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

Unpublished (1998)
electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored to the competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 bp mRNA linear EST 07-JT BES362.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3715611 3' similar to SW:COPB_RAT P23514 COATOMER BETA SUBUNIT ;, mRNA sequence.
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Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: T7 ET from Amersham
POLYA-No.
                                                                                                                                                                                                                                                                                             Length 25
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                                                                                                                                                                                                                                                                                          Score 11.6; DB 9;
Pred, No. 5.5e+05;
0; Mismatches 4;
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/sex="mixed"
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
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AUTHORS
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JOURNAL
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/Gell_type="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/clone lib="wagnaporthe grisea NS Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_l: EcoRI; Site_2:
Xhol; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on Xhol side of insert.
Nitrogen starvation library. Cells were inoculated into
minimal medium and grown for two days with shaking (150
rpm) at room temperature. Culture was harvested, blended,
inoculated into minimal medium as above for 24 h Cells
were harvested, washed with water and inoculated into
minimal medium base lacking nitrogen source for 6 h.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimed according to the
alignment, otherwise sequence quality was assessed using
phredPhrap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."
                                                                                                                                                                        CD029249 29 bp mRNA linear EST 07-MAY-2003 mgns012x001f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns012x001 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatterai, K. and Dean, R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                 Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                       Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence is available, see contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 6483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:148305"
/clone="mgns012x001"
/sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR PRIMERS
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgns012 row: O column: 01
Seq primer: T3.
Location/Qualifiers
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                     GGGTGACGTTCAGGGGGG 19
                                                              7 GGGTTAGGTGTAGGGGGG 24
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Best Local
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ORGANISM
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                sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Mixed stage fosmid library of P. pacificus var. California"
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
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Pristionchus pacificus
Eukaryota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.1%; Score 11.6; DB 1; Length 28; 77.8%; Pred. No. 5.5e+05; ive 0; Mismatches 4; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tat: 00497071601371
Fax: 00497071601498
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/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:54126"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
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Gaps

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Dictyostelium discoideum
Dictyostelium discoideum
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Dictyostelium discoideum

1 (bases 1 to 35)
Urushihara, H., Morio, T., Saito, T., Kohara, Y., Koriki, E., Ochiai, H., Maeda, M., Williams, J.G., Takkeuchi, I. and Tanaka, Y.
Analyses of cDNAs from growth and slug stages of Dictyostelium
                                                                     BI259582 34 bp mRNA linear EST 17-JUL-2001
602968347F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108146 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU263853 AD Dictyostelium discoideum CDNA clone VSD330 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="NIH MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies.
                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11261 row: m column: 11
                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 34)
NIH-MGC http://mgc.nci.nih.gov/.
NIHodo http://mgc.nci.nih.gov/.
Unational Institutes of Health, Mammalian Gene Collection (MGC)
Unational isbled (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.1%; Score 11.6; DB 2; Length 34; Best Local Similarity 77.8%; Pred. No. 5.6e+05; Matches 14; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /olone="IMAGE:5108146"
/tissue type="cervical carcinoma cell line"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .34
/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 2
Location/Qualifiers
                                                                                                         mRNA sequence.
B1259582
B1259582.
B1259582.1 GI:14817058
EST.
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                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                           Hominidae, Homo.
1 (bases 1 to 34)
                                                                                                                                                                                                                                                                 Homo sapiens
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BI259582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inductible Cylon Resources (documents/dnares). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwd92 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                            AZ783946 30 bp DNA linear GSS 16-FEB-2001
2M0026B08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0026B08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                      Bukaryocainus

Bukaryocainus

Mammalia; Butheria; Baarchontoglires; Glires; Rodentia;

Boirucognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.6; DB 9; Length 30;
Pred. No. 5.6e+05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 10000 Std Brror: 0.00 Plate: 0026 row: B column: 08 Seq primer: CGTTGTAAAACGACGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC2M0026B08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 30.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
                                                                                                                               AZ783946
AZ783946.1 GI:12919186
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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USA
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AZ783946/c
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Gaps

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discoideum Nucleic Acids Res. 32 (5), 1647-1653 (2004) 15010511 Contact: Hideko Urushihara

PUBMED COMMENT

JOURNAL

TITLE

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1 GGGGTGACGTTCAGGGGG 18

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14; Conservative

Best Local Similarity Matches 14; Conserva

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25 GGGGTGGGTGGAGGGGG

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/clone_lib="Sugano mouse liver mlia"
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA986717 37 bp mRNA linear EST 28-MAY-1998 uc73e01.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1431288 3' similar to SW:PRP2_MOUSE P05142 PROLINE-RICH PROTEIN MP-2 PRECURSOR. ;, mRNA sequence.
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1 (bases 1 to 37)

Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                   ch 61.1%; Score 11.6; DB 1; Length 35; 1 Similarity 77.8%; Pred. No. 5.6e+05; 14; Conservative 0; Mismatches 4; Indels
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Possible reversed clone: similarity on wrong strand
Institute of Biological Sciences
University of Tsukuba
1-1. Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hidekobiol.tsukuba.ac.jp.
                                                                                                                                                                /organism="Dictyostelium discoideum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: primer name ambiguous
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                    /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                              /strain="AX4"
/db_xref="taxon:44689"
/clone="VSD330"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B"
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Best Local S:
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/ncce="Organ: liver; Vector: pWE185-FL3; Site 1: DraIII (ACCTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pWE185-FL3 vector [5' site CACTGTGTG, 3' site CACTGTGTG, 3' site CACTGTGTG, 3' site CACTGTGTG, 1' sites of the pwe185-FL3 vector for solate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGTTGTAAAGGTGCG and 3' end primer CGACCTGGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)

ENKarycra, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ENKarycra, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzael, Oryza;

EN (M., J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S. I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

M. Umpublished (2003)

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14-AUG-2003

14ROOT--02-E03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E03, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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/dev_stage="14 days after germination"
/dev_stage="1.01i DH10B"
/lab host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-POR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/mol_type="mRNA"
/mol_tyne="Mackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-E03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.1%; Score 11.6; DB 1; Length 37; ilarity 77.8%; Pred. No. 5.6e+05; Conservative 0; Mismatches 4; Indels
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    Location/Qualifiers
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/mol_type="mRNA"
// db xref="taxon:9606"
/clone="IMAGE:1560394"
/tlssue_type="adacoarcinoma"
/tlssue_type="adacoarcinoma"
/tlssue_type="adacoarcinoma"
/lab host="mBH108"
/clone=lib="NCI CGAP_CO8"
/note="Organ: oclon" Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NII-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX569627 Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tse9f08_q1c, mRNA sequence.
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1 (Dases 1 to 44)

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Mamilton, J., Soares, M. B., Bonaldó, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                        61.1%; Score 11.6; DB 1; Length 43; 77.8%; Pred. No. 5.7e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality Insert Length: 1892 Std Error: 0.00 Seq primer: -40m13 fwd. Er from Amersham High quality sequence stop: 1. Location/Qualifiers
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/organism="Homo sapiens"
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Genome Biol. 4 (10), R63 (2003)
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Glossina morsitans morsitans
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Unpublished (1997)
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Matches 14; Conserv
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BX569627
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// organism="Homoo sapiens"
// organism="Homoo sapiens"
// mol_type="mRNA"
// bb_xref="taxon:9606"
// clone="MMGE:5314750"
// tissue_type="hypothalamus"
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// clone=lib="NIH_MGC_96"
// clone=lib="NIH_MGC_96"
// lost="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: Sall-XhoI gEcgag); Oligo-dT primed using primer
// stryrtyrtyrtyrtyrtyry, site_3: sall-xhoI grimer
// clone=lib="NIH_MGC_96"
// site_3: Stryrtyryrtyry, site_3: Sall-xhoI grimer
// site_3: Stryrtyryryryryry, site_3: Sall-xhoI grimer
// site_3: Stryrtyryryryryry, site_3: Sall-xhoI clones and constructed using the Cap-trapper method (Carninci, in preparation): Library constructed by M. Brownstein (NIHH/MHGRI, Mational Institutes of Health). Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Eutheria; Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4).

2 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999).

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Toshiyuki and Piero Carninci (RIKEN)

Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov mccolumn: 23

High quality sequence stop: 41.

Location/Qualifiers
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                                                                                                                                        BI669410 41 bp mRNA linear EST 12-SEP-2001
603295295F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314750 5',
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     32 GGCTGACGGCGAGGGGGG 15
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AA948503.1 GI:3109756
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Homo sapiens
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AA948503/c
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Gaps .. 0

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clone_lib="NIH_MGC_95"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="country: Zimbabwe; EST from adult gut infected with
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84112, USA
             The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 18A, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix qlc are reverse primer reads starting at 5' end of the CDNA all plc reads are from the 3' end.
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse9f08 qc1"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 45)
Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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    .44
    /organism="Glossina morsitans"

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Insert Length: 10000 Std Brror: 0.00
Plate: 0517 row: O column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 45.
Location/Qualifiers
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Pathogen Sequencing Unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.1
Best Local Similarity 73.7
Matches 14; Conservative
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Fax: 801 585 7177
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AZ648348
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AUTHORS
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KEYWORDS
SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWAPA2 (gil #1732114 [gb] API29072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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S I (bases 1 to 47)

S NIH-WGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

L Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: Gapba Famili nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CONTACT Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov

Plate: LLAM11719 row: a column: 01
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603242001F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284488 5',
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                /lab_host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/tissue_type="hippocampus"
/lab_host="DH108"
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/clone="UUGC1M0517013"
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/db_xref="taxon:9606"
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Location/Qualifiers
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Matches

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ORIGIN

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Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/Link at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled germ cell tumors"
/lab host="DH108"
/clone_lib="NCI_CGAP_GC4"
/note="Vectors: pT7130-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo (4T) primer: Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT773
vector. Library is normalized. Library was constructed by
Bento Soares and M. Patima Bonaldo. "
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BE615718
                        AA922976 49 bp mRNA linear EST 21-APR-1998 ok77e06.sl NCI CGAP GC4 Homo sapiens CDNA clone IMAGE:1520002 3' similar to TR:Q39614 Q39614 PROLINE-RICH PROTEIN: ;, mRNA sequence.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                       Hominidae, Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1520002"
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                                                                                                                                   AA922976.1 GI:3070285
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                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 49)
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     AA922976/c
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TITLE
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/lab_host="XL10 Gold"
/lab_host="XL10 Gold"
/clone lib="Whole Heart, Vector: pBluescript II SK; Site_I:
/note="Gorgan: Heart, Vector: pBluescript II SK; Site_I:
ECORI; Site_2: Mon! Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins WMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1, Site_2: Sall-XhoI (gtcgag); Oligo-dT primed using primer 5. "TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NIGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                   Score 11.6; DB 3; Length 47; Pred. No. 5.7e+05; 0; Mismatches 4; Indels
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Balija,V.S., Nascimento,L.U. and McCombie,W.R.
ESTS from Cannis familiaris whole heart (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 515 367 884
Fax: 516 367 884
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/db_xref="taxon:9615"
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Location/Qualifiers
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Canis familiaris
                                                                                                                                                                                                                                                                                                                        ch 61.1%;
l Similarity 77.8%;
14; Conservative
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nes 14; Conservative
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JOURNAL COMMENT

FEATURES

Matches

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ORIGIN

RESULT 32

REFERENCE AUTHORS TITLE

ACCESSION

VERSION KEYWORDS

SOURCE

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/organism="Homo sapiens"
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Matches 12; Conserv
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                                                                                          ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Hafe-1, Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Email: yeuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yebhitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Ganomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
http://mage.lln.gov
Dlate: LLCNL296 row: o column: 07.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.1%; Score 11.6; DB 2; Length 49; 77.8%; Pred. No. 5.7e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity 77.8 Matches 14; Conservative
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2 (Dases I to 32).

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission

Direct Submission

Buindited (Or-JAN-2002) Hong-Seog Park, Korea Research Institute of
Buindited (Or-JAN-2002) Hong-Seog Park, Korea Research Institute of
Buindited (Or-JAN-2002) Hong-Seog Park, Korea Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

[E-mail:redStone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:38-42-866-7181, Fax:82-42-866-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of Clone tracking errors.
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Pan troglodytes DNA, clone: RP43-090Kl3.T7, genomic survey
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43 (Unpublished 2 (bases 1 to 35)
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/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
Length 35;
                                                                                                                                                                         y Match 61.1%; Score 11.6; DB 1; Length 50; Local Similarity 77.8%; Pred. No. 5.7e+05; hes 14; Conservative 0; Mismatches 4; Indels
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    .35
    /organism="Pan troglodytes"

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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP43-090K13.T7"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
                                                                                                                                                                                                                                                                                                       2 GGGTGACGTTCAGGGGGG 19
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AG204798.1 GI:45236973
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/lab_host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/lab_host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWDA2 (gil 4732114) glo | AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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       Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypanosoma.

1 (bases 1 to 29)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Hallingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge (2B10 1SA, B-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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T. brucei sheared genomic DNA clone 246h09, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: G column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0072G21"
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Trypanosoma brucei
                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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                                                                                                                                                                                                                                                                                                                                                                                                [ (Dases I to 36) [ Randall T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C., Kelkar, H., Pong, A.M., Gates, K., Roberts, S., Yatzkan, E., Gaffney, T., Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, I., Mueller, E., Mindass, J., Binder, A., Birch, P.R.J., Gisi, U., Govers, F., Gow, N.A., Mauch, P., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S., Lam, S.T. and Judelson, H.S.
                                          EST 25-JAN-2005
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Mus musculus
Mus musculus
Mus repeata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Contrognathi; Muroidea; Muridae; Murinae; Mus.
Contrognathi; Muroidea; Muridae; Mus.
Contrognathi; Muroidea; Muridae; Mus.
Contrognathi; Muroidea; Muridae; Mus.
Contrognathi; Muroidea; Muridae; Mus.
Contrognathi; Manmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Miderhausern, A. and Wright, D., Weiss, R.
Miderhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
Phytophthora.
36 bp mRNA linear EST 25-
infestans CDNA, mRNA sequence.
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/note="Vector: pSPORT1"
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University of California
Webber Hall, Riverside, CA 92521,
Tel: 909 787 4199
Fax: 909 787 4294
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Contact: Robert B. Weiss
University of Utah Genome Center
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/strain="88069 and 618"
/db_xref="taxon:4787"
/sex="Al and A2"
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Location/Qualifiers
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (but it is a size distribution of the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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1 (basea 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Distand inserts
Unpublished (2000)
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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/mol_type="genomic DNA"
/strain="TREU927"
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Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0308 row: H column: 16
Seq primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/63"
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/clone="246h09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Laboracry Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalval [4]04]14[19]API129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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PRI0138b H10 2 - PRI0138b.BR (30) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/strain="California"
/db.xref="taxon:54126"
/db.xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
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Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 30)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppabB: an AcedB database for the nematode satellite organism
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Max-Planck-Institute for Developmental Biology
Speamannstr. 37-39. Tuebingen D-72076, Germany
Tel: 0049707160139.
Fax: 00497071601498
Email: ralf. sommer@tuebingen.mpg.de
Finis library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%; Score 11.2; DB 9; Length 30; ilarity 81.2%; Pred. No. 8.7e+05; Conservative 0; Mismatches 3; Indels
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
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Pred. No. 8.7e+05;
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81.2%;
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German Genetrap Consortium (GGTC)

Email: info@genetrap.de

FlipRoSAGeoct.2 gene trap. Sequence tag generated by 5'RACE.

Additional sequence information can be found at:

'http://genetrap.gsf.de/project/web_new/database/result_clone.html?

clone id=w090F07' ES cell line harboring insertion mutation of

target gene is available at:

'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html'

l'Inhouse Sequence Identifier: 18342
                                                                                                                              CZ294988 36 bp mRNA linear GSS 22-MAR-2005
M090F07 GGTC Gene Trap Library GV18C05 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                 Muse musculus muscus muscus, Muscus muscus musculus musculus musculus musculus musculus musculus muscus metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus. 1 (bases 1 to 36)

Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P. A large scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome

Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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tt15d10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240851 3'
similar to TR:Q12799 Q12799 T-COMPLEX PROTEIN 10A. ;, mRNA
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/cell_type="Bmbryonic stem cell"
/cell_line="ES cells [CS7BL/6J x 12986/SyEvTac] Fl"
/clone_lib="GGTC Gene Trap Library GV18C05"
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1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Best Local Similarity 68.4%; Pred. No. 8.8e+05;
Matches 13; Conservative 0; Mismatches 6;
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/clone="M090F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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/strain="129 Sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                           M090F07, mRNA sequence.
CZ294988
                                                                                                                                                                                                                                         CZ294988.1 GI:61682738
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31 GGGGACCTTCTGGGGG 16
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AI696220/c
LOCUS
DEFINITION
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db xref="taxon:722"
/clone_lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 33)
Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
Greer,K., Hartouni,S.R., Howie,B., Jakkula,L., Joo,D., Killpack,K.,
Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
A. complementary transposon tool kit for Drosophila melanogaster
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                                                                                                                                                                                                                                                                  d06009-5prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 5' end of P element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The P element insertion position is 26 in the 33 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailbrop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
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3; Indels
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Mismatches
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Nat. Genet. 36 (3), 283-287 (2004)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             genomic survey sequence.
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                                                     4 GTGACGTTCAGGGGG 19
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                                                                                                       10 GráAAGrrrcagaga
13; Conservative
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Matches 13; Conserv
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Gaps

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Length 39; Indele EST 16-AUG-1995

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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: 314 286 1800
Email: est@watson.wustl.edu
Insert Size: 2019
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infc@simage.llnl.gov)
for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand
Insert Length: 2019 Std Error: 0.00
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 18341
Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 bp mRNA linear EST 16-AUG-1 ym91g02.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:166322 S' similar to SP:S27887 S27887 NEUREXIN II-ALPHA PRECURSOR - ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

1 (bases 1 to 40)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hellman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                      /cell_type="Embryonic stem cell"
|/cell_line="ES cells [C57BL/6J x 129S6/SvEvTac] F1"
|/clone_lib="GGTC Gene Trap Library GV14C05"
|/note="Vector: FlipROSAceoC-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.2; DB 10;
Pred. No. 8.9e+05;
0; Mismatches 6;
                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
fstrain="129 Sv"
/db_xref="taxon:10090"
/clone="M093F02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:587017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
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/clone="IMAGE:166322"
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                             58.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                             /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R87616.1 GI:946429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
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Best Local S
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AUTHORS
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JOURNAL
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KEYWORDS
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R87616
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                                                                                                                                                                                                             Bonaldo, Ph.Ď.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seg primer: -40UP from Gibco

High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /.raz_nost_ming_CGAP_GGG"
//clone_lib="NGC CGAP_GGG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not_l; Site_2: Eco_RI; Plaemid DNA
from the normalized library NCT_CGAP_GG4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1228631, 1469064-1470983, and 1475592-1476743).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Genetrap Consortium (GGTC)

Email: info@genetrap.de

FlipROSACeoC-2 gene trap. Sequence tag generated by 5'RACE.

Additional sequence information can be found at:

'http://genetrap.gsf.de/project/web_new/database/result clone.html?

clone_id=M033F02' ES cell line harboring insertion mutaTion of

target_gene is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CZ294761 39 bp mRNA linear GSS 22-MAR-2005 M093F02 GGTC Gene Trap Library GV14C05 Mus musculus cDNA clone M093F02, mRNA sequence.
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Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
        National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled germ cell tumors"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGE:2240851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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COMMENT
                                                        JOURNAL
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        TITLE
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셤 ò

us-09-669-187a-80.szlm50.rst

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Query Match
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Matches
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AUTHORS
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                                                                                ACCESSION
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Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bX128210 41 bp DNA linear GSS 28-JAN-Danio rerio genomic clone DKEY-279M17, genomic survey sequence.
BX128210
                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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0
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                                                                                                                                                                                                                                                                                                                     Score 11.2; DB 8; Length 40;
Pred. No. 8.9e+05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="DKEY-279M17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                                                          Query Match 58.9%;
Best Local Similarity 81.2%;
Matches 13; Conservative (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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RESULT 47 W34290/c

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48 bp DNA linear GSS 25-APR-2002 1008098B12.2EL yl 1008 - RescueMu Grid I Zea mays genomic, genomic survey seguence. BH802996
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                                                                                                                                                                                                                                                                                              1 (bases 1 to 46)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                     .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
W34290 MRNA linear EST 12-SEP-
ma99007.rl Soares mouse p3NWF19.5 Mus musculus cDNA clone
IMAGE:318828 5' similar to SW:GBG3 BOYIN P29798 GDANINE
NUCLEOTIDE-BINDING PROTEIN G(I)/G($)/G(0) GAMMA-3 SUBUNIT. [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Pax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 58.9%; Score 11.2; DB 8; Length 46; Local Similarity 81.2%; Pred. No. 8.9e+05; es 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: -28Ml3 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                   Mus musculus (house mouse)
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Stanford University
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/tissue_type="loaf"
/tissue_type="loaf"
/dev stage="loaf"
/done="loaf"
/dev stage="loaf"
/dev stage="lo
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11191516D01.1EL x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
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Unpublished (2001)
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008098 row: 14
Class: transposon-taged.
Location/Qualifiers
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/mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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/clone lib="lilg - RescueMu Grid AA"
/rote="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units: For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with ampicillin."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.

| (bases 1 to 50)
| Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                       Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119150 row: 46
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/mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
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Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory
The Stalk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tex: 858 558 638 4100 x1752
Fax: 858 558 638 4100
Email: ecker@salk.edu
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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81.2%; Pred. No. 9e+05;
iive 0; Mismatches 3;
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Search completed: February 15, 2006, 21:10:07 Job time : 1283.74 secs

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                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                    1299706
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/A_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PB_COMB.seq:*
/cgn2_6/ptodata/1/ina/PB_COMB.seq:*
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US-09-565-101-63

US-09-538-873-18

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US-08-852-001-5

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US-09-396-1366-120261

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US-09-396-1366-120261

US-09-59-444-43

US-08-459-448-43

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US-09-547-422-43

US-09-588-462-43

US-09-588-462-43

US-09-68-652-12

US-09-698-652-12

US-09-696-774-90

US-09-030-701-63

US-09-030-701-63

US-09-030-701-63

US-09-080-749-59
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Maximum Match 100%
Listing first 300 summaries
                                                                            nucleic search, using sw model
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seq length: 50
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Minimum DB Maximum DB

Database

Result

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Searched:

Sequence 104710, Sequence 112560, Sequence 112560, Sequence 11360, Sequence 12361, Sequence 123, Appl Sequence 29, Appl Sequence 29, Appl Sequence 108, Appl Sequence 108, Appl Sequence 108, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 14, Ap	ance 40
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ORGANISM: Artificial Sequence
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US-09-538-873-18/c
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APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
FILE REPERBUCE: C. 1393/7009
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT PILING DATE: 1999-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 20
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US-09-965-101-63
is Sequence 63, Application US/09965101
j Patent No. 6821957
igeneral INFORMATION:
j APPLICANT: Davis, Heather L.
j APPLICANT: Schorr, Joachim
j APPLICANT: Schorr, Joachim
j APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Uberland North Man)
j CURRENT FILING DATE: 1039/7057 (HCL/MAT)
j CURRENT FILING DATE: 2001-09-26
j PRIOR FILING DATE: 1998-05-20
j PRIOR FILING DATE: 1997-05-20
j NUMBER OF SEQ ID NOS: 84
j SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                    Query Match

P4.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.7%; Score 14.2; DB 3; Length 20; Best Local Similarity 84.2%; Pred. No. 7.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: synthetic oligonucleotide US-09-082-649B-63
                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-082-649B-63
US-09-082-649B-63
Sequence 63, Application US/09082649B
Patent No. 6339068
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGTGACGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
STRANDEDNESS: single
                      ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-386-063-1
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TELEFAX: (202) 672-5399
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                                                                                FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
; OTHER INFORMATION: Primer
US-10-282-935-18
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Patent No. 6197556
GENERAL INFORMATION:
APPLICANT: Ulanovsky, Levy
TITLE OF INVENTION: BRANCHED PRIMERS
TITLE OF INVENTION: BRANCHED PRIMERS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEDE: BRINKS, HOFER, GILSON & LIONE
STREET: Plaza Drive
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.4; DB 3; Length 22;
Pred. No. 1.8e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                         Query Match 73.7%; Score 14; DB 3; Length 39; Best Local Similarity 100.0%; Pred. No. 9.5e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/852,001
FILING DATE: 06-MAX-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: MATELIN, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 6837/7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LOCATION: 18..19
CTHER INFORMATION: /product= "N = inosine"
US-08-852-001-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.5%;
93.3%;
                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGACGTTCAGGGGTG 16
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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: Illinois
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US-08-852-001-5
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SEQ ID NO 18
LENGTH: 39
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay

APPLICANT: Wohlgemuth, Jay

APPLICANT: Wohlgemuth, Jay

APPLICANT: Woodward

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTCHMUNE

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: 2002-09-06

PRIOR APPLICATION NUMBER: US 10/006,290

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR APPLICATION OF SEQ ID NOS: 9090

SOFTWARE PREDENTIN VERSION 3.1

SEQ ID NO 3663

LENGTH: 50
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KESOULY 9.

KESOULY 9.

Sequence 29, Application US/0866621B

Patent No. 6136544

GENERAL INFORMATION:

APPLICANT: Nutt, Stephen

TITLE OF INVENTION: GLUTAMATE RECEPTOR (OR EAA RECEPTOR)

TITLE OF INVENTION: DLYNUCLEOTIDES AND THEIR USES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLGY & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PALENTIN RELEASE

COMPUTER: DATENTIN RELEASE

CURRENT APPLICATION DATA:

SETTING DATENTING DATA:

CURRENT APPLICATION DATA:

STITMS DATENTING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.5%; Score 13.2; DB 3; Length 50; 83.3%; Pred, No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 20-JUN-1996
CLASSIPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATYORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 016777/0308
TELECOMMUNICATION INFORMATION:
Sequence 3663, Application US/10131827 Patent No. 6905827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-131-827-3663
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APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED NUMBER OF SEQUENCES: 94
                                                     SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.8; DB 2; Length 32;
Pred. No. 3.7e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/07/951,715A
FILING DATE: 2-5EP-1992
CLASSIFICATION NUMBER: US 07/772,027
ATTORNEY/AGENT INFORMATION:
NAME: SPUTILL WINDER: 32,933
REFERENCE/DOCKET NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 32,943
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
                                                         TITLE OF INVENTION: SYNTHETIC DNA SE
TITLE OF INVENTION: INSECTICIDAL ACT
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: CIBA-CERGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/08459448A Patent No. 5859336 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Koziel, Michael G. APPLICANT: Desai, Nalini M. APPLICANT: Lewis, Kelly S. APPLICANT: Kramer, Vance C. APPLICANT: Warren, Gregory W. APPLICANT: Bvola, Stephen V. APPLICANT: Crossland, Lyle D. APPLICANT: Wright, Martha S. APPLICANT: Weight, Martha S. APPLICANT: Merlin, Ellis J. APPLICANT: Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 32 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.4%;
Best Local Similarity 87.5%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GGTGCCGTACAGGGGG 3
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                                                                                                                                                                                                                                                                                              CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-951-715A-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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US-09-396-196G-120261/C
Sequence 120261, Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION:
APPLICANT: Mitcheal Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: 05/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120261
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 67.4%; Score 12.8; DB 3;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-08-666-2218-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-07-951-715A-43/c
; Sequence 43, Application US/07951715A
; Patent No. 5625136
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APPLICANT: Koziel, Michael G.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Wolly, Stephen V.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Leunis, Karen L.
APPLICANT: Launis, Karen L.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGTGACGTTCAGGGG 17
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Erik M.
Pace, Gary M.
Suttie, Janet L.
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Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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APPLICANT: Warren, Gregory W.
APPLICANT: Bvola, Stephen V.
APPLICANT: Bvola, Stephen V.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Marlin, Ellis J.
APPLICANT: Rothstein, Steven J.
APPLICANT: Rothstein, Steven J.
APPLICANT: Dawson, Cindy G.
APPLICANT: Dawson, Cindy G.
APPLICANT: Dawson, Cindy G.
APPLICANT: Sutie, APPLICANT: Sutie, Janet L.
APPLICANT: SUTIE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                      CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Ru., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER: READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COS/MS-DOS
COMPUTER: DEAD FORM:
COMPUTER: DEAD FO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATION SYSTEM:

OPERATION OF PREACTION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,595A

FILING DATE: 02-JUN-1995

CLASSIFICATION #00

PRIOR APPLICATION BOO

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGRNT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: CGC 1577/CIP/DIV3

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 10FORMATION:

TELECOMMUNICATION 10FORMATION 10FORMAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /desc = "primer P5(a)"
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other nucleic acid
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Desai, Nalini M.
Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGTGACGTTCAGGGGG 18
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STRANDEDNESS: single
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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DESCRIPTION:
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APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Sutie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.4%; Score 12.8; DB 2; Length 32;
87.5%; Pred. No. 3.7e+03;
tive 0; Mismatches 2; Indels
                               ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
                                                                                                                                                                                      COUNTRY: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: GG C1577/CIP/DIV4
TELECOMMUTCATION INFORMATION:
NAME: CALL CALL SALESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other nucleic acid
/desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 derecceracadedes
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08-459-595A-43/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-459-448A-43
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
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RESULT 16

US-09-547-422-43/C

J Sequence 43, Application US/09547422

Sequence 43, Application US/09547422

Sequence 43, Application US/09547422

Return 60-520100

Beai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warner, Vance C.
Warner, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
ITILE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road

CITY: Research Triangle Park
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APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995
CLASSIFICATION *CINKNOWN>
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 02-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Making J. Timochy
REGISTRATION NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.8; DB 3;
Pred. No. 3.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO: 43:
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGTGACGTTCAGGGGG 18
                                                                                            ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GGTGCCGTACAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.5
Matches 14; Conservative
                                                                      USA
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ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.4%; Score 12.8; DB 3; Length 32; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                    COMPUTER: USA

ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-401-1995
FILING DATE: 02-5EP-1992
RICK APPLICATION NUMBER: US 07/951,715
FILING DATE: 02-5EP-1992
RAPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs J. Timochy
REGISTRATION NUMBER: CGC1577/CIP/DIV
TEMECOMMUNICATION NUMBER: CGC1577/CIP/DIV
  INSECTICIDAL ACTIVITY IN MAIZE
                                        AUDRESSEE: No. 6075185artis Corporation STREET: 3054 Cormwallis Road CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other nucleic acid
/desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-459-444-43/C
US-08-459-444-43/C
Sequence 43, Application US/08459444A
Parent No. 6121014
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
  TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                          COUNTRY:
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Ngoc
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE OF INVENTION: CRRONIC INFLAMMATORY DISEASES
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506412000120
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4733
LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.4%; Score 12.8; DB 3;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2;
                      APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. 6720488-2001
CLASSIFICATION: -(UNKNOWN)
PRIOR APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APP-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8689
TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-09-988-462-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4733, Application US/10131827; Patent No. 6905827; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGTGACGTTCAGGGGG 18
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CORGANISM: Homo sapiens
US-10-131-827-4733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
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                      COMPUTER: IEAM PC compatible
COMPUTER: IEAM PC compatible
SOFTWARE: PACE COMPUTER:
SOFTWARE: PACE COMPUTER:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-UN1-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Maciss 10. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/OCKET NUMBER: 5-18805H
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.4%; Score 12.8; DB 3; Length 32; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSER: Syngenta Biotechnology, Inc.
STREET: 3054 COrnwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: /desc = "primer P5(a)" HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-09-547-422-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18. Application US/09988462
Sequence 18. Application US/09988462
GENERAL INFORMATION:
CENTRAL INFORMATION:
MATCH NO.
CENTRAL NO.
CENTRAL NO.
MATCH C.
MATCH 
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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US-09-988-462-43/c
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Gaps

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GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Schwartz, David M.

TITLE OF INVENTION: UNMETHYLATED CDG DINUCLEOTIDE IN THE TREATMENT OF TITLE OF INVENTION: LES-ASSOCIATED DISORDERS

TITLE OF INVENTION: LES-ASSOCIATED DISORDERS

TITLE OF INVENTION: LES-ASSOCIATED DISORDERS

FILE REFERENCE: C1039/7011

CURRENT FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/039,405

PRIOR APPLICATION NUMBER: 60/039,405

PRIOR APPLICATION NUMBER: 60/039,405

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 63

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Krieg et al.,
APPLICANT: Krieg et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES:
AUDRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
TURING DATE: 30-October-1997
CLASSIFCATION: 514
PRICR APPLICATION DATA:
APPLICATION DATE: U.S. Serial No. 6239116 08/738,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                               4; Indels
                                                                                          Query Match
66.3%; Score 12.6; DB 3;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.3%; Score 12.6; DB 3; 78.9%; Pred. No. 4.4e+03; tive 0; Mismatches 4;
          ; OTHER INFORMATION: Synthetic oligonucleotide US-08-738-652-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: synthetic oligonucleotide US-09-030-701-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 90, Application US/08960774
Patent No. 6239116
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Best Local Similarity 78.9
Matches 15; Conservative
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CITY: La Jolla
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US-08-960-774-90
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FEATURE:
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Sequence 12, Application US/08738652B

Sequence 12, Application US/08738652B

Sequence 12, Application US/08738652B

SERENAL INFORMATION:

APPLICANT: Krieg, Arthur M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

FILE REFERENCE: C1039/7004 HCL

CURRENT APPLICATION NUMBER: US/08/738,652B

CURRENT APPLICATION NUMBER: US 08/276,358

EARLIER FILING DATE: 1994-07-15

EARLIER FILING DATE: 1994-07-15

SEALIER FILING DATE: 1995-02-07

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 12

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 19;
                                                                                                            Sequence 2.7, Application US/09672126B

APPLICANT: Hartmann, Gunther AppliCANT: Bratzler, Robert L.

APPLICANT: Bratzler, Robert L.

TITLE OF INVENTION: Methods Related to Immunostimulatory, TITLE OF INVENTION: Methods Related to Interferon FILE REFERENCE: C1039/7044

CURRENT APPLICATION NUMBER: US/09/672,126B

CURRENT FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 169

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEX: misc_feature
LOCATION: (1)...(2)
OTHER INFORMATION: Backbone has phosphorothioate linkages.
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NAME/KEY: misc_feature
LOCATION: (14)...(18)

OTHER INFORMATION: Backbone has phosphorothioate linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (3)...(13)
OTHER INFORMATION: Backbone has phosphodiester linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (19)...(19)
OTHER INFORMATION: Backbone has phosphodiester linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
66.3%; Score 12.6; DB 3;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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     21 GTGACGTTCTGGGAGG
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                                                                                                    US-09-672-126B-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 27
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
NAME/KSY: misc feature
LOCATION: (0) - (0)
OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5'
OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages
US-09-082-649B-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                              APPLICANT: Schort, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
FILE REPERENCE: C1039/7009
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT PILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 60/047,233
PRIOR APPLICATION NUMBER: US 60/047,209
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FASTERQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: for Activating Dendritic Cells
FILE REFERENCE: C1039/7017
CURRENT APPLICATION NUMBER: US 08/960,774
EARLIER FILING DATE: 1998-11-13
EARLIER PILING DATE: 1997-10-30
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 08/738,652
EARLIER APPLICATION NUMBER: US 08/736,653
EARLIER APPLICATION NUMBER: US 08/276,358
EARLIER FILING DATE: 1995-02-07
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Ratise FastsEQ for Windows Version 3.0
EENGTH: 20
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66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.3%; Score 12.6; DB 3; Length 20; 78.9%; Pred. No. 4.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/09191170 Patent No. 6429199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGTGACGTTCAGGGGGG 19
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                    Krieg, Arthur M.
Schorr, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.9
Matches 15, Conservative
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US-09-191-170-47
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APPLICANT: Krieg, Arthur M.
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Genor, Joachim
APPLICANT: WL, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1039/7009
CURRENT APPLICATION NUMBER: US 60/047,233
FRIOR FILING DATE: 1999-05-20
FRIOR FILING DATE: 1997-05-20
FRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.6; DB 3; Length 20;
Pred. No. 4.4e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
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NAME/KEY: misc_feature
; LOCATION: (0) ...(0)
; OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 66.3%; Score 12.6; DB 3; 1 Similarity 78.9%; Pred. No. 4.4e+03; 15; Conservative 0; Mismatches 4;
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELEPAK: 619/678-5070
TELEFAK: 619/678-5070
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 52, Application US/09082649B
Patent No. 63139068
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24
US-09-082-649B-59
Sequence 59, Application US/09082649B
Patent No. 6339068
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGTGACGTTCAGGGGGG 19
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Best Local Similarity 78.9%;
Matches 15; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: CDNA
US-08-960-774-90
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Best Local Similarity
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Query Match
Best Local Similarity 78.9
Matches 15; Conservative
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US-09-65-101-52
Sequence 52, Application US/09965101
Patent No. 6821957
GENERAL INFORMATION:
APPLICANT: Davis, Heather I.
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Wi, Tong
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1039/1057 (HCL/MAT)
CURRENT APPLICATION NUMBER: US 09/085,101
CURRENT APPLICATION NUMBER: US 09/082,649
PRIOR FILING DATE: 1997-05-20
PRIOR PLICATION NUMBER: US 60/047,233
PRIOR APPLICATION NUMBER: US 60/047,209
PRIOR PLICATION NUMBER: US 60/047,209
PRIOR PLICATION NUMBER: US 60/047,209
PRIOR PLICATION NUMBER: US 60/047,209
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 52
LENGTH: 20
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                                              GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Methods of Treating Cancer Using
TITLE OF INVENTION: Immunostimulatory Oligonuclectides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTHER INFORMATION: Has a phosphorothioate backbone. US-09-965-101-52
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Pred. No. 4.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-337-619-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: synthetic oligonucleotide
                                                                                                                                     TILE REFERENCE: C1039/JO21/HCL
CURRENT APPLICATION NUMBER: US/09/337,619
CURRENT FILING DATE: 1999-06-21
EARLIER APPLICATION NUMBER: US 08/960,774
EARLIER APPLICATION NUMBER: US 08/960,774
EARLIER APPLICATION NUMBER: US 08/36,063
EARLIER APPLICATION NUMBER: US 08/36,063
EARLIER FILING DATE: 1997-10-30
EARLIER FILING DATE: 1996-10-30
EARLIER FILING DATE: 1994-07-05
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PRESEQ for Windows Version 3.0
SSEQ ID NO 12
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
Sequence 12, Application US/09337619
Patent No. 6653292
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Best Local Similarity 78.9%;
Matches 15; Conservative
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JAPPLICANT: Krieg, Arthur M.

APPLICANT: Krieg, Arthur M.

JAPPLICANT: Schort, Joachim

JAPPLICANT: Schort, Joachim

APPLICANT: Schort, Joachim

APPLICANT: Will Tong

TITLE OF INVENTION: Vectors and Methods for Immunization or

TITLE OF INVENTION: Therapeutic Protocols

FILE REFERENCE: C1039/7057 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/965, 101

FRIOR PELING DATE: 1998-05-20

PRIOR FILING DATE: 1998-05-20

PRIOR APPLICATION NUMBER: US 60/047,233

PRIOR FILING DATE: 1997-05-20

NUMBER OF SEQ ID NOS: 84

SOFTWARRE: FastSEQ for Windows Version 3.0

LENGTH: 20
Query Match 66.3%; Score 12.6; DB 3; Length 20; Best Local Similarity 78.9%; Pred. No. 4.4e+03; Matches 15; Conservative 0; Mismatches 4; Indels
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; GENERAL INCORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory;
TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 200-09-27
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFFWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
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; Sequence 1, Application US/09672126B
; Patent No. 6949520
                                                                                                                                                                                                                                                                          Sequence 59, Application US/09965101
Patent No. 6821957
GENERAL INFORMATION:
                                                                                                     1 GGGGTGACGTTCAGGGGGG 19
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Query Match 66.3%; Score 12.6; DB 3; Length 20; Best Local Similarity 78.9%; Pred. No. 4.4e+03; Matches 15; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 136, Application US/09672126B
; Sequence 136, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
    APPLICANT: Hartmann, Gunther
; APPLICANT: Brateler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory;
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FESTESEQ for Windows Version 3.0
; SEQ ID NO 136
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
            APPLICANT: Bratzler, Robert L.
APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Nucleic Acid-Induced Interferon
FILE REPERENCE: C1039/7044
CURRENT APPLICATION NUMBER: US/09/672,126B
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/156,147
PRIOR FILING DATE: 1999-09-29
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Patent No. 6949520
Patent INCORMATION:
APPLICANT: Bratchann, Gunther
APPLICANT: Bratzler Robert L.
APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Nucleic Acid-Induced Interferon
                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-672-126B-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 169
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 135
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGTGACGTTCAGGGGGG 19
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APPLICANT: Hartmann, Gunther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.9°
Matches 15, Conservative
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US-09-672-126B-136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mattaler, Robert L.
APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Nucleic Acid-Induced Interferon
FILE REFERENCE: C1039/7044
CURRENT APPLICATION NUMBER: US/09/672,126B
CURRENT APPLICATION NUMBER: 60/156,147
PRIOR APPLICATION NUMBER: 60/156,147
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 169
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5:
LENGTH: 20
                                                                                             NAME/KEY: misc_feature
COCATION: (1)...(2)
COCATION: (1)...(2)
COTHER INFORMATION: Backbone has phosphorothioate linkages.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3)...(14)
OTHER INFORMATION: Backbone has phosphodiester linkages.
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)...(19)
OTHER INFORMATION: Backbone has phosphorothioate linkages.
PEATURE:
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; OTHER INFORMATION: Backbone has phosphorothioate linkages.
US-09-672-126B-5
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LOCATION: (20) ...(20)
OTHER INFORMATION: Backbone has phosphodiester linkages.
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Pred. No. 4.4e+03;
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OTHER INFORMATION: Synthetic Oligonucleotide
                                                 OTHER INFORMATION: Synthetic Oligonucleotide
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US-09-672-126B-135
Sequence 135, Application US/09672126B
Patent No. 6949520
GENERAL INFORMATION:
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Patent No. 0549520
GENERAL INFORMATION:
APPLICANT: Hartmann, Gunther
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78.9%;
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 78.9
Matches 15; Conservative
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US-09-672-126B-5
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US-09-907-794A-225/c

Sequence 225, Application US/09907794A

; Patent No. 6655468

; GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan, James
      US-09-672-126B-165
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APPLICANT:
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                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1)...(2)
OTHER INFORMATION: Backbone has phosphorothioate linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (16)...(20)
OTHER INFORMATION: Backbone has phosphorothioate linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (21)...(21)
OTHER INFORMATION: Backbone has phosphodiester linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (3).7.(15)
OTHER INFORMATION: Backbone has phosphodiester linkages
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US-09-396-196G-78259/C

Sequence 78259 Application US/09396196G

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Number: Nn.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1 the
CURRENT APPLICANTION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
SPRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
FILE REFERENCE: C1039/7044

CURRENT APPLICATION NUMBER: US/09/672,126B

CURRENT FILING DATE: 2000-09-27

FRIOR APPLICATION NUMBER: 60/156,147

PRIOR FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 169

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 21
                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic Oligonucleotide
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                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 15; Conserv
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RESULT 35

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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Sequence 165, Application US/09672126B
; Sequence 165, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
    APPLICANT: Hartmann, Gunther
; APPLICANT: Brainler, Robert L.
    APPLICANT: Brainler, Robert L.
    APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory;
    TITLE OF INVENTION: Methods Related to Immunostimulatory;
    TITLE OF INVENTION: Nucleic Acid-Induced Interferon;
    FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.6; DB 3;
Pred. No. 4.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-672-126B-165
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66.3%; Score 12.6; I
Best Local Similarity 78.9%; Pred. No. 4.66
Matches 15; Conservative 0; Mismatches
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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APPLICANY: ROY, MARGAREA ANII.
APPLICANY: Stewart, Initiothy A.
APPLICANY: Williams, Daniel
APPLICANY: None
APPRICANY: None
APPLICANY: None
APPLICANY: None
APPLICANY: None
APPRICANY: None
AP
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; Sequence 225, Application US/09902775A
; Patent No. 6666451
; GENERAL INFORMATION:
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                       Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-03
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US-09-905-125A-225/c
; Sequence 225, Application US/09905125A
; Patent No. 6664376
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Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Best Local Similarity 78.9
Matches 15; Conservative
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Gao, Wei-Qiang
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Williams, F. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR PELICATION NUMBER: PCT/USOO/04414
PRIOR PELLING DATE: 1090-00-18
PRIOR PELLING DATE: 1090-00-07-18
PRIOR PELLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-30
PRIOR PELLING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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FILING DATE: 1999-12-20
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                                                                                                                                                                                                                                      US-09-906-700-225/c
; Sequence 225, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
1 GGGGTGACGTTCAGGGGGG 19
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Oiang
Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                    19 GGAGCGTCGCTCAGGGGGG
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Goddard, A.
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Eaton, Dan L.
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic FILE REPRESENCE: 10466-14

CURRENY ERPLICATION NUMBER: US/09/902,775A

CURRENY ELLING DATE: 2010-07-10

PRIOR APPLICATION NUMBER: US/09/00.4414

PRIOR FILING DATE: 1099-07-20

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR PRILOR PRIOR NUMBER: PCT/US99/2094

PRIOR PRILOR DATE: 1999-09-13

PRIOR PRILOR DATE: 1999-09-12

PRIOR APPLICATION NUMBER: PCT/US99/28014

PRIOR PRILOR DATE: 1999-10-20

PRIOR PRILOR DATE: 1999-10-20

PRIOR PRILOR DATE: 1999-10-30

PRIOR PRILOR DATE: 2000-01-05

PRIOR PRINAPER OF SEQUID NOTE: 1999-10-30

PRIOR PRILOR DATE: 1999-10-30

PRIOR PRILOR DATE: 2000-01-05

PRIOR PRINAPER OF SEQUID NOTE: 1999-10-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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ORGANISM: Artificial Seguence
                                                                                                                                                                     Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
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                                                                                                                                                                                                                                                            Goddard, A.
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICATION NUMBER: PCT/US99/28214
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APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acids Encoding the Same
FILE RPERERNCE: GNE. 161892218
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2000-02-22
RIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: POSP-09-15
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Sequence 225, Application US/09903603A

Patent No. 6767995

GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E
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Filvaroff, Ellen
                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 225
LENGTH: 44
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APPLICANT: Ashkenzi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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and Transmembrane Polypeptides and Nucleic
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION WUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
PRIOR PILING DATE: 4999-12-30
PRIOR PILING DATE: 4999-12-30
PRIOR PILING DATE: 4000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-904-920A-225/c
; Sequence 225, Application US/09904920A
; Patent No. 6806352
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Filvaroff, Ellen
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers, Luc
Eaton, Dan L.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-905-381A-225/c
Sequence 225, Application US/09905381A
Patent No. 6818746
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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                                              Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
FEATURE:
                        Paoni, Nicholas F.
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Patent No. 6818449
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-909-064-225/c
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0; Gaps

Indels

4

0; Mismatches

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15; Conservative
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Matches
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/145,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                 Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                         Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                         Goddard, A.
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66.3%; Score 12.6; DB 3; Length 44; 78.9%; Pred. No. 4.8e+03;

Query Match Best Local Similarity

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PPLICANT: Roy, Margaret Ann
PPLICANT: Stewart, Indothy A.
PPLICANT: Tunas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Williams, P. Mickey
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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PRIOR PELICATION NUMBER: PCT/INSO0/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
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CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/21547
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                                                                                                                                             US-09-906-618-225/c
; Sequence 225, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
1 GGGGTGACGTTCAGGGGGG 19
                                                19 GGAGCGTCGCTCAGGGGGG 1
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Goddard, A.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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                    PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-36
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CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/665,350
     APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 225, Application US/09904462 Patent No. 6878807 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: Oligonucle
US-09-906-646-225
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Filvaroff, Ellen
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
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Best Local Similarity
Matches 15; Conserv
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US-09-904-462-225/c
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APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT FILING DATE: 2002-01-22
PRIOR FILING DATE: 1999-00-2-22
PRIOR PLING DATE: 1999-00-2-22
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
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US-09-906-618-225
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                                                                                                                                                                                                                                                                                                                                   Length 44;
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66.3%; Score 12.6; DB 3;
Best Local Similarity 78.9%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 4;
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 225
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 225, Application US/09906646
Patent No. 6852848
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Javi
APPLICANT: Bosnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard, A.
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US-09-906-646-225/c
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APPLICANT:
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APPLICANT:
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APPLICANT
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-15
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-902-736A-225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR PELICATION NUMBER: PCT/US99/21089
PRIOR PELICATION NUMBER: PCT/US99/21089
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 44
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US-09-906-722A-225/c
US-09-906-722A-225/c
; Sequence 225, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                        Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
             Hillan, Kenneth, J.
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                                                                                                                                            Paoni, Nicholas F.
                                                   Kljavin, Ivar J.
Aather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                              Pan, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-904-462-225
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1990-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-0-28
PRIOR PLING DATE: 1999-0-09
PRIOR PLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR DATE: 1999-12-07
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US-09-902-736A-225/c
Sequence 225, Application US/09902736A
Patent No. 689414B
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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66.3%; Score 12.6; DB 3; Length 44; 78.9%; Pred. No. 4.8e+03; ive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                        US-09-641-638-1255/c; Sequence 1255, Application US/09641638; Patent No. 6432648
                                                                                                                                        1 GGGGTGACGTTCAGGGGGG 19
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APPLICANT: Blumenfeld, Marta
                     Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
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ORGANISM: Homo Sapiens
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nes 15; Conserv
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Best Local S
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERBACE: GNB.16182261
CURRENT APPLICATION NUMBER: US/09/06,722A
CURRENT PELLING DATE: 2001-07-16
PRIOR PLLING DATE: 2000-02-22
PRIOR PLLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLLING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-07
PRIOR PELLOR APPLICATION NUMBER: US 60/146,222
PRIOR PELLOR APPLICATION NUMBER: US 60/146,222
PRIOR PELLOR APPLICATION NUMBER: US 60/146,222
PRIOR PELLOR DATE: 1999-07-28
PRIOR PELLOR DATE: 1999-07-28
PRIOR PELLOR DATE: 1999-09-08
PRIOR PELLOR DATE: 1999-09-15
PRIOR PELLOR DATE: 1999-01-15
PRIOR PELLOR DATE: 1999-01-15
PRIOR PELLOR DATE: 1999-01-15
PRIOR PELLOR DATE: 1999-11-20
PRIOR PELLOR DATE: 1999-12-20
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CRGANISM: Artificial Sequence
FRATURE:
CTHEN INFORMATION: Description of Artificial Sequence: Synthetic
CTHEN INFORMATION: oligonucleotide probe
US-09-906-722A-225
                                                                                                                                                                                                                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                                                    Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                           Ferrara, Napoleone
Filvaroff, Ellen
                           Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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SEQ ID NO 225
LENGTH: 44
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REPRENDE: GENEST: 051CP1
CURRENT APPLICATION NUMBER: US 09/502,330
PRIOR PAPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 1099-02-11
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR PRICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-03-23
PRIOR PRILING DATE: 1999-02-12
PRIOR PRILING DATE: 1999-02-12
PRIOR PRILING DATE: 1999-02-12
PRIOR PLILING DATE: 1999-02-13
PRIOR PLILING DATE: 1999-02-12
PRIOR PLILING DATE: 1999-02-13
PRIOR PLILING DATE: 1999-02-13
PRIOR PLILING DATE: 1999-03-23
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j Sequence 1255, Application US/10170097

j Patent No. 6794143

j GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2000-08-16

PRIOR FILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: US 69/502,330

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 1999-05-07
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Gaps
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; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-387-371 : polymorphic base C or T
US-09-641-638-1255
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5 9 US-10-809-189-120261 Sequence 5 9 US-10-956-157-186456 Sequence 9 US-10-956-157-265641 Sequence 5 9 US-10-956-157-280869 Sequence 5 9 US-10-956-157-280869 Sequence	1 25 9 US-10-956-157-280870 Sequence 280870, 1 25 10 US-11-036-317-42252 Sequence 42252, A 2 10 US-11-036-317-503552 Sequence 503752.	1 25 10 US-11-036-317-703160 Sequence 703160, 1 25 10 US-11-036-317-894738 Sequence 894738,	1 25 10 US-11-016-317-954962 Sequence 954962,	1 26 10 US-11-027-767A-13 Sequence 13, Appl	1 31 3 US-09-801-274-1698 Sequence 1698, Ap 1 32 3 US-09-988-462-43 Sequence 43, Appl	41 7 US-10-035-833A-822 Sequence 822, App	3 19 3 US-09-776-479-976 Sequence 976, App	3 19 3 US-09-776-479-1046 Sequence 1046, Ap	3 19 3 US-09-776-479-1046 Sequence 1046, Ap	3 19 5 US-10-112-653-930 Sequence	3 19 5 US-10-017-995-1046 Sequence 1046, Ap	3 19 6 US-10-314-578-976 Sequence 976, App	3 19 8 US-10-314-5/8-1046 Sequence 1046, Ap 3 19 8 US-10-831-778-976 Sequence 976, App	3 19 8 US-10-831-778-1046 Sequence 104	3 19 10 US-11-056-463-27 Sequence 27	2 2 3 US-09-888-326-437 Sequence 437	3 20 3 US-09-888-326-443 Sequence 443	3 US-09-818-918-12 Sequence 12,	3 20 3 US-09-776-479-767 Sequence 767	3 20 3 US-09-776-479-968 Sequence 968	3 20 3 US-09-776-479-969 Sequence 969	3 20 3 US-09-776-479-519 Sequence 519	3 20 3 US-09-776-479-767 Sequence 767	3 20 3 US-09-776-479-968 Sequence 968	3 20 3 US-09-776-479-969 Sequence 965	3 20 3 US-09-965-101-59 Sequence 59,	3 20 5 US-10-112-653-496 Sequence 496 3 20 5 US-10-112-653-740 Sequence 740	3 20 5 US-10-112-653-878 Sequence 878, App	3 20 5 US-10-112-653-923 Sequence 923, App 3 20 5 US-10-112-653-1040 Sequence 1040, Ap	3 20 5 US-10-017-995-519 Sequence 519, App	3 20 5 US-10-017-995-767 Sequence 767, App 3 20 5 US-10-017-995-909 Sequence 909, App	3 20 5 US-10-017-995-968 Sequence 968, App	3 20 5 US-10-017-995-969 Sequence 965 3 20 5 US-10-161-229-47 Sequence 47,	3 20 6 US-10-194-035-89 Sequence 89, Appl	3 20 6 US-10-224-523-35 Sequence 35, Appl 3 20 6 US-10-187-264A-12 Sequence 12, Appl	3 20 6 US-10-306-522-12 Sequence 12,	3 20 6 US-10-314-578-519 Sequence 519	3 20 6 US-10-314-578-767 Sequence 767 3 20 6 US-10-314-578-909 Sequence 909	20 6 US-10-314-578-968 Sequence 968, App	3 20 6 US-10-314-578-969 Sequence 969, App	3 20 6 US-10-455-247-3 Sequence 3, Appli 3 20 7 112-10-719-493-12 Sequence 12. Appl	3 20 7 US-10-627-331-12 Sequence 12, Appl	3 20 7 US-10-743-625-12 Sequence 12, Appl	3 20 7 US-10-679-710-12 Sequence 12, Appl C
1 25 9 US-10-809-189-120261 Sequence 1 25 9 US-10-956-157-186456 Sequence 1 25 9 US-10-956-157-26541 Sequence 1 25 9 US-10-956-157-280869 Sequence 1 25 9 US-10-956-157-280869 Sequence	2.8 67.4 25 9 US-10-956-157-280870 Sequence 280870, 2.8 67.4 25 10 US-11-036-317-42252 Sequence 42252, A 2.8 67.4 25 10 HS-11-036-3177-507752 Sequence 503752	2.8 67.4 25 10 US-11-036-317-303-32 Sequence 703160, 2.8 67.4 25 10 US-11-036-317-809138 Sequence 703160, 2.8 67.4 25 10 US-11-036-317-894738 Sequence 894738,	2.8 67.4 25 10 US-11-036-317-954962 Sequence 954962,	2.8 67.4 26 10 US-11-027-767A-13 Sequence 13, Appl	2.8 67.4 31 3 US-09-801-274-1698 Sequence 1698, Ap 2.8 67.4 32 3 US-09-988-462-43 Sequence 43, Appl	2.8 67.4 41 7 US-10-035-833A-822 Sequence 822, App	2.6 66.3 19 3 US-09-776-479-976 Sequence 976, App	2.6 66.3 19 3 US-09-776-479-1046 Sequence 1046, Ap	2.6 66.3 19 3 US-09-776-479-1046 Sequence 1046, Ap	2.6 66.3 19 5 US-10-112-653-930 Sequence	2.6 66.3 19 5 US-10-017-995-1046 Sequence 1046, Ap	2.6 66.3 19 6 US-10-314-578-976 Sequence 976, App	2.6 66.3 19 6 US-10-314-5/8-1046 Sequence 1040, Ap. 2.6 66.3 19 8 US-10-831-778-976 Sequence 976, App	2.6 66.3 19 8 US-10-831-778-1046 Sequence 104	2.6 66.3 19 10 US-11-056-463-27 Sequence 27	2.6 66.3 20 3 US-09-888-326-437 Sequence 437	2.6 66.3 20 3 US-09-888-326-443 Sequence 443	2.6 66.3 20 3 US-09-818-918-12 Sequence 12,	2.6 66.3 20 3 US-09-776-479-767 Sequence 767	2.6 66.3 20 3 US-09-776-479-968 Sequence 968	2.6 66.3 20 3 US-09-776-479-969 Sequence 969	2.6 66.3 20 3 US-09-764-5 Sequence 519 Sequence 519	2.6 66.3 20 3 US-09-776-479-767 Sequence 767 5 6 66 3 20 3 US-09-776-479-909 Sequence 909	2.6 66.3 20 3 US-09-776-479-968 Sequence 968	2.6 66.3 20 3 US-09-776-479-969 Sequence 969	2.6 66.3 20 3 US-09-965-101-59 Sequence 59,	2.6 66.3 20 5 US-10-112-653-496 Sequence 496 2.6 66.3 20 5 US-10-112-653-740 Sequence 740	2.6 66.3 20 5 US-10-112-653-878 Sequence 878, App	2.6 66.3 20 5 US-10-112-653-923 sequence 923, App 2.6 66.3 20 5 US-10-112-653-1040 Sequence 1040, Ap	2.6 66.3 20 5 US-10-017-995-519 Sequence 519, App	2.6 66.3 20 5 US-10-017-995-767 Sequence 767, App 2.6 66.3 20 5 US-10-017-995-909 Sequence 909, App	2.6 66.3 20 5 US-10-017-995-968 Sequence 968, App	2.6 66.3 20 5 US-10-017-995-969 Sequence 963 2.6 66.3 20 5 US-10-161-229-47 Sequence 47.	2.6 66.3 20 6 US-10-194-035-89 Sequence 89, Appl	2.6 66.3 20 6 US-10-224-523-35 Sequence 35, Appl 2.6 66.3 20 6 US-10-187-264A-12 Sequence 12, Appl	2.6 66.3 20 6 US-10-306-522-12 Sequence 12,	2.6 66.3 20 6 US-10-314-578-519 Sequence 519	2.6 66.3 20 6 US-10-314-578-767 Sequence 767 2 6 66 3 20 6 US-10-314-578-909 Sequence 909	2.6 66.3 20 6 US-10-314-578-968 Sequence 968, App	2.6 66.3 20 6 US-10-314-578-969 Sequence 969, App	2.6 66.3 20 6 US-10-455-247-3 Sequence 3, Appli 2.6 66.3 20 7 US-10-719-493-12 Sequence 12, Appl	2.6 66.3 20 7 US-10-627-331-12 Sequence 12, April	2.6 66.3 20 7 US-10-743-625-12 Sequence 12, Appl	2.6 66.3 20 7 US-110-679-710-12 Sequence 12, Appl C

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; CTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends US-09-888-326-447
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APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REPERENCE: C103/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/176,479
PRIOR APPLICATION NUMBER: US 60/176,991
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR PRILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 19
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100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels
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Publication No. US20040067902A9
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
 CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SSEQ ID NO 447
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80, Application US/09776479; Publication No. US20030087848A1; GENERAL INFORMATION:
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US-09-776-479-80
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; Sequence 447, Application US/0988326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
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S-09-906-760A-225

IS-09-907-623-225

IS-09-902-572A-225

IS-09-902-979-225

IS-09-905-149-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-815A-225

IS-09-906-818-225

IS-09-906-818-225

IS-09-906-818-225
US-09-906-742-225
US-09-906-838-225
US-09-907-6138-225
US-09-907-6138-225
US-09-907-6138-225
US-09-904-86-225
US-09-904-86-225
US-09-904-86-225
US-09-904-905-225
US-09-903-749A-225
US-09-903-749A-225
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US-09-903-749A-225
US-09-903-749A-225
US-09-903-749A-225
US-09-903-744-225
US-09-903-904-462-225
US-09-903-904-462-225
US-09-903-904-462-225
US-09-903-904-485-225
US-09-903-904-88-225
US-09-904-88-225
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US-09-906-618-225
US-09-907-728-225
US-09-904-805-225
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US-10-017-995-80
US-10-017-995-80

Sequence 80, Application US/10017995

Publication No. US20030055014A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

TILE REPERENCE: C1037/7025 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/017,995

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: US 60/255,534

PRIOR PLING DATE: 2001-12-14

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels
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   CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 80
LENGTH: 19
                                                                                                                                                                           ) OTHER INFORMATION: Synthetic Sequence US-09-776-479-80
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-112-653-74
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LENGTH: 19
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; Sequence 80, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: USE MECHANA
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                           GENOLIC ALL STR-80

Sequence 80, Application US/10314578

Publication No. US20030212026A1

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Schetter, Christian

APPLICANT: Schetter, Christian

APPLICANT: Vollmer, Jorg

TITLE OF INVENTION: Immunostimatory Nucleic Acids

FILE REFERENCE: C1039/7035 (HCL/MAT)

CURRENT APPLICATION NUMBER: US 60/156,113

PRIOR APPLICATION NUMBER: US 60/156,113

PRIOR FILING DATE: 1999-09-25

PRIOR FILING DATE: 1999-09-27

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 1145

SOFTWARE: FastERC for Windows Version 3.0

LENGTH: 19

TYPE: DNA

PRATURE: ARTHICIAL SEQUENCE

CREATH: 19

TYPE: DNA

TYPE: DNA

PRATURE: ARTHICIAL SEQUENCE
                                                                                       Query Match
100.0%; Score 19; DB 5;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0;
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FEATURE:
OTHER INFORMATION: Synthetic Sequence
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; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-80
; OTHER INFORMATION: Synthetic Sequence US-10-017-995-80
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Best Local Similarity 100.0
Matches 19; Conservative
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US-10-831-778-80
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Sequence 76, Application US/10112653
; Publication No. US2003005026841
; GENERAL INFORMATION:
    APPLICANT: Berg, Daniel J.
    TITLE OF INVENTION:
    TITLE OF INVENTION: TRANTWORTHWILATORY NUCLEIC ACID FOR
    TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES;
    FILE REPERENCE: C01039/70060(AWS)
    CURRENT APPLICATION NUMBER: US/10/112,653
    CURRENT APPLICATION NUMBER: US 60/279,642
    PRIOR PILING DATE: 2001-03-29
    NUMBER OF SEC ID NOS: 1040
    SOFTWARE: EastSEC for Windows Version 3.0
    LENGTH: 19
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                                                                                                                                                                                        US-09-776-479-82

US-09-776-479-82

Sequence 82, Application US/09776479

Publication No. US20040067902A9

GENERAL INFORMATION:

APPLICANT: Bratiler, Robert L.

APPLICANT: Fouron, Ves

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the

TITLE OF INVENTION: Transferent of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT APPLICATION NUMBER: US 60/179,991

PRIOR FILING DATE: 2000-02-03

FRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 82

LENGTH: 19
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91.6%; Score 17.4; DB 3; Length 19; 94.7%; Pred. No. 1.3e+02;
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91.6%; Score 17.4; DB 5;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1;
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                                               0; Mismatches
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                                                                                          1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                   1 GGGGTGTCGTTCAGGGGGG 19
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FEATURE:
                     Best Local Similarity 94.7
Matches 18; Conservative
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Matches 18; Conservative
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US-10-112-653-76
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  Query Match
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Sequence 82, Application US/09776479

Publication No. US20030087848A1

GENERAL INFORMATION:
APPLICANT: Ratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Pouron, Yves

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT FILING DATE: 2001-02-02

RRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SEQ ID NO 82

LENGTH: 19
                                                                                                                                                                                                                                                                              ; sequence 448, Application US/0988326; Bublication No. US20030026801A1; GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Welner, George; APPLICANT: Welner, George; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced; TITLE OF INVENTION: Methods for Enhancing Cancer; FILE REFERENCE: C1039/7052 (AMS); CURRENT FILING DATE: 2001-06-22 PRIOR PRIOR FILING DATE: 2000-06-22 NUMBER OF SEQ ID NOS: 848; SOFTWARE: PSELESQ for Windows Version 3.0; SEQ ID NO 448
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                                           100.0%; Score 19; DB 8; Length 19; 100.0%; Pred. No. 21;
                                                                                          0; Indels
                                                                ; Pred. No. 21;
0; Mismatches
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ORGANISM: Artificial Sequence
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                                           Query Match
Best Local Similarity 100.
Matches 19; Conservative
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US-09-776-479-82
US-10-831-778-80
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WS-11-036-317-815104/c
Sequence 815104, Application US/11036317
Sequence 815104, Application US/11036317
Sequence 815104, Application US/1036317
Sequence 815104, Application No. 220050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TILLE OF INVENTION METHOD of Analysis of Alternative Splicing in Mouse;
FILE REPERENCE: 3664.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR FILING DATE: 2004-01-13
; Sequence 82, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
   APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
   APPLICANT: FOULDN: Yeas
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT); CURRENT FAPLICATION NUMBER: US (10/2) 991
; CURRENT FILING DATE: 2004-04-23
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; TENCHAL 100 82
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SOFTWARE: Micrarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 815104
LENGTH: 25
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Publication No. US2003002678241
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: INMUNOMODULATORY OLIGONUCLECTIDES
FILE REPERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/09/415,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.4; DB 10;
Pred. No. 1.2e+03;
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91.6%; Score 17.4; DB 8;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1;
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Best Local Similarity 94.1%;
Matches 16; Conservative (
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US-09-415-142-1
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                                                                                                                                 Sequence 82, Application US/10017995
; Sequence 82, Application US/20030055014A1
; GENERAL INFORMATION:
    APPLICANT: BETAZIZET, Robert L.
    TILLE REFERENCE: C1037/7025 (HCL/MAT)
    CURRENT APPLICATION NUMBER: US/10/017,995
    CURRENT APPLICATION NUMBER: US/10/017,995
    CURRENT FILING DATE: 2000-12-18
    PRIOR PILING DATE: 2000-12-14
    NUMBER OF SEQ ID NOS: 1093
    SEQ ID NO 82
    LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.6%; Score 17.4; DB 5; Length 19; Best Local Similarity 94.7%; Pred. No. 1.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
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US-10-314-578-82
Sequence 82, Application US/10314578
Publication No. US20030212026A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: Clo39/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 82
LENGTH: 19
TUBER OF SEQ ID NOS: 1145
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, OTHER INFORMATION: Synthetic Sequence US-10-314-578-82
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                        1 GGGGTGTCGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-831-778-82
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NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic Oligonucleotide
PRIOR APPLICATION NUMBER: US 09/415,142
PRIOR FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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APPLICANT: Krieg, Arthur
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred
TITLE OF INVENTION: Methods and Products for Treating HIV Infection
FILE REFERENCE: C1039/7053(HCL)
CURRENT APPLICATION NUMBER: US/09/931, 583
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
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APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REPERENCE: C1039/7052 (AMS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT PILING DATE: 2001-06-22
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE FASTESQ for Windows Version 3.0
SET ILENGTH: 20
                                                                                                                                                                                                                                                                                                        Score 14.2; DB 3; Length 20;
Pred. No. 4.6e+03;
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                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic oligonucleotide US-09-415-142-1
                                                                                                                                                                                                                                                                                                          Query Match 74.7%; Score 14.2; Dest Local Similarity 84.2%; Pred. No. 4.6e Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
    CURRENT FILING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 449, Application US/09888326; Publication No. US20030026801A1; GENERAL INFORMATION:
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                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 16; Conservative
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US-09-888-326-449
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US-09-931-583-1
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US-09-776-479-224

i Sequence 224, Application US/09776479

j Sequence 224, Application US/09776479

j Publication No. US20030087848A1

j GENERAL INFORMATION:
    APPLICANT: Petersen, Deanna M.
    TITLE OF INVENTION: Treatment of Asthma and Allergy
    FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT PLING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

NUMBER OF SEQ ID NOS: 1093

SEQ ID NO 224

LENGTH: 20
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Sequence 224 Application No. US20040067902A9
Fublication No. US20040067902A9
GENERAL INPORMATION:
APPLICANT: Patersen, Deanna M.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy; TITLE OF INVENTION: UNUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR SEQ ID NOS: 1093
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
           Length 20;
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Query Match
74.7%; Score 14.2; DB 3;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3;
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84.2%; Pred. No. 4.6e+03;
iive 0; Mismatches 3;
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Gaps

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Length 20 Indels

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US-010.17-995-224

Sequence 224, Application US/10017995

Publication No. US20030055014A1

GENERAL INFORMATION:

TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

TITLE OF INVENTION INDER: US/10/017,995

CURRENT APPLICATION NUMBER: US/10/017,995

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-14

NUMBER OF SEQ ID NOS: 1093

SOGTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 224, Application US/10314578

Publication No. US20030212026A1

GENERAL INFORMATION:

APPLICANT: Schetter, Christian

APPLICANT: Schetter, Christian

APPLICANT: Vollmer, JOSS

TITLE OF INVENTION: Immunostimulatory Nucleic Acids

FILE REFERENCE: C1039/7035 (HCL/MAT)

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: US 60/156,113

PRIOR APPLICATION NUMBER: US 60/156,113

PRIOR FILING DATE: 1999-09-25

PRIOR FILING DATE: 1999-09-27

PRIOR FILING DATE: 1999-09-27

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 1145

SOFTWARE: FastSEQ for Windows Version 3:0

LENGTH: 20
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Pred. No. 4.6e+03;
0; Mismatches 3;
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Pred. No. 4.6e+03;
                                                                      ; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-0-112-653-216
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
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LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2%;
Matches 16; Conservative
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US-10-314-578-224
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Publication No. US20030050268A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REPERENCE: C01039/70060(AMS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 6/279,642
PRIOR FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                          RESULT 21
US-09-565-101-63
US-09-565-101-63

Sequence 6, Application US/09965101

Publication No. US20040186067A1

GENERAL INFORMATION:

APPLICANT: Davis, Heather I.

APPLICANT: Schort, Joachim

APPLICANT: Schort, Joachim

TITLE OF INVENTION: Therapeutic Protocols

FILE REFRENCE: C1039/7057 (4CL/MAT)

CURRENT APPLICATION NUMBER: US/09/965,101

CURRENT APPLICATION NUMBER: US 60/047,233

PRIOR FILING DATE: 1998-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR PLICATION NUMBER: US 60/047,233

PRIOR FILING DATE: 1997-05-20

PRIOR APPLICATION NUMBER: US 60/047,209

PRIOR PLING DATE: 1997-05-20

NUMBER OF SEQ 1D NOG 63

LENGTH: 70
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Pred. No. 4.6e+03;
0; Mismatches 3; Indels
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Pred. No. 4.6e+03;
0; Mismatches 3; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 216
                                                                                            FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-224
                                                                                                                                                                                                                                                                               1 GGGGTGACGTTCAGGGGGG 19
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Best Local Similarity 84.2%;
Matches 16; Conservative C
  SEQ ID NO 224
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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84.28;
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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US-10-112-653-216
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Publication No. US20040152656A1

GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klimman, Dennis
APPLICANT: Steinberg, Alfred D.
FILE DE INVENTION: IMMNOMODULATORY OLIGONUCLECTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/788,191
CURRENT APPLICATION NUMBER: US 08/386,063
PRIOR PILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
                                                                                                                                                                                     APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODILATORY OLIGONUCLEOTIDES
FILE REFERENCE: CLO39/7029
CURRENT APPLICATION NUMBER: US/10/690,495
CURRENT APPLICATION NUMBER: US/08/306,063
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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                                                                                                            US-10-690-495-1; Sequence 1, Application US/10690495; Publication No. US20040143112A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-789-536-1
; Sequence 1, Application US/10789536
1 GGGGTGACGTTCAGGGGGG 19
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nes 16; Conserv
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Matches
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                                            Length 20;
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                                                                                         3; Indels
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
TITLE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/631,676
CURRENT APPLICATION NUMBER: US 08/366,063
PRIOR PILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMOULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/789,051
CURRENT APPLICATION NUMBER: US 08/386,063
PRIOR APPLICATION NUMBER: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
                                          74.7%; Score 14.2; DB 6;
84.2%; Pred. No. 4.6e+03;
Live 0; Mismatches 3;
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Pred. No. 4.6e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10631676 Publication No. US20040087534A1 GENERAL INFORMATION:
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; Publication No. US20040142469A1
; GENERAL INFORMATION:
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                                                                                                                                 1 GGGGTGACGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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84.2%;
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Best Local Similarity 84.2'
Matches 16; Conservative
                                        Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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Matches 16; Conserv
US-10-314-578-224
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US-10-789-051-1
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Pred. No. 4.6e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
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| Sequence 1, Application US/10787737 |
| Sequence 1, Application US/10787737 |
| Publication No. US20040171150A1 |
| GENERAL INFORMATION: |
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Kriman, Dennis |
| APPLICANT: Steinberg, Alfred D. |
| TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES |
| FILE REPERENCE: C1039/7029 |
| CURRENT APPLICATION NUMBER: US/10/787,737 |
| CURRENT APPLICATION NUMBER: US 08/386,063 |
| PRIOR FILING DATE: 1995-02-07 |
| NUMBER OF SEQ ID NOS: 27 |
| SEQ ID NO 1 |
| SEQ ID NO 1 |
| LENGTH: 20 |
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Publication No. US20040181045A1
General INPORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Kliman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT FILING DATE: 204-02-26
CURRENT FILING DATE: 1955-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.2; DB 7;
Pred. No. 4.6e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Synthetic oligonucleotide US-10-789-353-1
CURRENT APPLICATION NUMBER: US/10/789,353
CURRENT FILING DATE: 2004-02-26
PRIOR PILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASLSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Pred. No. 4.6e+03;
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Publication No. US20040162258A1

GENERAL INFORMATION

APPLICANT: Klinman, Dennis

APPLICANT: Klinman, Dennis

APPLICANT: Steinberg, Alfred D.

TILE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES

FILE REFERENCE: C1039/7029

CURRENT APPLICATION NUMBER: US/10/769,626

CURRENT PILING DATE: 2004-01-30

PRIOR APPLICATION NUMBER: US 08/386,063
                                    GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinmur Dennis
APPLICANT: Klinmur Dennis
APPLICANT: Klinmur Dennis
APPLICANT: Klinmur Dennis
TILLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/789,536
CURRENT FILING DATE: 2004-02-26
FRIOR PELING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FARENSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.7%; Score 14.2; DB 7; Best Local Similarity 84.2%; Pred. No. 4.6e+03; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Synthetic oligonuclectide US-10-769-626-1
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGTGACGTTCAGGGGGG 19
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84.28;
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ORGANISM: Artificial Sequence
                Publication No. US20040152657A1
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-789-353-1
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OTHER INFORMATION: synthetic oligonucleotide
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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PRIOR APPLICATION NUMBER: US 09/965,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63, Application US/10838659 Publication No. US20050032734A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               Sequence 1, Application US/10888885
Publication No. US20050009774A1
GENERAL INFORMATION:
                                                                                                                   1 GGGGTGACGTTCAGGGGG 19
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               Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 16; Conservative
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; Sequence 224, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT FILING DATE: 2004-04-23
; PRIOR PAPLICATION NUMBER: US 60/179,991
; PRIOR PILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                              Query Match 74.7%; Score 14.2; DB 8; Length 20; Best Local Similarity 84.2%; Pred. No. 4.6e+03; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.2; DB 8; Length 20;
Pred. No. 4.6e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMOULATORY OLIGONUCLEOTIDES
TITLE OF INVENTION: IMMUNOMOULATORY OLIGONUCLEOTIDES
FILE REPERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/847,650
CURRENT APPLICATION NUMBER: US 08/386,063
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASCESQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
                                                                                         ) OTHER INFORMATION: Synthetic oligonucleotide US-10-788-199-1
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US-10-847-650-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Synthetic Sequence US-10-831-778-224
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                    TYPE: DNA
ORGANISM: Artificial Sequence
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84.28;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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US-10-831-778-224
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LENGTH: 20
LENGTH: 20
                                                                       FEATURE:
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  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Davis, Heather L.
APPLICANT: Davis, Arthur M.
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1039-70057109(10)(838,659)
CURRENT APPLICATION NUMBER: US/10/838,659
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOWODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION WUMBER: US/10/888,885
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
Score 14.2; DB 8;
Pred. No. 4.6e+03;
0; Mismatches 3;
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PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 09/082,649
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FELING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FRESEQ for Windows Version 3.0
SSEQ ID NO 63
LENGTH: 20
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US-11-016300

15-20-017-185300

15-20-017-185300

15-20-017-185300

15-20-017-185300

15-20-017-185300

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15-20-017-185300
                                                                                      Gaps
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                                     74.7%; Score 14.2; DB 8; Length 20; 84.2%; Pred. No. 4.6e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                    Sequence 1, Application US/11067516;
Publication No. US20050239736A1
| GENERAL INFORMATION:
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Steinberg, Alfred D. |
| TILLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES |
| FILE REFERENCE: C1039/7029 |
| CURRENT APPLICATION NUMBER: US/11/067,516 |
| CURRENT FILING DATE: 2003-10-21 |
| PRIOR FILING DATE: 2003-10-21 |
| PRIOR APPLICATION NUMBER: US/80,495 |
| PRIOR APPLICATION NUMBER: US 08/386,063 |
| PRIOR FILING DATE: 1995-02-07 |
| NUMBER OF SEQ ID NOS: 27 |
| SEQ ID NO 1 |
| LENGTH: 20 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.7%; Score 14.2; DB 10; Best Local Similarity 84.2%; Pred. No. 4.6e+03; Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic oligonucleotide US-11-067-516-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGTGACGTTCAGGGGGG 19
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                                                                                        16; Conservative
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US-11-036-317-185300
                                            Query Match
Best Local Similarity
Matches 16; Conserve
                                                                                                                                                                                                                                                         RESULT 40
US-11-067-516-1
US-10-649-584-1
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APPLICANT: Klimman, Dennis
APPLICANT: Klimman, Dennis
APPLICANT: Steinberg, Alfred
TITLE OF INVENTION: Methods and Products for Treating HIV Infection
FILE REFERENCE: C1039.70084US00
CURRENT APPLICATION WHBER: US/10/649,584
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION WHBER: US 09/931,583
PRIOR FILING DATE: 1994-07-15
PRIOR PILING DATE: 1994-07-15
PRIOR FILING DATE: 1994-07-15
PRIOR FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 20
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                                          Query Match 74.7%; Score 14.2; DB 8; Length 20; Best Local Similarity 84.2%; Pred. No. 4.6e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: INVUNMONULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/888,089
CURRENT FILING DATE: 2004-709
FRIOR APPLICATION NUMBER: US/10/690,495
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FABELSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic oligonucleotide
US-10-888-089-1
                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10888089; Publication No. US20050037403A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/10649584; Publication No. US20050037985A1; GENERAL INFORMATION:
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                                                                                                                                            1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                         2 gegricacerrrregeege 20
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ORGANISM: Artificial Sequence
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    US-10-838-659-63
                                                                                                                                                                                                                                                                 RESULT 38
US-10-888-089-1
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-282-935-18/C
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                                                                                                                                                           APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERRNCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 202532
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 365-01
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NOS: 991174
SEQ ID NO 382608
LENGTH: 25
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; Publication No. US20050214823A1
; GENERAL INFORMATION:
APPLICANT: Williams, Alan
; ATTLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
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Pred. No. 4.4e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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US-11-036-317-382608
; Sequence 382608, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
                                                                                               ; Sequence 282532, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGAGACGTICAIGGGCG 24
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7 GGGGAGACGTTCATGGGCG
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84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-382608
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-282532
                                                                               US-11-036-317-282532
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Sequence 18, Application US/10282935

Publication No. US20030143193A1

GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHW, ADANN
APPLICANT: BALLUAR, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: COMPOSITIONS COMPOUNDS
FILE REFERENCE: UTSON 1984US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-00-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
TYPE: DNA
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TILE REFERENCE: 3654.1
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PLIANG DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 398410
LENGTH: 25
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; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FLILING DATE: 2005-01-13
; PRIOR FLILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 395403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-395403
                                                                                                                                                                                                                                                                                                 Length 25;
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Pred. No. 4.4e+03;
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84.2%; Pred. No. 4.4e+03;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Publication No. US20050214823A1
GENERAL INFORMATION:
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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Length 25;

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Sequence 18, Application No. US20040009148A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WILLEN S.
APPLICANT: BALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
APPLICANTON NUMBER: US/10/440,796
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US/09/538,873
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 18
LENGTH 39
LENGTH 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 292133, Application US/11036317; Sequence 292133, Application US/11036317; Publication No. US20050214823A1; Publication No. US20050214823A1; Publication No. US20050214823A1; GENERAL INFORMATION:
; APPLICANT: Williams, Alan; APPLICANT: Williams, John; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse; FILE REFERENCE: 3654.1; CURRENT APPLICATION NUMBER: US/11/036,317; CURRENT FILING DATE: 2004-01-13; PRIOR FILING DATE: 2004-01-13; NUMBER OF SEQ ID NOS: 991174; SEQ ID NO 292133
; SEQ ID NO 292133
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) ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Primer

US-10-282-935-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Primer US-10-440-796-18
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                                                                                                                                                            Length 39
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                                                                                                                                                       Ouery Match 73.7%; Score 14; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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US-11-036-317-292133
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US-11-036-317-292133
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US-10-440-796-18/c
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Sequence 822290, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION:

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLIANG DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
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Sequence 815105, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

TILE REPERENCE: 3654-11

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION UNMER: US 60/536,639

PRIOR APPLICATION UNMER: US 60/536,639

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

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88.2%; Pred. No. 7e+03;
iive 0; Mismatches 2;
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88.2%; Pred. No. 7e+03;
tive 0; Mismatches 2;
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Best Local Similarity 88.2
Matches 15; Conservative
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CORGANISM: Mus musculus
US-11-036-317-815105
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ORGANISM: Mus musculus
US-11-036-317-822290
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Matches 15; Conserva
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US-11-036-317-822290
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Seguence:

Searched:

Database

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Sequence 83693,
Sequence 83694,
Sequence 896494,
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Sequence 97, Appl
Sequence 14533,
Sequence 76814,
Sequence 76517,
Sequence 7653,
Sequence 246915,
Sequence 246915,
Sequence 411534,
Sequence 111534,
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Sequence 321322,
Sequence 1319423,
Sequence 1319423,
Sequence 132868,
Sequence 22043, A
Sequence 22043, A
Sequence 121131,
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Sequence 62, Appl
  Sequence 114797,
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Sequence 9
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US-10-310-914A-321292
US-10-310-914A-321322
US-10-310-914A-437868
US-10-310-914A-1295431
US-10-310-914A-1319423
US-10-310-914A-13122628
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US-10-750-185-22043
US-10-750-232-22043
US-10-310-9144-181131
US-10-310-9148-1198901
US-10-310-914A-114797
US-10-310-914A-456901
US-10-310-914A-818042
US-10-310-914A-896593
US-10-310-914A-896494
US-10-310-914A-897004
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US-10-939-294A-17580
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Sequence 1185206,
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Sequence 673587,
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                                                                                                                                     February 16, 2006, 02:03:53; Search time 177.124 Seconds (without alignments) 98.157 Million cell updates/sec
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1: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
2: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
3: /cgn2_6/prodata/2/pubpna/USOS_NEW_PUB.seq:*
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5: /cgn2_6/prodata/2/pubpna/USOS_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubpna/USOS_NEW_PUB.seq:*
7: /cgn2_6/prodata/2/pubpna/USOS_NEW_PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-127-803-1
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US-10-310-914A-1202061
US-10-310-914A-895375
US-10-310-914A-1185102
US-10-310-914A-1185206
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US-11-127-654-501
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11 US-11-136-527-338521 7 US-10-310-914A-477171 7 US-10-310-914A-860573 7 US-10-310-914A-550477 7 US-10-209-208-33 7 US-10-209-208-34 11 US-11-218-880-33 11 US-11-218-880-34	הססה	1 7 7		-ii 1				νονο	σσ	7		7	7			7	7	7		7	7,	-		- 1	~ ~						-
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APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMINOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US, 11/127, 654
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 60/219, 642
PRIOR APPLICATION NUMBER: US 60/279, 642
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SEQ ID NO 76
LENGTH: 19
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TITLE OF INVENTION: INFLAMMATORY DISEASES;
FILE REFERENCE: C1039.7006 CUS01
CURRENT PPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-05-12;
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR PILING DATE: 2002-03-29
PRIOR PLING DATE: 2001-03-29;
NUMBER OF SEQ ID NOS: 1040
SEQ ID NO 74
LENGTH: 19
LENGTH: 19
CREANISM: Artificial sequence
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Sequence 296043,
Sequence 351683,
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Sequence 70487, A
Sequence 954555,
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Sequence 543421,
Sequence 673169,
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Sequence 13934,
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Sequence 1122826,
Sequence 1181622,
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Sequence 369887,
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US-10-310-914A-147289
US-10-310-914A-369060
US-10-310-914A-795738
US-10-310-914A-873292
US-10-310-914A-873292
US-10-310-914A-1049795
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US-10-310-914A-142175
US-10-310-914A-154172
US-10-310-914A-269187
US-10-310-914A-369187
US-10-310-914A-369187
US-10-310-914A-543421
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US-10-310-914A-673169
US-10-310-914A-961314
US-10-310-914A-1021596
US-10-310-914A-1024378
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US-11-136-527-13933
US-11-136-527-13934
US-11-136-527-13936
US-11-136-527-13946
US-11-136-527-13946
US-11-136-527-13946
US-11-136-527-13946
US-11-136-527-94751
US-11-136-527-94751
US-11-136-527-96001
US-11-136-527-265981
US-11-136-527-266981
US-11-136-527-266001
US-11-136-527-2960024
US-11-136-527-2960024
US-11-136-527-296024
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-10-310-914A-1352469
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US-10-310-914A-53127
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Sequence 1228446, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000332A1
Publication No. US2006000332A1
Publication No. US2006000332A1
Publication No. US200600032A1
PUBLICANT: Bentwich, Isaac
PAPLICANT: Shiler, Kvuzat
PITLE OF INVENTION: uses thereof
PITLE OF INVENTION: uses thereof US-10-310-914A-1228446

Sequence 74, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

RESULT 1 US-11-127-654-74

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-803-1
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ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                  Query Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNMODULATORY OLIGONUCLEOTIDES
TITLE OF INVENTION: IMMUNMONE: US/11/127,803
CURRENT APPLICATION NUMBER: US/11/127,803
CURRENT APPLICATION NUMBER: US/11/127,803
PRIOR FILING DATE: 2005-05-11
PRIOR PELICATION NUMBER: US/803/86,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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74.7%; Score 14.2; DB 9;
Best Local Similarity 84.2%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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Publication No. US20050244379A1
GENERAL INFORMATION:
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   CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1228446
LENGTH: 19
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                                                                                                                                                                     Best Local Similarity 68.4
Matches 13; Conservative
                                                                                                                      US-10-310-914A-1228446
                                                                                       TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                        RESULT 4
US-11-127-797-1
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US-11-127-803-1
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## Sequence 216, Application US/11127654

## Sequence 216, Application US/11127654

## Sequence 216, Application US. US2050250726A1

## Sequence 216, Application No. US2050250726A1

## SPELICANT: Krieg, Arthur M.

## APPLICANT: Krieg, Arthur M.

## APPLICANT: Berg, Daniel J.

## TITLE OF INVENTION: INPLAMMATORY DISEASES

## TITLE OF INVENTION: INPLAMMATORY DISEASES

## TITLE OF INVENTION: UNPLAMMATORY DISEASES

## CURRENT APPLICATION NUMBER: US/11/12,653

## CURRENT APPLICATION NUMBER: US 10/112,653

## PRIOR PILING DATE: 2002-03-29

## PRIOR PILING DATE: 2001-03-29

## PRIOR PILING DATE: 2001-03-29

## NUMBER OF SEQ ID NOS: 1040

## SEQ ID NO 216

## SEQ ID NO 216

## DEBOTT NOTE: 2001-03-29

## SEQ ID NO 216

## DEBOTT NOTE: 2001-03-29

## DEBOTT NOTE: 2001-03-29
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            Length 20;
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| Sequence 1, Application US/11128127
| Sequence 1, Application Wo/11128127
| Publication No. US20050244380A1
| GENERAL INFORMATION:
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Steinberg, Alfred D. |
| TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES |
| FILE REFERENCE: C1039/7029 |
| CURRENT APPLICATION NUMBER: US/11/128,127 |
| CURRENT APPLICATION NUMBER: US/10/690,495 |
| PRIOR FILING DATE: 2003-10-21 |
| PRIOR FILING DATE: 1995-02-07 |
| PRIOR FILING DATE: 1995-02-07 |
| NUMBER OF SEQ ID NOS: 27 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| LINGTH: 20 |
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Score 14.2; DB 9;
Pred. No. 8.1e+02;
0; Mismatches 3;
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; OTHER INFORMATION: Synthetic oligonucleotide
US-11-128-127-1
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Sequence 895439, Application US/10310914A
Publication No. US/20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Tasac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
                   GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Youzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses 1,000.000.
CURRENT PEPLICATION NUMBER: U$/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 895375
LENGTH: 20
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| Sequence 1185102, Application US/10310914A
| Publication No. US20060003322A1
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: uses thereof
| TITLE REFERENCE: 06087.0200.CPUS01
| CURRENT APPLICATION WIMBER: US/10/310,914A
| CURRENT FILING DAFE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 1185102
| LENGTH: 20
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Pred. No. 1.3e+03;
0; Mismatches 2; Indels
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88.2%;
Publication No. US20060003322A1
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Best Local Similarity 88.2
Matches 15; Conservative
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US-10-310-914A-1185102
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US-10-310-914A-1185102
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ORGANISM: Human
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US-10-310-914A-1202061/C
; Sequence 1202061, Application US/10310914A
; Publication No. US2060003322A1
; Publication No. US2060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bhiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06097.0200. CPUSO1
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1202061
: LENGTH: 28
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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                                                                      Score 14.2; DB 11; Length 20;
Pred. No. 8.1e+02;
0; Mismatches 3; Indels
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OTHER INFORMATION: Synthetic oligonucleotide
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 14; Conservative
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US-10-310-914A-895375/c
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US-10-310-914A-524757
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US-10-310-914A-524757
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LENGTH: 20
        ; OTHER INFORMATION OF 11-127-654-216
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GENERAL INVORVATION:

APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILIOS DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/20/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO : 188547
                     APPLICANT: KNOOTOVA, ANGELASIA
APPLICANT: KNOOTOVA, ANGELASIA
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134,99US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PELING DATE: 2003-09-10
PRIOR PELING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PEOPTIERARY
LENGTH: 19
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Pred. No. 1.9e+03;
0; Mismatches 1;
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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Best Local Similarity 93.3
Matches 14; Conservative
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US-11-101-244-1188547
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US-10-310-914A-673587/C
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US-10-314A-1185206
US-10-310-0-14A-1185206
Sequence 1185206, Application US/10310914A
Sequence 1185206, Application US/10310914A
Sequence 1185206, Application US/10310914A
Sequence 1185206, Application No. US2066003322A1
GENERAL INFORMATION:
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06097.0200.CPUSO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
LENGTH: 22
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                                Query Match 72.6%; Score 13.8; DB 7; Length 21; Best Local Similarity 88.2%; Pred. No. 1.3e+03; Matches 15; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 70.6
Matches 12; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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US-11-101-244-1188547/c
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US-10-310-914A-1185206
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US-10-310-914A-895439
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Sequence 872061, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: Uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 972061
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMMUNOSTIMULATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT PEPLICATION NUMBER: US/11/12,653
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Astentin version 3.2
SEQ ID NO SOIL
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                                                                                                                                                                                 Score 13.2; DB 11;
Pred. No. 2.4e+03;
0; Mismatches 3;
                                            TYPE: DNA
CRGANISM: Artificial sequence
FEATURE:
THER INFORMATION: Synthetic oligonucleotide
US-11-127-654-498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-501
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 501, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 15; Conservative
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ORGANISM: Human
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  SEQ ID NO 498
LENGTH: 20
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                                  APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUSO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
FEQ ID NO 673587
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Sequence 308426, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof;
FILLE REFERENCE: 06087.0200.CPUS01;
CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT PILLIO DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PATEUTIN version 3.3
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APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMINOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
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Publication No. US20060003322A1
GENERAL INFORMATION:
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Best Local Similarity 93.5.
Best Local 14; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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US-10-310-914A-308426/c
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ORGANISM: Human
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LENGTH: 18
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Thu Feb 16 12:20:50 2006

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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CURNENT PRILIS APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARER Patentin version 3.3 SEQ ID NO 518042
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US-10-314A-896494/C
US-10-310-914A-896494/C
Sequence 896494, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bantwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200.CF08301
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
LENGTH: 23
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Publication No. US20060003322A1
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
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Pred. No. 2.4e+03;
0; Mismatches 3;
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Pred. No. 2.4e+03;
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83.3%;
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
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Matches 12; Conserv
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Best Local Similarity
                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-518042
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US-10-310-914A-836953
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CORGANISM: Human
US-10-310-914A-896494
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Sequence 114797, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich Isoinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 114797
LENGTH: 22
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Pred. No. 2.4e+03;
0; Mismatches 3; Indels
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83.3%; Pred. No. 2.4e+03;
ive 0; Mismatches 3; Indels
                                   Indels
              Pred. No. 2.4e+03;
2; Mismatches 3;
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US-10-310-914A-518042/C
US-10-310-914A-518042/C
'Sequence 518042, Application US/10310914A
'Publication No. US20060003322A1
'GENERAL INFORMATION:
                                                                         2 GGGTGACGTTCAGGGGGG 19
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Best Local Similarity 83.3%;
Matches 15; Conservative
              L Similarity 72.2%;
13; Conservative
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Best Local Similarity 83.50,
Thes 15; Conservative
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; APPLICANT: Shiler, Kvuzat
                                                                                                                                                                          RESULT 22
US-10-310-914A-114797/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-114797
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LENGTH: 23
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              Best Local
Matches 1
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF FILE REPERRORS: 017733-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
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US-11-012-353-97
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              CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 00/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 16126
LENGTH: 25
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                                                                                                                                                                                                                                                                                                        69.5%; Score 13.2; DB 11; 83.3%; Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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PRIOR APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-20
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN VET: 3.3
SOFTWARE: PATENTIN VET: 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGTGACGTTCAGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGGGAGACGCTCAGGAGG
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Matches 15; Conservative
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ORGANISM: Homo sapien
US-11-121-849-16126
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US-10-310-914A-1145336
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 066097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-112-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN VETSION 3.3
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2006-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 509542
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
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83.3%; Pred. No. 2.4e+03;
ive 0; Mismatches 3; Indels
Indels
3;
0; Mismatches
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US-10-310-914A-509542/C
US-10-310-914A-509542, Application US/10310914A
; Sequence 509542, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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                                            GGGTGACGTTCAGGGGG 19
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Best Local Similarity 66.73
Matches 12; Conservative
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Best Local Similarity 83.37
Matches 15; Conservative
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-837004
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US-11-121-849-16126
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ORGANISM: Human
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Matches
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us-09-669-187a-80.szlm50.rnpbn

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Sequence 966777, Application US/10310914A

Fublication No. US20060003322A1

FUBLICANT: BENEVATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
STANDER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 966777
LENGTH: 22
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Publication No. US20060003322A1
GERREAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION UNMERS: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOOFWARE: Patentin version 3.3
SEQ ID NO 746353
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.4%; Score 12.8; DB 7; Length 20; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                    67.4%; Score 12.8; DB 7;
87.5%; Pred. No. 3.7e+03;
ative 0; Mismatches 2;
                                                                  TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM:
FEATURE:
NAME/KEY: misc_feature
JCCATION: (1)...(23)
US-10-522-362-49
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                           4 GTGACGTTCAGGGGG 19
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Best Local Similarity 87.5<sup>†</sup>
Matches 14<sup>‡</sup>, Conservative
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US-10-310-914A-746353/C
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US-10-310-914A-746353
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                       SEQ ID NO 49
LENGTH: 20
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US-10-914A-966814/c
US-10-310-914A-966814/c

i Sequence 966814, Application US/10310914A

j Publication No. US2060003322A1

i GENERAL INFORMATION:
    APPLICANT: Bentwich, Isaac

    APPLICANT: Bhiler, Kvuzat

    TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
    TITLE OF INVENTION: Uses thereof
    TITLE OF INVENTION: Uses thereof
    FILE REFERENCE: 06087.0200.CPUS01
    CURRENT APPLICATION NUMBER: US/10/310,914A
    CURRENT FILING DATE: 2002-12-06
    NUMBER OF SEQ ID NOS: 1388402
    SOFTWARE: PatentIn version 3.3
    SEQ ID NO 966814

. LENGTH: 19
                  GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Vuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFRENCE: 06087.0200.CPUSO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
SUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1145336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/1052362;
Sequence 49, Application US/1052362;
Publication No. US20050281788A1
GENERAL INPORMATION:
APPLICANT: De Bari, Cosimo
APPLICANT: De Bari, Cosimo
TITLE OF INVENTION: Compositions Comprising Muscle
TITLE OF INVENTION: Drogenitor Cells and Uses Thereof;
FILE REFERENCE: 50304/030001
CURRENT FILING DATE: 2005-01-26;
PRIOR FILING DATE: 2003-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.8; DB 7;
Pred. No. 3.7e+03;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            67.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGACGTTCAGGG 16
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  Publication No. US20060003322A1
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Best Local Similarity 87.5
Fig. 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                        US-10-310-914A-1145336
                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 33
US-10-522-362-49
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Sequence 15921, Application US/11121849
Fublication No. US20050272080A1
Fublication No. US20050272080A1
Fublication No. US20050272080A1
Fublication No. US20050272080A1
FUBLICANT: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
FRIOR APPLICATION NUMBER: 60/567,949
FRIOR APPLICATION NUMBER: 60/567,949
FRIOR APPLICATION NUMBER: 60/567,949
FRIOR SEQ ID NOS: 673904
SOFTWARER: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 15921
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-121-849-22103/C
US-11-121-849-22103, Application US/11121849
Sequence 22103, Application US/11121849
Publication No. US20050272080A1
Sequence 22103, Application No. US20050272080A1
SEMERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
SPRIOR FILING DATE: 2004-05-03
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Pred. No. 3.7e+03;
0; Mismatches 2;
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87.5%; Pred. No. 3.7e+03;
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Pred. No. 3.7e+03;
2; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 1145337
                                                                                                                                                                                                                               67.4%;
75.0%;
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                               Query Match 67.4
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                    US-10-310-914A-1145337
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US-11-121-849-15921/C
                                                                                                                                        TYPE: RNA
ORGANISM: Human
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                                                                                                                                             Sequence 240915, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200. CPUSOI;
FILE REFERENCE: 06087.0200. CPUSOI;
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 240915
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Publication No. US2006000332A1

REMERAL INFORMATION:

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION WUBBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ INVENTION: 24

LENGTH: 24
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US-10-914A-1145337
US-10-914A-1145337
Sequence on No. US20060003322A1
Sequence on No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
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Pred. No. 3.7e+03;
1; Mismatches 2; Indels
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81.2%;
  1 GGGGTGACGTTCAGGG 16
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                                           GGGGAGACGCTCAGGG 2
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                   RESULT 36
US-10-310-914A-240915/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Human
US-10-310-914A-240915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-411534
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US-10-310-914A-411534
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Squence 476399, Application US/11121849

Fubilication No. US20050272080A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
HIGH STILLS OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Statistic OF INVENTION: Microarrays
FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

FRIOR PAPLICATION NUMBER: 06/56.03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NO 476398

LENGTH: 25
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Sequence 568167, Application US/11121849

Publication No. US20050272080A1

Fublication No. US20050272080A1

GENERAL INFORMATION:

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Selection NUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: G0/567,949

PRIOR FILING DATE: 2004-05-03

PRIOR FILING DATE: 2004-05-03
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TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 115643
LENGTH: 25
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SOFWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 568167
LENGTH: 25
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Pred. No. 3.7e+03;
0; Mismatches 2;
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Pred. No. 3.7e+03;
0; Mismatches 2;
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87.5%;
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-115643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapien
US-11-121-849-476398
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; ORGANISM: Homo sapien
US-11-121-849-568167
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Sequence 24138, Application US/11121849

Fublication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

FRIOR FILING DATE: 2004-05-03

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
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                                             3 GGTGACGTTCAGGGGG 18
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Matches 14; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-107577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
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US-11-121-849-115643/c
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US-11-121-849-107577
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APPLICANT: Furnet, Daniel
APPLICANT: Pingle, Maneesh
APPLICANT: Pingle, Maneesh
APPLICANT: Pingle, Maneesh
APPLICANT: Pingle, Maneesh
APPLICANTON: Methods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT PELLING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US 60/502/731
PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SOFTWARE: Patentin version 3.3
SEQ ID NO 19843
LENGTH: 32
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87.5%; Pred. No. 3.7e+03;
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87.5%; Pred. No. 3.7e+03;
iive 0; Mismatches 2;
                                       FILING DATE: 20-Nov-2001
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APP-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INPORMATION:
NAME: Meigs, J. Timochy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide probe US-10-939-294A-19843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19843, Application US/10939294A Publication No. US20050266417A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 87.5
Matches 14; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 48
US-10-939-294A-19843
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US-11-121-849-570964

US-11-121-849-570964

Sequence 570964, Application US/11121849

Publication No. US200222080A1

GENERAL INFORMATION:

APPLICANT On Palma

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT FILING DATE: 2005-05-03

PRIOR PILING DATE: 2005-05-03

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 570964
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                                              Gaps
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Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Rllis J.
Launis, Kene L.
ITILE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
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Query Match 67.4%; Score 12.8; DB 11; Length 25; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels C
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ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/755,092

FILING DATE: 08-Jan-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/10755092;
Publication No. US20660021095A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
                                                                                         1 GGGGTGACGTTCAGGG 16
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Best Local Similarity 87.5
Warches 14; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-570964
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US-10-755-092-43/c
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0
                        Sequence 51905, Application US/11175859
; bublication No. US20060024715A1
; GRNERAL INFORMATION:
    APPLICANT: Affymetrix, Inc.
; APPLICANT: Affymetrix, Inc.
; TILE OF INVENTION: Method of Analysis of Human Polymorphism
; TILE OF INVENTION: Method of Analysis of Human Polymorphism
; CURRENT APPLICATION UNDHER: US/11/175,859
; CURRENT APPLICATION NUMBER: US/05-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; ROWERS FLING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 51905
; LENGTH: 50
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, ORGANISM: homo sapien
US-11-175-859-51905
RESULT 49
US-11-175-859-51905/c
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Biocceleration Ltd.  Biocceleration Ltd.  Search time 575.802 Seconds ithout alignments) 69.293 Million cell updates/sec	2097806	٠ ټ ټ	Descriptio  Descriptio  Descriptio  AX10389 S  AX355412 S  AX355412 S  AX35612 S  AX36301 S  AX351117 S  AX35111 S  AX35111 S  AX35111 S  AX35111 S  AX3511 S  AX351 S  AX
GenCore version pyright (c) 1993 - 2006 search, using sw model uary 15, 2006, 17:51:58;	S-09-669-187A-81  4  ggggtccagcgtgcgccatggggg DENTITY_NUC app 10.0 , Gapext 1.0  883141 seqs, 28421725653 r  its satisfying chosen para ngth: 0 ngth: 0 minimum Match 0% Maximum Match 100% Listing first 300 summarie	* nn:* nn:* nn:* nn:* nn:* nn:* v:* v:* v:* v:* pl::* pl::* pl::* pl::*	
Co OM nucleic - nucleic Run on: Febr	Title:  Sequence:  Scoring table:  Searched:  Total number of h Minimum DB seq le Maximum DB seq le Post-processing:	Database : 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Regult Score great and is derically Mo. Score

BD168552 Cells pro AR199548 Sequence AR374700 Sequence AR409315 Sequence AR60967 Sequence AR239597 Sequence AR239597 Sequence AR718919 Nicotiana AR086618 Sequence AR766504 Sequence AR766504 Sequence CQ878195 Sequence BD189694 A method CQ897034 Sequence BD002997 A method BD002997 A method BD002999 A sequence CS083838 Sequence CS083838 Sequence AR477055 Sequence	AR606811 Sequence BAR60812 Sequence BD096170 Novel pol AX47581 Sequence AX47683 Sequence AX47683 Sequence AX477683 Sequence AX65975 Sequence AX650224 Sequence AR050225 Sequence AR050225 Sequence AR044090 Sequence AR044091 Sequence AR041711 Sequence AR091715 Sequence AX901715 Sequence AX1917490 Sequence AX1917490 Sequence AX1917490 Sequence AX23347 Sequence AX23347 Sequence AX23347 Sequence AX5087848 Sequence AX17725 Sequence AX477725 Sequence AX477725 Sequence	CS124138 Sequence CS124089 Sequence CS124089 Sequence BD008994 Inhibitio AR052603 Sequence AR176022 Sequence AR176022 Sequence AR176022 Sequence BD187522 REGULATIO 196082 Sequence BD187522 REGULATIO 196082 Sequence AR30673 Sequence AR30673 Sequence AX211670 Sequence AX211670 Sequence AX211670 Sequence AX277461 Sequence AX277461 Sequence AX27761 Sequence AX27761 Sequence AX27761 Sequence AX27761 Sequence AX27761 Sequence AX27761 Sequence AX2762671 Sequence AX27761 Sequence AX27761 Sequence AX27661 Sequence AX27761 Sequence BD05773 Pusion pr BD08152 Soluble s BD133294 Process f A61400 Sequence
13.8 57.5 45 6 13.8 57.5 45 6 13.8 57.5 45 6 13.8 57.5 45 6 13.8 57.5 45 6 13.8 57.5 45 6 13.8 57.5 45 6 13.6 56.7 21 6 13.6 56.7 30 6 13.6 56.7 34 6 13.6 56.7 34 6 13.6 56.7 34 6 13.6 56.7 34 6 13.6 56.7 34 6 13.6 56.7 34 6 13.6 56.7 34 6 13.6 56.7 34 6 13.6 56.7 35 6 13.6 56.7 35 6 13.6 56.7 35 6 13.6 56.7 35 6	1886 13.4 4 55.8 19.8 19.8 19.8 19.8 19.8 19.8 19.8 19	13 54.2 13 54.2 14 54.2 15 54.2 16 54.2 17 54.2 18
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ignthetic construct synthetic construct other sequences; artificial sequences.

REFERENCE

VERSION AX103889.1 GI:13920086  KEYWORDS SOURCE SOURCE ORGANISM Synthetic construct ORGANISM Synthetic construct ORGANISM Synthetic construct OTHER SYNTHETIC AND STATEMENT OF THE STATEMENT OF THE STATEMENT OF TOWN RESEARCH FOUNDATION (US); Coley Pharmaceutical GmbH (DE)  FEATURES I Cocation/Qualifiers SOURCE   OCCATION   Cocation   Cocatio	Query Match 100.0%; Score 24; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 33; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GGGGTCCAGGGGGGGG 24	440	REFERENCE 1 AUTHORS Weiner, G. and Hartmann, G. TITLE Methods for enhancing antibody-induced cell lysis and treating cancer. JOURNAL Parent: WO 0197843-A 440 27-DEC-2001, UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) FEATURES Location/Qualifiers 124 /organism="synthetic construct" //mol_type="unassigned DNA" //db xref="taxon:32630"	/noTe="Synthetic oligonuclectide	RESULT 3 AX54642 LOCUS LOCUS DEFINITION Sequence 81 from Patent W002053141. DEFINITION AX546942 VERSION AX546942 VERSION AX546942 VERSION AX546942 SOURCE SOURCE SOURCE ORGANISM Synthetic construct
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BD263032
BD853032.1 GI:3372800
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1 (bases 1 to 33)
Dickman,M.B.
Trans-species transfer of apoptotic genes and transgenic plants
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/organism='Artificial Sequence'
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   /note="Single strand DNA oligonucleotide"
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1 (bases 1 to 33)

Horlick, R. A. and Chelsky, D.
Method for maintenance and selection of episomes
Patent: US 6417002-A 11 09-JUL-2002;
Pharmacopeia, Inc.; Cranbury, NJ
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Patent: JP 20022388769-A 5 19-NOV-2002;
UNINESITY OF NEBRASKA LINCOLN
OS Artificial Sequence
PN JP 2002538769-A/5
PD 19-NOV-2002
PF 29-OCT-1999 JP 2000579763
PR 30-OCT-1999 US 60/106321,09-JUN-PR
PR 30-OCT-1999 US 60/106321,09-JUN-PC A01H5/00,C12N5/10,C12N15/09,C12O1/61
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6e+04;
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Sequence 11 from patent US 6417002.
AR217874 GI:23317768
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Jevnikar, A.M., Ma, S. and Stiller, C.R.
Methods and products for controlling the immune response of a mammal to glutamic acid decarboxylase
Patent: US 6338850-A 1 15-JAN-2002;
Location/Qualifiers
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100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 24; Conservative 0; Mismatches 0; Indels
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Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 81 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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other sequences; artificial sequences.
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Sequence 2 from Patent WO2004072225.
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 90 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
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chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiner, G. and Hartmann, G. Methods for enhancing antibody-induced cell lysis and treating
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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100.0%; Pred. No. 1.7e+05;
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 85.0%; Pred. No. 1.3e+05;
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Sequence 533 from Patent W00197843.
AX355505
AX355505.1 GI:18620173
                    0; Mismatches
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AXX03898
AXI03898.1 GI:13920095
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Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, M.Y. and Bruice, T.W.

Promoters for regulated gene expression
Patent: US 6938555-A 69 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F., Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A., Sheppard,L.T., Lim,M.Y. and Bruice,T.W. Promoters for regulated gene expression parent: WO 01946001-A 69 13-DEC-2001; GENELABS TECHNOLOGIES, INC. (US)
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                                                                                                        66.7%; Score 16; DB 6; Length 33; 100.0%; Pred. No. 5.9e+04; rive 0; Mismatches 0; Indels
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85.0%; Pred. No. 1.3e+05;
ive 0; Mismatches 3;
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other sequences; artificial sequences.
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Sequence 69 from patent US 6838556.
AR630015.1 GI:59762210
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 Location/Qualifiers
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Matches 17; Conservative
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AX754696/c
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Unclassified.
1 (bases 1 to 27)
1 (bases 1 to 27)
Reed,J.C. and Sato,T.
Reed,J.C. and Sato,T.
Nucleic acids encoding Fas associated proteins and screening assays using same
Patent: US 5747245-A 13 05-MAY-1998;
Patent: US 5747245-A 13 05-MAY-1998;
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                                                                                                                                                           Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 90 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                         1. .16
/organism="synthetic construct"
/nol_type="unassigned DNA"
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                                                   DNA
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Sequence 13 from patent US 5632994.
143661.1 GI:2468759
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Sequence 90 from Patent WO02053141.
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Sequence 13 from patent US 5747245.
AR004426
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synthetic construct
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143661/c
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PAT 10-JUN-1998
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Regulation of gene transcription by the variable number of tandem repeats (vntr) domain of the dopamine transporter gene patent: WO 03038099-A 1 08-MAY-2003;
TCS Cellworks Ltd (GB)
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Reed.J.C. and Sato, T.
Interaction of proteins involved in a cell death pathway
Patent: US 5702897-A 8 30-DEC-1997;
Location/Qualifiers
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1 (bases 1 to 27)
Reed, J.C. and Sato, T.
Fas associated proteins
Patent: US 5632994-A 13 27-MAY-1997;
Location/Qualifiers
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Sequence 1 from Patent W003038099.
AX754696.1 GI:32167230
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/organism="unknown"
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Sequence 8 from patent US 5702897.
186720
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Homo sapiens
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                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Submitted (21-FEB-1995) A. Villa, ITBA- CNR, Via Ampere 56, 20131
                                                 Gaps
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                       Length 40;
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                                                                                                                                                                                    linear
                                                 5; Indels
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                  Score 15; DB 6; I
Pred. No. 1.5e+05;
0; Mismatches 5;
                                                                                                                                                                             H.sapiens tfe3 gene, third intron donor.
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synthetic construct
other sequences; artificial sequences.
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/gene="tfe3"
/note="third intron donor"
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Sequence 12 from Patent EP1217072.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="X"
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7490085
                                                                               1 GGGGTCCAGCGTGCGCCATGGGG 23
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Homo sapiens (human)
Homo sapiens
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/gene="tfe3"
                    / Match 62.5%;
Local Similarity 78.3%;
Les 18; Conservative
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Villa,A.
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                    Query Match
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HSTFE3ID3/c
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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VERSION
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1 (bases 1 to 47)
Larocca,D., Kassner,P. and Baird,A.
METHODS USING GENETIC PACKAGE DISPLAY FOR DETECTING AND IDENTIFYING
METHODS USING GENETIC PACKAGE DISPLAY FOR DETECTING AND INTERACTIONS THAT FACTLITATE INTERNALIZATION AND
TRANSGENE EXPRESSION AND CELLS OR TISSUES COMPETENT FOR THE SAME
AND METHODS FOR WOUVING GENE DELIVERY VECTORS
PATENT: US 6723512-A 5 20-APR-2004;
Selective Genetics Inc., San Diego, CA
Location/Qualifiers
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Larocca,D., Baird,A. and Kassner,P.
Methods using genetic package display for selecting internalizing ligands for gene delivery
Patent: US 6451527-A 5 17-SEP-2002;
Selective Genetics, Inc.; San Diego, CA
Location/Qualifiers
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                            1. .20
/organism="synthetic construct"
/organism="synthetic bna"
/mol_type="unassigned bna"
/mol_type="taxon:32630"
/ob_xref="taxon:32630"
/ob_type="ranslational consensus WAP-EPO with NotI modification"
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9
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ilarity 88.9%; Pred. No. 2e+05;
Conservative 0; Mismatches
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Sequence 5 from patent US 6451527.
AR229744
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Location/Qualifiers
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1 (bases 1 to 29)
Aujame, L., Bouchardon, A., Renauld-Mongenie, G., Rokbi, B., Nassif, X.,
Tinsley, C. and Perrin, A.
Nucleic acids and polypeptides specific of the neisseria genus
                                                                                                           PAT 14-FEB-2005
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                                                                                                                                                                                                                                                                                                         pathogenic strains 12.28-DEC-2004;
Patent: US 6835384-A 127 28-DEC-2004;
Aventis Pasteur and Institut National de la Sante et de la
Recherche Medicale (INSERM); Lyons;
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Bouchardon,A. and Renauld,M.G.
Patent: FR 2785293-A 127 05-MAY-2000;
PASTEUR MERIEUX SERUMS VACC (FR)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="amorce de"
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synthetic construct
other sequences; artificial sequences.
                                                                                                      Sequence 127 from patent US 6835384.
AR628538
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/organism="unknown"
/mol_type="genomic DNA"
               2 GGGATCCAACCTGCTTCATGGGTG 25
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GGGGTCCAGCGTGCGCCATGGGGG
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BD002993/c
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VERSION
KEYWORDS
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AR628538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT 16-NOV-2004
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: amorce
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Aventis Pasteur (FR); INSTITUT NATIONAL DE LA SANTE ET :
RECHERCHE MEDICALE (INSERM) (FR)
Location/Qualifiers
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                             60.8%; Score 14.6; DB 6; Length 47;
81.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 26;
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60.0%; Score 14.4; DB 6;
Best Local Similarity 93.8%; Pred. No. 2.8e+05;
Matches 15; Conservative 0; Mismatches 1;
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Bacl-2 splicing variants
Patent: WO 2005012357-A 1 10-FEB-2005;
Milmer, Jo (GB)
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Seguence 1 from Patent WO2005012357.
CS019648
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/organism="unidentified"
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                                                                                              1 GGGGTCCAGCGTGCGCCATGG 21
                                                                                                                    GGGTTCCCGCGTGGGCGATGG 30
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Best Local Similarity 75.0
Matches 18; Conservative
                                                               17; Conservative
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                                               Best Local Similarity
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CS019648/c
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PAT 16-JAN-2004
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1 (bases 1 to 19)
Rao,M.S., Proschel,M.M. and Kalyani,A.J.
Liheage-restricted neuronal precursors
Patent: JP 200515071-A 14 21-MAY-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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PN JP 200251671-A/14
PD 21-MAY-2002
PD 21-MAY-2002
PF 03-UUJ-1998 UP 1999507430
PR 04-UUJ-1997 US 08/909435,02-JUL-1998 US 09/109858 PI
MAHENDRA S RAO, MARGOT MAYER PROSCHEL, ANJALI J KALYANI PC
A61K48/00,A61K35/30,C12N5/00,C12N5/08 CC
Lineage-restricted neuronal precursors
FH Key
        Gaps
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof baten: WO 0147944-A 7160 05-JUL-2001;
Curagen Corporation (US)
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/note="Nucleotide deleted between bases 25 and 26
Accession number cg40388639"
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                                                                                                                                                                 linear
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          Indels
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BD194701
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Sequence 7160 from Patent W00147944.
CQ008520.1 GI:41015226
          0; Mismatches
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JP 2005515071-A/14.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                             26 GGCGCTCGCGTGCGCCAGGCGGG
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          18; Conservative
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Key Location/Qualifiers
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    .35
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/organism='Artificial Sequence'
Location/Qualifiers
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35 bp DNA line
A method for determining DNA methyltransferase.
BD002993
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Patent: JP 2000232889-A 4 29-AUG-2000;
DAIICHI FHARMACEUTICAL CO LTD
OS ARTÍFICIAL Sequence
PP JP 2000232889-A/4
PD 29-AUG-2000
                                                                                                                                                                            A method for determining DNA methyltransferase
Patent: JP 2000232889-A 2 29-AUG-2000;
DAIICHT PHARMACEUTICAL CO LTD
OS Artificial Sequence
N JP 2000232889-A/2
PD 29-AUG-2000

    .35
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other sequences; artificial sequences.
1 (bases 1 to 35)
Aonuma.M.
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other sequences; artificial sequences.
1 (bases 1 to 35)

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    /organism="synthetic col/mol_type="genomic DNA"
    /db_xref="taxon:32630"

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BD002995.1 GI:18630956
JP 2000232889-A/4.
                                                           BD002993.1 GI:18630954
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PAT 29-SEP-1999
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0;
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Sequence 17 from patent US 5831066.
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Sequence 10 from patent US 5734033.
196091
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                                                                                                     17 bp
Sequence 9 from patent US 5734033.
                 37 GTTCAGCGGCGCCAGGGG 19
GTCCAGCGTGCGCCATGGG 22
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/db xref="taxon:32630"
/noTe="Description of Artificial Sequence: oligonucleotide
(45mer) used for in s i tu hybridization for Kv3.3 mRNA"
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Rao,M.S., Mayer-Proschel,M. and Kalyani,A.J.
Lineage-restricted neuronal precursors and methods of isolation
Patent: US 6787353-A 14 07-28P--2004;
University of Utah Research Foundation; Salt Lake City, UT
                                                                                                                      Gaps
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                                                                                       Query Match
Best Local Similarity 84.2%; Pred. No. 3.6e+05;
Matches 16; Conservative 0; Mismatches 3;
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1. .19
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                          DNA
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synthetic construct
other sequences; artificial sequences.
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Sequence 9 from Patent EP1348964.
AX839895

    19
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    /mol_type="genomic DNA"

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AR580293
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PAT 16-JUN-2001

FEATURES TITLE

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Unknown.
Unclassified.
1 (bases 1 to 18)
1 (bases 1 to 18)
Krieg,A.M. and Weiner,G.
Methods and products for stimulating the immune system using immunotherapeutic oligonocleotides and cytokines
Patent: US 6218371-A 59 17-APR-2001;
Location/Qualifiers
                                                                                                                                                                           1 (bases 1 to 18)
Krieg, A.M., Kline, J., Klinman, D. and Steinberg, A.D.
Immunostimulatory nucleic acid molecules
Patent: US 6207646-A 55 27-MAR-2001;
Location/Qualifiers
                                                                          linear
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100.0%; Pred. No. 4.4e+05;
tive 0; Mismatches 0;
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100.0%; Pred. No. 4.4e+05;
tive 0; Mismatches 0;
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                                                                   Sequence 55 from patent US 6207646.
AR140496.
AR140496.1 GI:14482992
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/organism="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59 from patent US 6218371.
AR146347
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Brown, L.R. and Xu, C.
Pluorescent diberazole derivatives and methods related thereto
Patent: US 6140051-A 131-OCT-2000;
Location/Qualifiers
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Pred. No. 4.4e+05;
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100.0%; Pred. No. ...
0; Mismatches
Reed, J.C.
Regulation of bcl-2 gene expression
Patent: US 5831066-A 24 03-NOV-1998;
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/organism="unknown"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 24 from patent US 5831066.
AR052624
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1 (bases 1 to 18)
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AR116926
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other sequences; artificial sequences.

I (bases 1 to 18)
S Schwartz,D.A. and Krieg,A.M.
S Schwartz,D.A. and Krieg,A.M.
Use of nucleic acids containing unmethylated CPG dinucleotide in the treatment of LPS-associated disorders
L Patent: JP 2001513776-A 27 04-SEP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN D 2001513776-A/27
PN 04-SEP-2001
PP 25-FEB-1998 JP 1998537810
PR 25-FEB-1997 US 60/039405
PR 28-FEB-1997 US 60/039405
PR AGINARTZ,ARTHUR KRIEG
PC AGINAGO, COTHZI/04, A01N43/04
CC Synthetic oligonucleotide
PH Key Location/Qualifiers
FT Source Location/Qualifiers
FT FT Source //organism='Artificial Sequence'.
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Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
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PF 28-SEP-1998 JP 2000515030
PR 02-COT-1997 US 60/06073,18-AUG-1998 US 09/136
TIMOTHY A RIBEY,BOB D BROWN, FYLE J ARNOLD
PC C12Q1/68,C07H21/04,C12N15/09,C12P19/34,C12N15/00 CC
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mythetic construct
other sequences; artificial sequences.

1 (bases 1 to 18)
Riley.T.A. Brown, B.D. and Arnold, L.J.
Combined antisense library
Patent: JP 2001519170-A 45 23-OCT-2001;
OASIS BIOSCIENCES INC
OS Artificial Sequence

    .18
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/db_xref="taxon:32630"

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   Mismatches
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JP 2001513776-A/27.
synthetic construct
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BD076451.1 GI:22622054
JP 2001519170-A/45.
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                                    CCAGCGTGCGCCAT 19
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 14; Conservative
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BD069938
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Semple,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansell,S.M.,
Cullis,P., Scherrer,P. and Debeyer,D.
Charged therapeutic agents encapsulated in lipid particles
containing four lipid components
Patent: US 6287591-A 14 11-SEP-2001;
Location/Qualifiers
1 (bases 1 to 18)

Krieg, A.M. and Weiner, G.
Methods and products for stimulating the immune system using immunotherapeutic oligonucleotides and cytokines
Patent: US 6218371-A 104 17-APR-2001;
Location/Qualifiers
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                                                                                                                                                                                    Length 18;
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Pred. No. 4.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory nucleic acid molecules
Patent: US 6239116-A 45 29-MAY-2001;
Location/Qualifiers
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100.0%; Pred. No. ...
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    .18
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    .18
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                                                                                                                   /organism="unknown"
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Seguence 45 from patent US 6239116.
ARIS4716
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Krieg, A.M. and Kline, J.N.
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Best Local S:
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AR167448
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lipid vesicles
Patent: JP 2002501511-A 14 15-JAN-2002;
INEX PHARMACEUTICALS CORP
DD 15-JAN-2002
PF 14-MAY-1998 D 1998548646
PI SEAN C SEMPLE, SANDRA K KLIMUK, TROY HARASYM, MICHAEL J HOPE, PI
STEVEN M ANSELL,
PI PIETER CULLIS, PETER SCHERRER, DAN SUITE DEBEYER PC A61K9/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description of Artificial Sequence: Designed DNA based on bcl-
1 (bases 1 to 18)
Semple.S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansel,S.M.,
Cullis,P., Scherrer,P. and Debeyer,D.S.
High efficiency encapsulation of charged therapeutic agents in
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100.0%; Pred. No. 4.4e+05;
tive 0; Mismatches 0;
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    .18
        /organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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Patent: JP 2003026609-A 17 29-JAN-2003;
John C REED
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 18)
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    .18
    /organism="Chlamydia sp./mol_type="genomic DNA" /db_xref="taxon:35827"

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JP 200302669-A/17
29-JAN-2003
19-JUN-2003
20-SEP-1993 US 08/124256
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   REFERENCE
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High efficiency encapsulation of charged therapeutic agents in
lipid vesicles.
BD106497 BD106497.1 GI:23201315
JP 2002501511-A/14.
Chlamydia sp.
Chlamydia sp.
Chlamydia sp.
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
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N JP 2001515087-A/4

PN JP 2001515087-A/4

PD 18-SEP-2001515087-A/4

PR 18-AUG-1999 JP 2000509723

PR 18-AUG-1997 CH

1931/97

PC CO7H19/106, CO7FT/118, CO7H19/106, CO7H19/106, CO7FT/118, CO7H19/106, CO7H19/10
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JP 2001515087-A/4.
synthetic construct
synthetic synthetic
1 (bases 1 to 18)
pitsch,5., Weiss,P.A and Jenny,L.
pitsch,5., Weiss,P.A and Jenny,L.
synthetic syntheti
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                                                           1. .18 /organism='Artificial Sequence'.
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                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Pred. No. 4.4e+05;
                             Location/Qualifiers

    .18
    ^organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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/organism="synthetic construct"
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100.0%; Pred. No. ...
0; Mismatches
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/db_xref="taxon:32630"
                                                                                                                             Location/Qualifiers
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FH Key Locat
FT source 1. .1
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Best Local Similarity 100.0
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Matches 14
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BD080525/c
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BD106497
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Gaps

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PAT 17-JUL-2003

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Gaps

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Other sequences; artificial sequences.

NCE 1 (bases 1 to 18)

ORS Magner, H. and Lipford, G.

Barent: JP 2002514397-A 59 21-MAY-2002;

CORY PHARMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

CORY PARAMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

CORY PARAMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

CORY PHARMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

CORY PHARMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

ND 19 2005514397-A/59

PP 14-MAY-1999 US 09/241653 PI

HERMANN WAGNER, GRAXSON LIPFORD

PC C12N15/09, A6IX31/70, A6IX39/39, CO7H21/04//A6IX45/00, C12N15/00

CC Synthetic Sequence

FH Key Location/Qualifiers

FT SOURCE /Organism='Artifinial Cammon',

FT FOURTH IN COMMON CORY CONTRACTOR CONTRACTOR CORTACTOR CORTACTO
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synthetic construct

ISM synthetic construct

other sequences, artificial sequences.

CB (bases 1 to 18)

RS Wagner, H. and Lipford, G.

Re Medner, H. and Lipford, G.

Method of controlling hematopoiesis by using CpG oligonucleotide

No PRARMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

OS Artificial Sequence

NO D 2002514397-A/104

PD 21-MAX-2002

PF 14-MAX-1999 JP 2000547949
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Method of controlling hematopoiesis by using CpG oligonucleotide.
BD205614
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Method of controlling hematopoiesis by using CpG oligonucleotide.
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                                                                         ch 58.3%; Score 14; DB 6; Length 18; Similarity 100.0%; Pred. No. 4.4e+05; 14; Conservative 0; Mismatches 0; Indels
                                                                               Length 18;
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100.0%; Pred. No. 4.4e+05;
tive 0; Mismatches 0;
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JP 2002514397-A/59.
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consolidates artificial sequences.

E l'bases 1 to 13
Compositions and methods for the delivery of oligonucleotides via the alimentary canal
compositions and methods for the delivery of oligonucleotides via the alimentary canal
L Patent: JP 2002510319-A 34 02-APR-2002;
SS PHARMACEUTICALS INC
OS Artificial Sequence
N JP 2002510319-A/34
PD 02-APR-2002
PR 01-JUL-1998 US 08/886829
PR 01-JUL-1997 US 08/886829
                                                                                                                                        synthetic construct
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other sequences; artificial sequences.

I (bases i to 18)

Barackman, J., Simph, M., Ugozoli, M., Kazazu, J., Donnelly, J.,
Ott, G.S. and Ohagan, D.
Microemulations with Adsorbed Macromoelecules and Microparticles
Artificial Sequence
OS Artificial Sequence
N JP 2002537102-A/4
PD 05-NOV-2002
PP 05-NOV-2002
PP 05-NOV-2002
PR 29-JUL-1999 US 60/146391, 28-OCT-1999 US 60/161997, PR
26-FEB-1999 US 60/121858
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                       BD190420 18-2003 Macromoelecules and Microparticles.
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JP 2002510319-A/34.
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DUAZZEOU9 18 bp DNA linear PAT 17-JUL-2003 Compositions of CPG and saponin adjuvants and uses thereof. BD222609
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PN JP 2002522510-A/1
PD 23-JUL-2002
PF 06-AUG-1998 US 60/095913,08-APR-1999 US 60/128608 PI
CHARLOTTE A KENSIL
PC A61K39/39,A61K39/00,C12N15/09,C12N15/00
CC Compositions of CPG and saponin adjuvants and uses thereof FH
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JP 200222510-A/1.
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Sulkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Quillajaceae; Quillaja.

Kensil, C.A.
Kensil, C.A.
PR 14-MAY-1998 US 60/085516,02-FEB-1999 US 09/241653 PI
HERMANN WAGNER, GRAYSON LIPPORD
PC C12N15/09,A61K31/70,A61K39/39,C07H21/04//A61K45/00,C12N15/00
CC Synthetic Sequence
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FH Key Location/Qualifiers
FT source 1 .18
/organism='Artificial Sequence'.
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    70 reganism="synthetic construct"
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    .18
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GenCore version Copyright (c) 1993 - 2006	OM nucleic - nucleic search, using sw model	Run on: February 15, 2006, 17:25:23; (v.	Title: US-09-669-187A-81 Perfect score: 24 Sequence: 1 ggggtccagcgtgcgccatggggg 24	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 4996997 segs, 3332346308 resi	Total number of hits satisfying chosen parame	Minimum DB seq length: 0 Maximum DB seq length: 50	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 300 summaries	* 21 . *	1: genesedn1980	genesequi genesequ2000 genesequ2001	geneseqn2001bs qeneseqn2002as	geneseqn2002bs	genesedn2003bs	1: geneseqn2003d 2: geneseqn2004a	3: geneseqn20 4: geneseqn20	24 [	Fred. No. 18 the number of results predictions of score greater than the score	derived by analysis of the		Result No. Score Match Length DB ID	100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	24 100.0 24 6	24 100.0 24 6 24 100.0 24 9	24 100.0 24 9	24 100.0 24 13 17.2 71.7 26 2	8 16 66.7 30 13	9 16 66.7 33 3 0 16 66.7 33 3	11 15.2 63.3 35 6	3 15 62.5 16 6	4 15 62.5 16 6 5 15 62.5 16 9	6 15 62.5 16 9	17 15 62.5 16 13 ADU89406 c 18 15 62.5 25 9 ACI96181	9 15 62.5 27 2

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12-JUN-2001 (first entry)

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response. The method comprises administering an immunostimulatory uncleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory nucleic acid immunostimulatory incleic acid. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophlus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redurect a Th1 to a Th1 immune response and to activate immune cells. Note: the
                                                                       Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infections disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
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                                   Immunostimulatory nucleic acid #72.
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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AAF98956 RESULT 1

AAF98956 standard; DNA; 24

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ALIGNMENTS

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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder ancer, chone cancer, barain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, leukaemia, liver cancer, eye cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, larynx cancer, pancreatic cancer, prostate cancer, rhaddomyosarcoma, skin cancer, prostate cancer, rhaddomyosarcoma, skin cancer, stonach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
                                                                                                                                                                            Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 24; DB 6; Length 24; 100.0%; Pred. No. 0.58;
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22-JUN-2000; 2000US-0213346P.
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                                              (IOWA ) UNIV IOWA RES
                                                                                          Hartmann G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       administering at least one antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted anglogenesis. The method is useful for inhibiting anglogenesis associated with solid tumour growth, tumour metastasis, precancerous lession, theumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, myocardial anglogenesis, plaque neovascularisation, telanglectasia, haemophiliac joints, anglofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypertrophic scars. The present sequence is an antianglogenic nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising
  rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
plaque neovascularisation; telangiectasia; haemophiliac joint;
angiofibroma; wound gramulation; intestinal adhesion; atherosclerosis;
scleroderma; hypertrophic scar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to inhibiting angiogenesis in a subject,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunostimulatory nucleic acid SEQ ID NO: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 21; 276pp; English
                                                                                                                                                                                                                                                                                                                                          (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                    14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                                14-DEC-2000; 2000US-025534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001; 2001WO-US020154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL39036 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-566690/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                              WO200253141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200197843-A2
                                                                                                                                                                                                                                                                                                                                                                                        Bratzler RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-2001.
                                                                                                                                                                                                          11-JUL-2002
                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL39036;
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Local Matches

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Mismatches

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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                  The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulocrative collitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
                                                                                                                                                                                                                              Gaps
        allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                    100.0%; Score 24; DB 9; Length 24; 100.0%; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 9; Length 24;
Pred. No. 0.58;
                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                             Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 C; 13 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fouron Y;
                                                                                                                                                                                                                                                                    1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                     1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                              Disclosure; Page 10; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulatory nucleic acid #72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-0179991P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-2001; 2001US-00776479
                                                                                                                                                                                                                                                                                                                                       ADB36458 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                              24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRATZLER R L.
PETERSEN D M.
FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 2 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-657977/62.
                                                                                                                                                                                                                  Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003087848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; allergy;
                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PETE/) I
(FOUR/) 1
                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                               ADB36458
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                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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0
                                                                                                                                                                                                                                                                                                                                                Allergic response suppressor oligonucleotide #81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of an immunostimulatory nucleic acid.
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24
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GGGGTCCAGCGTGCGCCATGGGGG
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                                                                                                                                                                                       ВР
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02-FEB-2001; 2001US-00776479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-2004; 2004US-00831778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ86577 standard; DNA; 26
                                                                                                                                                                                       ADU89397 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method of the invention.
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J Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-833006/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRAT/) BRATZLER
(PETE/) PETERSEN
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004235774-A1
                                                                                                                                                                                                                                                                                                10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                          ADU89397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
AAQ86577
ID AAQ8
                                                                                                                                                              ADU89397
                                                                                                                                    RESULT
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us-09-669-187a-81.szlm50.rng

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The present invention describes a filamentous fungus (I) comprising an exogenous polynucleotide capable of expressing a Bcl-2 polypeptide or its active portion, and exhibiting accelerated growth as compared to a wild-type filamentous fungus. Also described: (I) enhancing (M1) growth of filamentous fungus, involving providing the filamentous fungus with a Bcl cilamentous fungus, involving providing the filamentous fungus with a Bcl cilamentous fungus storied at aboptimal temperature; (3) increasing of a filamentous fungus storied at aboptimal temperature; (3) increasing culture medium (II) suitable for growth of fungus, comprising Bcl-2 culture medium (II) suitable for growth of fungus, comprising Bcl-2 culture medium (II) suitable for growth of fungus, comprising Bcl-2 culture medium (II) suitable for growth of fungus, comprising Bcl-2 colletorics active portion, and a carbon source; and (5) a colletorichum gloeosporioides f.sp. aeschynomene. (M1) is useful for cocoding a suitable gene. Bcl-2 has herbicide activities. (I) is colletorichum gloeosporioides f.sp. aeschynomene. (M1) is useful for cradicating an unwanted weed growing in a crop field, which is nuclea weed spreading (I) in the crop field which is pathogenic to the unwanted weed spreading (I) in the crop field which is pathogenic to the unwanted weed spreading (I) in the crop field which is pathogenic to the unwanted weed scand drug production, paper and pulp industry, agriculture and collection. (I) remains viable in storage for a time period longer than the wild-type filamentous fungus when grown on solid media. (I) chartess, as compared to the wild-type filamentous fungus. The present sequence represents a PCR primer for the human Bcl-2 gene, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                              Novel filamentous fungus having exogenous polynucleotide expressing Bcl-2 polypeptide, and exhibiting accelerated growth compared to wild- type filamentous fungus, useful for eradicating unwanted weed growing in crop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; human; episome; transfection; selection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30 BP; 7 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 16; DB 100.0%; Pred. No. 2e+ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2; 57pp; English
                                                                                                                       (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                Sharon A, Goldstein-Barhoom S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                      10-FEB-2004; 2004WO-IL000132.
                                                                                12-FEB-2003; 2003US-0446513P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA50259 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGCGTGCGCCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-2000 (first entry)
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Best Local Similarity 100.'
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl2 gene 5' PCR primer
                                                                                                                                                                                                       WPI; 2004-625842/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
26-AUG-2004
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                                                                                                                                                                                                                                                                                                            field
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The signal sequence was isolated from barley alpha-amylase cDNA by PCR using the primers given in AAQ86577-78. The product was cloned into BBLUBSCTIPILI together with a mouse MHC II alpha chain mature peptidenence to obtain plasmid p8M155, for expression in tobacco cv. SRI transformants. (Updated on 25-MAR-2003 to correct PN field.) (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressing a mammalian antigen in transformed plants to provide a source of plant material - for oral or enteral admin. to a mammal to produce tolerance to the antigen.
                                                                                                                                                           Barley; Hordeum vulgare; alpha-amylase; signal peptide; PCR; primer; polymerase chain reaction; major histocompatibility complex; MHC; transgenic plant; allograft refection suppression; plasmid pSM155; tobacco; Nicotiana tabacum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             filamentous fungus; Bcl-2; herbicide;
Colletotrichum gloeosporioides f.sp. aeschynomene; food production;
drug production; paper; pulp industry; agriculture; bioremediation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 BP; 4 A; 8 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNLO ) UNIV HOSPITAL LONDON HEALTH ASSOC.
                                                                                                                    Alpha-amylase signal sequence primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Bcl-2 PCR primer SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 17; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                            94WO-CA000530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stiller
                                                                                                                                                                                                                                                                                                                                                                                                                                   93GB-00019429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR29366 standard; DNA; 30
                                                        (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-139392/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004072225-A2.
                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-1994;
                                                                                                                                                                                                                                                                                                          WO9508347-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jevnikar AM,
                                                        25-MAR-2003
25-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                 30-MAR-1995.
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                   AAQ86577;
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Gaps

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RESULT

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DB 13; Length 30; 2e+03; 0; Indels

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Transgenic plants with improved resistance characteristics comprising
                                                                                                                                                                                                                                                                                                                                                                                                           Cyclin D1
HBV promot
                                                                                                                                                             conferred
                                                                                                                                                                                                                                                                                                                                              ABK29920;
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                              ABK29920/
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                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                             The present 5' primer was used with the 3' primer given in AAA50260 for the PCR amplification of Bcl2 DNA, introducing a 5' BsiWI site and a 3' MneI site. The PCR product was incorporated into an episome to demonstrate a method of the invention. The method relates to the maintenance and selection of episomes in transfected eukaryotic cells in vitro or in vivo, e.g. for gene therapy. It involves transfecting the cells with an episome under conditions in which cells that survive are successfully transfected with the episome. The resulting cells express a first protein whose expression causes cell death and a second protein whose expression causes cell death and a second protein first protein. In an example of the method, bcl2 and bad, and df445 and cide-1, were used as kill antegonist and kill agonist pairs in episomes used to transfect 293E cells. The method allows the rapid establishment
                                                                                                                                                                                                                                                                                                                       eukaryotic cells that stably and reliably express a gene of interest
                                                                                                                            Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis; bcl-2; resistance; bacterial; viral; pathogens; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutagenic PCR primer Bc12-5 targeted to anti-apoptotic gene bc1-2.
                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                  Score 16; DB 3; Length 33;
Pred. No. 2e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              Sequence 33 BP; 9 A; 9 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                             Example 1; Page 29; 53pp; English
                                                                                                                                                                                                                                                                                                                                                           66.7%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYNE-) UNIV NEBRASKA-LINCOLN
                     11-FEB-2000; 2000WO-US003547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0106321P.
99US-0138303P.
                                          99US-00249585
                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                 27 ccaecerececcares 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US025522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA48984 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            6 CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                              (PHAR-) PHARMACOPEIA INC.
                                                                                   Chelsky D;
                                                                                                       WPI; 2000-515062/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365634/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200026391-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                          11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-1999;
17-AUG-2000.
                                                                                  Horlick RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dickman MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA48984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA48984/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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                                                                                                                        The present invention relates to the use of apoptotic genes in the the production of transgenic plants with improved resistance characteristics. The present sequence is the mutagenic PCR primer Bc12-5. This primer was used with primer Bc12-3 (AAA48985) to introduce a 5' Ncol site and a 3' Xbal site in the human apoptotic gene bc1-2. Specifically the primer introduced an Ala residue between the Met (position 1) and His (position 2) residues of the native protein. The altered bc1-2 sequence was used in the creation of the final vector used to transform plants. The improved resistance characteristics of the plants helps protect against bacterial, viral and other pathogens. Resistance to abiotic challenges may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid regulatory sequences, which are able to regulate expression of a gene operably linked to a promoter, useful for regulating the expression of transgenes and for treating e.g., cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vanH promoter; androgen receptor promoter; AR promoter; human epidermal growth factor receptor 2 promoter; her2 promoter; hera lactamase promoter; Bla promoter; transgene; cancer; breast cancer; colon cancer; immunological disorder; prostate cancer; cytostatic; autoimmune disease; HBV pre-S promoter; HBV-X promoter; Enterococcus infection; immunosuppressive; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in D1 promoter; CD40L promoter; hepatitis B virus promoter; promoter; vancomycin-resistant enterococci promoter; VRE promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression modulator; multiple sclerosis; MS; chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma; systematic lupus erytheatecous; SLE; graft-vs-host disease; GVHD; familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laurance ME, Michelotti EF;
omas RL, Kongpachith A, Sheppard LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Lens.
o. 2e+03;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human epidermal growth factor receptor 2 (Her2), primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 BP; 3 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 3
Pred. No. 2e+0
0; Mismatches
nucleic acids encoding apoptotic proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tam AW, Daux
                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%; Pines 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK29920 standard; DNA; 35 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2001; 2001WO-US018343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%;
                                                                 Example 3; Page 58; 109pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 ccaecerececares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim JP, Starr DB, Tam AV
Velligan MD, Latour DR,
Lim MY, Bruice TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-130595/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic; ds.
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Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bratzler RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS77606;
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                                               8
                                         The invention describes an isolated nucleic acid regulatory sequence for a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci (VRE) promoter, an HBV promoter, and receptor (RR) promoter. Human epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase regulate expression of the endogenous, autologous or heterologous genes operably linked to the promoter, and may be incorporated into heterologous nucleic acid constructs for use in regulated expression of transgenes. Regulated expression of cyclin D1 can be used in cancer therapies, such as breast, colon or pancreatic cancers and familial adenomatous polyposis. Regulation of the activity of CD40L gene promoter may be used in the treatment of immunological disorders, such as activity of ED40L gene promoter autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus erythematosus (SLE), graft-ve-host disease (GVHD) and rhematoid arthitis. Regulated expression of genes under the control of the HBV (hepaticis B)-specific core, pre-S and X promoters can be used in the therapy of HBV disease, chronic hepatic insufficiency, cirrhosis, hepatocellular carcinoma, and in the regulated expression of the vall gene promoter can be used in treatment of Enterococcus infection, while regulated expression of the androgen receptor gene can be used in the invention to determine the regulatory regions involved in gene expression, codescribed in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection; bacterial infection; fungal infection, parasitic infection, cancer, asthma, infections allergy, immune deficiency, phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                               63.3%; Score 15.2; DB 6; Length 35; 85.0%; Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                       Seguence 35 BP; 3 A; 13 C; 14 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunostimulatory nucleic acid #81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vollmer J;
                        Example 6; Page 52; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTCCAGCCGGAGCCATGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTCCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF98965 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLEY PHARM GMBH
immunological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-273485/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF98965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
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                                                                        The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immuno response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to inhibiting angiogenesis in a subject, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%; Score 15; DB 4; Le 100.0%; Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis inhibitory oligonucleotide #90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
Disclosure; Page 40; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 21; 276pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-2001; 2001WO-US048458.
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nes 15; Conservative
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present sequence is an immunostimulatory oligonucleotide described in the

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              included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler Webber Syndrome, myocardial angiogenesis, plaque meovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, barain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larymx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, nelanoma, melanoma, oral cavity cancer, ovarian cancer, pandreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
  administering at least one antiangiogenic nucleic acid molecule. Also
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                         Score 15; DB 6; Length 16;
Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                   Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory nucleic acid SEQ ID NO: 533.
                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis; metastasis; cytostatic; ss
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                                                                                                                                                                                                                                                                                                                           62.5%;
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                                                                                                                                                                                                                                                                                                                      Query Match
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inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as
                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                Immunostimulatory, antiinflammatory, dermatological, antipsoriatic; antiulcer; gene therapy, vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating non-allergic inflammatory diseases, such as psoriasis, ecze allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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                             Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                         Score 15; DB 6; Le
Pred. No. 5.4e+03;
0; Mismatches 0;
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100.0%; Pred. No. 5.4e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 10; 229pp; English.
                                                                                                                                                                                                                                                                                                                                    Immunostimulatory nucleic acid #84.
exemplification of the invention
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                                                                             100.08;
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                                                             62.5%;
                                                                                                                        5 TCCAGCGTGCGCCAT 19
                                                                                                                                          5 TCCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                     ACD99398 standard; DNA; 16
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                                                                                          15; Conservative
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                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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ACD99398
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RESULT 16

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The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimmlatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allery, including rhinitis, uricaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                    Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 15; DB 13; Length 16; 100.0%; Pred. No. 5.4e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human microarray DNA oligonucleotide SEQ ID NO 96172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 90; 235pp; English.
                                                                                                                                                                                            Bratzler RL, Petersen DM, Fouron Y;
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              23-APR-2004; 2004US-00831778.
                                                       03-FEB-2000; 2000US-0179991P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method of the invention.
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                                                                                                                (BRAT/) BRATZLER R
(PETE/) PETERSEN D
(FOUR/) FOURON Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              se; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; baccerial infection; viral infection.
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                                                                                                                                                                          ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 6; 221pp; English.
                                                                                                                                       Immunostimulatory nucleic acid #81.
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100.08; Fr
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                    ADB36467 standard; DNA; 16 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                  BRATZLER R L.
PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-657977/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (BRAT/) BRATZLER
(PETE/) PETERSEN
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                            US2003087848-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bratzler RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2005
                                                                                                  04-DEC-2003
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                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                             ADB36467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADU89406,
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Query Match Local

Matches

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Gaps

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismacch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, or analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises nor nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-bothybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of mRNA molecules by contact and a contact an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/sequence.html
New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas-associated protein; tumour necrosis factor receptor; PTP-BAS; apoptosis; PAP; cell surface protein; autoimmune disease; HIV virus; hybridoma; cell death; DNA primer; PCR; polymerase chain reaction; s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%; Score 15; DB 9; Length 25; 78.3%; Pred. No. 5.5e+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 3 A; 9 C; 9 G; 4 T; 0 U; 0 Other;
                                                  sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                  Claim 1; SEQ ID NO 96172; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGTCCAGCGTGCGCCATGGGG 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Bcl-2 forward DNA primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT18388 standard; DNA; 27 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00410804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed JC, Sato T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9534661-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-1994;
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New Fas associated proteins PTP-BAS types 4 and 5 - involved in

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the invention traces to a mucier active computation at the control of the signal sequence having at least one signal sequence unit or a mixture of units, the signal sequence causing a transmembrane transport of the nucleic acid, the solological system. The invention also relates to a vector containing the nucleic acid, a host organism containing at least the nucleic acid or the vector, a method of producing the nucleic acid, the vector, a pharmaceutical composition comprising the nucleic acid, the vector or the host organism and optionally a pharmaceutical carrier and/or diluent and a kit comprising the nucleic acid, the vector or the host organism. The conclectide sequence further contains at least one second nucleotide sequence to be transported and/or one or more components covalently linked and/or forming a complex with the first and/or second nucleotide sequence, where the covalently linked and/or complexed components are biologically active. The nucleic acid, vector or host organism is useful for preparing a pharmaceutical composition for treating genetically based disorders. This sequence represents a signal sequence-containing
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programmed cell death, used for modulating apoptosis, e.g. for treating cancer, and for identifying other modulators.
                                                                                         The cDNA sequence encoding the cytoplasmic domain of human Fas (AA 191-335) was modified by PCR mutagenesis using this primer along with the corresponding reverse primer (AAT18389) and another forward (AAT18386) and reverse (AAT18337) primer set. It was then subcloned in frame into plasmid pEG202 to produce plasmid pEG/Fas(191-135). The cDNA sequence the cytoplasmic domain of human Fas was then subcloned into the ECORI site of pEG302, in-frame with the upstream LexA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a nucleic acid comprising a first nucleotide
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid promoting transmembrane transport of nucleic acids,
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                                                                                                                                                                                                                                                  Sequence 27 BP; 7 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           Score 15; DB 2; Le
Pred. No. 5.5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treating genetically based disorders
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                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                         Disclosure; Page 42; 84pp; English.
                                                                                                                                                                                                                                                                             62.5%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
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                                                                                                                                                                                                                                                                                                                                                                                             21 CCAGCGTGCGCCATG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADY71779 Standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                           Local Similarity 100.
les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005024033-A2
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(first entry)

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human; ds; dopamine transporter; DAT; enhancer; expression vector; reporter gene; antiparkinsonian; neuroleptic; antidepressant; Parkinson's disease; schizophrenia.
                                                                                                                                    Human dopamine transporter enhancer SEQ ID NO:1.
                                                      ADF70717 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                               01-NOV-2001; 2001GB-00026268.
                                                                                                                                                                                                                                                                                                     01-NOV-2001; 2001GB-00026268.
                                                                                                                                                                                                                                                                                                                                                          (TCSC-) TCS CELLWORKS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-432825/41.
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                GB2381525-A.
                                                                                                          12-FEB-2004
                                                                                                                                                                                                                                                                          07-MAY-2003
                                                                                 ADF70717;
                                                                                                                                                                                                                                                                                                                                                                                     Quinn J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid comprising a first nucleotide sequence having at least one signal sequence unit or a mixture of units, the signal sequence causing a transmembrane transport of the nucleic acid in a biological system. The invention also relates to a vector containing the nucleic acid, a host organism containing at least the nucleic acid or the vector, a method of producing the nucleic acid, the vector, a nethod of producing the nucleic acid, the vector or the host organism and optionally a pharmaceutical carrier and/or diluent and a kit comprising the nucleic acid, the vector or the host organism. The nucleotide sequence further contains at least one second nucleotide sequence further contains at least one second nucleotide sequence to be transported and/or one or more components covalently linked and/or second nucleotide sequence. Where the covalently linked and/or complexed components are biologically active. The nucleic acid, vector or host organism is useful for preparing a pharmaceutical composition for treating genetically based disorders. This sequence represents an oligonucleotide used in the scope
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                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid promoting transmembrane transport of nucleic acids, useful for treating genetically based disorders.
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                                                      Score 15; DB 14; Length 28;
Pred. No. 5.5e+03;
                                                                               0; Indels
oligonucleotide used in the scope of the invention.
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                            Sequence 28 BP; 3 A; 9 C; 8 G; 8 T; 0 U; 0 Other;
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                                             62.5%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                          ADY71781 standard; DNA; 28 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-2003; 2003EP-00020437.
                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2004; 2004WO-EP010162.
                                                                                                                           CCAGCGTGCGCCATG 19
                                                                                                            6 ccadcerececare 20
                                                                                                                                                                                                                                                                                        Control oligonucleotide #18
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                                                                                 15; Conservative
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                                                                                                                                                                                                                                                                                                                   Cellular transport; ss
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                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                    Matches
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                                                                                                                                                                                                                                     The invention relates to a novel expression vector comprising an enhancer sequence and a reporter gene. The enhancer sequence comprises a variable number of tandem repeat (VWTR) and is found in the 3' non-coding region of the human dopamine transporter (DAT) gene. The enhancer sequence is expession vector of the invention has antiparkinsonian, neuroleptic, and antidepressant activity, and may act as a dopamine transporter gene expression vector of the invention has antiparkinsonian, neuroleptic, and antidepressant activity, and may act as a dopamine transporter gene expression vector is useful for identifying a compound capable of regulating the expression of a target gene (preferably human dopamine transporter gene) that comprises an enhancer sequence. A compound of the invention is useful for treating Parkinson's disease and schizophrenia that are associated with reduced and increased levels of dopamine, respectively. The present sequence is used in the exemplification of the
Novel expression vector comprising reporter gene and a reporter genetranscription promoting enhancer sequence that has a variable number of tandem repeat and is found in 3'non-coding region of human dopamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 40 BP; 8 A; 15 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                               Claim 1; SEQ ID NO 1; 52pp; English.
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les 18; Conserv
                                                                                                                 transporter
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Gaps

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6 CCAGCGTGCGCCATG 20

15; Conservative

Matches

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Local Similarity

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, or at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more tocleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The mucleic acid probes and detecting the hybridisation. The mucleic acid probes and detecting the hybridisation. Each of the nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primare extensions or in screening SDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been contained and previously sequence. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly from USPTO at sequence thml
                                                                                                                                                                                          New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.8%; Score 14.6; DB 9; Length 25; Best Local Similarity 81.0%; Pred. No. 8.2e+03; Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human microarray DNA oligonucleotide SEQ ID NO 87909.
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                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 35445; 9pp; English
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16-MAR-2001; 2001US-0276759P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-2003 (first entry)
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                                              (AFFY-) AFFYMETRIX INC
                                                                                                                                              WPI; 2003-567953/53.
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                                                                                                Mittmann MP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapeutic protein production, characterized by the utilization of sequence motifs for restriction endonucleases NotI or NooI to connect the gene segments (including promoter regulatory regions) with the gene segments (including structural fragments of the gene coding the required protein). The method is useful for preparing an expression vector for therapeutic protein production, in particular human erythropoietin (BPO). The vector produced by the method is useful for BPO expression in suitable transfected eukaryotic cells or in the mammary gland of transgenic organisms. The present sequence represents a translational consensus WAP-EPO sequence with NotI modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the preparation of an expression vector for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing vectors for therapeutic protein production in transgenic animals, based on utilization of modified translational Kozak consento connect promoter regulatory sequences with coding structural gene
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                       Translational consensus WAP-EPO with NotI modification sequence.
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                                                                      Therapeutic; erythropoietin; EPO; transgenic; WAP; ss.
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                                                                                                                                                                                                                                                                                                                                                                        (BIOP-) BIOPHARM VU BIOFARMACIE A VETERINARNICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 32pp; English.
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ACI35454
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Gaps

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, or analysis of genetic variation or in hybridisation of rag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises morrises of at least one target sequence. The method of analysis comprises more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises mointoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The sequence or specific matations of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the containing the containing of DNA that have been isolated and previously sequenced. The sequence presented is one of the form of the containing the microarray. Note: The sequence of the form of the containing the contain
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                                                                                                                                           New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 3 A; 7 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 87909; 9pp; English.
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Best Local Similarity 81.0'
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(AFFY-) AFFYMETRIX INC
                                                                                                WPI; 2003-567953/53.
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                                                Mittmann MP
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library. In analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid set least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are strached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring of amily members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes in situ hybridisation, in Southern, Northern or dottober thybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly
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                                                                         New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.8%; Score 14.6; DB 9; Length 25; 81.0%; Pred. No. 8.2e+03; ive 0; Mismatches 4; Indels
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                                                                                                                                                            Claim 1; SEQ ID NO 55179; 9pp; English
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tes 17; Conservative
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                                      WPI; 2003-567953/53.
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Mittmann MP
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The present sequence is a PCR primer used to amplify the EGF sequence in COS cells infected with non-targeted M13 phage and EGF-phage. The maplification primers have sequences located on each side of the EGF sequence in the gene III coding sequence. The PCR products were digested with restriction endonucleases and ligated into a new phage vector and used to transform competent bacterial cells by electroporation. Plaques consider the analysed via PCR using oligonucleotides which included the present sequence. Four rounds of selection were sufficient to enrich the targeted EGF-phage to 100%. This selection procedure is a useful example of a novel method of selecting internalising ligands displayed on a genetic package carries a gene encoding a detectable product expressed on internalisation. The method is referred to as Ligand Ingends that may be useful as antibacterial agents or in gene therapy. The method is also useful for studying protein-protein interactions that lead to cell transduction and identifying cells which are transduced by the ligands. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                   Selecting internalized ligands displayed on a genetic package by contacting them with a cell, where each package carries a gene encoding detectable product expressed on internalization, useful for identifying
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81.0%; Pred. No. 8.3e+03;
tive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                          Example 19; Page 65; 112pp; English.
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                                                                                      Kassner P;
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                                            (SELE-) SELECTIVE GENETICS INC.
99US-00258689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US025361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 81.0%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD14864 standard; DNA; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                              ligands for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kassner P,
                                                                                      Baird A,
                                                                                                                                WPI; 2000-387775/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LARO/) LAROCCA D.
(KASS/) KASSNER P.
(BAIR/) BAIRD A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002068272-A1
26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36-JUN-2002.
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                                                                                      Larocca D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD14864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 29
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#X#X#X#X#####X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                   The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, or an analysis of genetic variation or in hybridisation to a DNA library, of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of the probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of mucleic acid subsciling in situ hybridisation, in Southern, Northern or dotprobes is useful in in situ hybridisation, in Southern, Northern or dotprobes is useful in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence and previously sequenced. The sequence presented is one of the norther more containing be obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                       New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phage display, biopanning; fusion protein; antibacterial; ligand internalisation; cell transduction; library screening; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.8%; Score 14.6; DB 9; Length 25; 81.0%; Pred. No. 8.2e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 3 A; 7 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF sequence biotinylated PCR primer AnchorlM8f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                Claim 1; SEQ ID NO 87293; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "biotinylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GICCACTGTGCTCCATGGGTG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA30408 standard; DNA; 47 BP.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteria phage M13.
WPI; 2003-567953/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200029555-A1
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17-NOV-1998;
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11-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA30408;
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Gaps

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bacterial infections, and cancer, e.g. biliary tract cancer, breast
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modified_base
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                                                                                                                                                                       The invention relates to a method for selecting ligands that internalise and facilitate transgene expression, comprising displaying on a phage carrying a transgene encoding a detectable product, and recovering a nucleic acid molecule encoding the ligands from the cell expressing the detectable product. The methods are useful in selecting and identifying ligands displayed on a phage that internalise and facilitate transgene expression, and also in identifying transduction facilitating peptides. Internalising ligands identified by the methods are useful in gene delivery methods and as anti-bacterial agents. The ligands and antiligands identified by the treatment of e.g., cancer and restenosis. The method is also useful in that it allows identification of molecules that are targets for new discovery. This sequence represents a PCR primer used to amplify a ligand gene III fusion of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonuclectides, useful for treating allergy or asthma, viral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral infection; bacterial infection; cancer; lymphoma;
intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                           Genetic package display method useful for detecting and identifying protein-protein interactions that facilitate internalization and transgene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.8%; Score 14.6; DB 10; Length 47; 81.0%; Pred. No. 8.3e+03; cive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 47 BP; 6 A; 10 C; 18 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vollmer J, Uhlmann E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CpG immunostimulatory oligonucleotide #52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                          Example 19; Page 24; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGTCCAGCGTGCGCCATGG 21
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25-SEP-2003; 2003US-0506108P.
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les 17; Conservative
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         WPI; 2003-776567/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004053104-A2
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modified_base
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ADP86181
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                                                                                                           The invention relates to a class of CpG immunostimulatory oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, gastric cancer, lymphomas, intraepithelial neoplasms, endometrial cancer (e.g. small cell and non-small cell), melanoma, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, soracomas, thyroid cancer, ocsophageal cancer, brain and CNS cancer, connective tissue cancer, ocsophageal cancer, eye cancer, testicular cancer, as well as other carcinomas and sarcomas. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CpG immunostimulatory oligonucleotide; immune response; allergy; asthma; viral infection; bacterial infection; cancer; lymphoma; intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma; carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention is also useful in gene therapy. The present sequence is a CpG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.0%; Score 14.4; DB 12; 93.8%; Pred. No. 1e+04; ive 0; Mismatches 1;
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                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunostimulatory oligonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COLE-) COLEY PHARM GROUP INC. (COLE-) COLEY PHARM GMBH.
                                                               Example; SEQ ID NO 52; 104pp;
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25-SEP-2003; 2003US-0506108P.
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Best Local Similarity 93.8
Matches 15; Conservative
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/*tag=
cancer, cervical cancer
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nucleic acid; polypeptide or nucleotide probe, which

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chemical; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA15383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA15383
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                                                        The invention relates to a class of CpG immunostimulatory of objigonucleotides containing a 5TCG motif or a CG at or the 5' end that are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, cervical cancer, choricoarcinoma, colon cancer, endometrial cancer, gastric cancer, invaphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer, testicular cancer, as well as other carcinomas and sarcomas. The invention is also useful in gene therapy. The present sequence is a CpG invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a method of regulating apoptosis in a cell comprising targeting an abnormally or alternatively spliced mRNA, an abnormally or alternatively structured mRNA, or a product of either. Also described are: a nucleotide construct with a nucleotide sequence which is homologous to mRNA transcribed from an abnormally spliced gene; an agent selected from small molecule or protein; polypeptide; peptide; aptamer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulating apoptosis in a cell, useful for treating cancer, comprises targeting an abnormally or alternatively spliced mRNA, an abnormally or alternatively structured mRNA, or a product of either.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; apoptosis modulation; pharmaceutical; cancer; cytostatic; neoplasm; Bcl-2; reverse transcriptase PCR; RT-PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                          60.0%; Score 14.4; DB 12; Length 18; 93.8%; Pred. No. 1e+04; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                      ie+04;
.hes 1; Indels
                                                                                                                                                                                                                                                                                                             Seguence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
                            Example; SEQ ID NO 53; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 14; 35pp; English.
                                                                                                                                                                                                                                                                            immunostimulatory oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Bcl-2 RT-PCR primer Bcl-2up.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADW88846 standard; DNA; 26 BP
                                                                                                                                                                                                                                                                                                                                                                                                        4 GICCAGCGIGCGCCAI 19
                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCAGCGTGCGCCAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2004; 2004WO-GB003326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2003; 2003GB-00017988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
 cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-123281/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milmer J, Jiang M;
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILM/) MILMER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2005012357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADW88846;
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 32
ADW88846/c
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continuents authorate, actual purpreparture of nuclear agent interacts with or binds with a protein expressed by an abnormally spliced mRNA for use as a medicament or for the manufacture of a medicament for the treatment of cancerous cell growth, a pharmaceutical composition comprising a nucleotide construct such as siRNA, anti-sense RNA, shRNA or miRNA; or the agent cited above, and a pharmaceutical composition comprising a nucleotide construct such as paramaceutical diluent or carrier; a DNA or RNA expression vector comprising an expression cassette including the nucleotide sequence selected from: the nucleic acid sequence of the abnormally spliced gene element as given in the specification; a nucleic acid molecule which hybridizes to the nucleic acid sequence of (a); and a nucleic acid molecule which hybridize to the nucleic acid sequence of (a); and a nucleic acid molecule which hybridized to the sequences in (a) and (b) and any sequence which is complementary to any of the above sequences, where the expression cassette is cannoformed to a pronder sequence. The method is useful for regulating apoptosis in a cell or for treating cancer. The agent or conclectide construct is useful as a medicament for the treatment of cancerous cell growth. The DNA or RNA expression can an expension of an anoisottic construct is used in the targeting of an abnormally spliced construct is used in the targeting of an abnormally spliced construct is a seed in the targeting of an abnormally spliced construct is also as a medicament for treatment of construct is used as a medicament for treatment of construct is used as a medicament for treatment of construct is used in the targeting of an abnormally spliced construct is also an enterest treatment of construct is used as a editor or coll growth. The DNA or RNA expression vector is used as a delivery means or the product. This sequence represents a reverse transcripture of construct is also an entered or an enter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a PCR primer that was used to amplify DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide specific for pathogenic Neisseria useful in therapeutic or preventative vaccines and for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pathogenic strain; Neisseria; vaccine; Neisseria infection; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer used to isolate alternatively nspliced Bcl-2 polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer for a Neisseria pathogenic strain DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.4; DB 14; Length
Pred. No. 1e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rokbi B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 BP; 6 A; 8 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERUMS & VACCINS SA. SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouchardon A, Renauld-Mongenie G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 30; 187pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98FR-00013693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-FR002643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Query Local Similarity 93.00,
Best Local Similarity 93.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccaecerececcarce s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA15383 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INMR ) PASTEUR MERIEUX
(INRM ) INSERM INST NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perrin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-365622/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200026375-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2000.
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Gaps

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Length 31; Indels

60.0%; Score 14.4; DB 10; 93.8%; Pred. No. 1e+04;

0; Mismatches

AGCGTGCGCCATGGTG 16

8 AGCGTGCGCCATGGGG 15; Conservative

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Best Local Similarity Matches 15; Conserv

Query Match

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encoding a protein that is specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequence is also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that overexpress it, or express it in a non-toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New engineered human skin equivalent that becomes perfused in vivo after engraftment on an immunodeficient animal, useful for treating conditions involving impaired angiogenesis, e.g. diabetes, chronic leg ulcers or
                                                                                                                                                                                                                                                                                                                                                                              Bcl-2; endothelial cell; mutant; vascularisation; human; antidiabetic; antiulcer; vulnerary; cardiovascular; cell therapy; ss.
                                                                                                                                                           Gaps
                                                                                                                                                         ö
                                                                                                                              60.0%; Score 14.4; DB 3; Length 29; 75.0%; Pred. No. 1e+04; ive 0; Mismatches 6; Indels
                                                                                                      Sequence 29 BP; 5 A; 8 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     Caspase-resistant Bcl-2 5'-end terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schechner JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 3; 144pp; English.
                                                                                                                                                                                   24
                                                                                                                                                                                                           GGGATCCAACCTGCTTCATGGGTG 25
                                                                                                                                                                                   1 GGGGTCCAGCGTGCGCCATGGGGG
                                                                                                                                                                                                                                                                           ADF28077 standard; cDNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-2003; 2003WO-US011371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2002; 2002US-0371677P.
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                             Local Similarity 75.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bothwell ALM, Pober JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-833725/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003087337-A2.
                                                                                                                                                                                                                                                                                                                             12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                     ADF28077;
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wounds.
                                                                                 mutant
                                                                                                                                                           Matches
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Human; D34A caspase-resistant Bcl-2; Bcl-2; mutant; vasotropic; vascularisation; angiogenesis; tissue transplantation; grafting; organ transplantation; gene; ss.

Human 5' end of Bcl-2 DNA SEQ ID NO:3.

(first entry)

03-APR-2002

ABA92890;

ВР

ABA92890 standard; DNA; 32

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The present invention describes a synthetic composition, which comprises collagen, fibronectin and at least one cell. Also described are: (1) a construct prepared by a method (MI) comprising: (a) preparing a solution comprising collagen and fibronectin; (b) suspending endothelial cells in the solution of step (a), where the suspended endothelial cells in the solution of step (a), where the suspended endothelial cells comprise a nucleic acid encoding a caspase-resistant Bel-2 polymetries, and (C) polymerising the collagen within the solution of step (b) to form a three construct produced by the method of (1); (a) a method (M2) of animal implantation comprising comprising in a method (M3) for forming endothelial cells into tubbes within a comprisity; (4) a method (M3) of producing endothelial cell tubules in vivo; (5) a method (M3) of producing endothelial cell tubules in vivo; (5) a method (M3) of sacularisation; (7) a method (M7) of composition in a tissue or an organ, or in animal; (6) methods (M6) for identifying genes or gene products involved in the process of vascularisation; (7) a method (M7) of composition is useful in methods for forming cultured endothelial cells into tubes within a composition is useful in methods for forming cultured endothelial cells into tubes of forming cultured endothelial cells into tubes within a confinence of kinn only or recipients with impaired vascularisation or impaired engineered skin onco recipients with impaired vascularisation or impaired angiogenesis, or in all aspects of tissue and organ transplantation and grafting. The present sequence represents the 5' end of human Bol-2, with the present sequence represents the sequence represents and organ transplantation and construction and present invention and example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 55; 99pp; English.
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comprise a nucleic acid encoding a caspase-resistant BC1-2 polypeptide, adjusting the solution of step (b) to about pH 7.0-8.0, and warming the solution of step (c) to about 25-40 &degric to form a three-dimensional gel. The method of endothelial cell transplantation promotes vascularisation of human skin equivalents in vivo. Administration can be orthotopic or subcutaneous. The engineered human skin equivalents and methods are useful in treating diseases or conditions involving impaired angiogenesis, such as diabetes, chronic leg ulcers, wounds, acardiovascular disease or burnis. The present sequence represents a Caspase-resistant BC1-2 5'-end terminal fragment

Sequence 31 BP; 7 A; 10 C; 8 G; 6 T; 0 U; 0 Other;

The invention relates to an engineered human skin equivalent, where the skin equivalent becomes perfused in vivo after engraftment on an immunodeficient animal. The method involves implanting onto a skin surface wound of an animal a construct prepared by a method comprising: preparing a solution comprising collagen and fibronecth; suspending endothelial cells in the solution where the suspended endothelial cells

cells,

New synthetic composition comprising collagen, fibronectin and useful for forming cultured endothelial cells for tissue/organ transplantation or grafting onto recipients with impaired

vascularization.

Zheng

Schechner JS,

Pober JS,

Bothwell ALM,

(UYYA ) UNIV YALE.

WPI; 2002-130568/17.

05-JUN-2001; 2001WO-US018034. 05-JUN-2000; 2000US-0208931P. 30-MAR-2001; 2001US-0279797P.

WO200193880-A1.

13-DEC-2001

Homo sapiens

Gaps

; 0

Indels

1;

Pred. No. 1e+04; Mismatches

93.8%;

15; Conservative

Best Local Similarity Matches 15; Conserv

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The invention relates to a hybrid oligomer comprising a cyclic AMP response element (GRE) sequence and a sequence that hybridises to the bcl cancer cells in vitro, which comprises contacting the growth of cancer cells in vitro, which comprises contacting the cancer cells with a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a CRE decoy oligomer and a CRE decoy oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a Carrier. The pharmaceutical composition of the invention is useful for preventing or treating cell-proliferative disorders e.g., cancer, hyperplasia or tumourigenesis and also bacterial infection, viral infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and bol-2 antisense oligomer are also useful for preventing or treating hepatitis B virus infection. The hybrid oligomers can also be used for secening candidate transcription factors or other molecules e.g., gene are also very contact or other molecules e.g., gene are also to the paratitis and parasitic disconsise or other molecules e.g., gene are also to the parameter or other molecules e.g., gene are also were the parameter or other molecules e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cAMP response element, bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic; autoimmune disorder; parasitic infection; virucide; hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybrid oligomer comprises a cyclic AMP response element sequence sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
                                                                                          ö
                                          60.0%; Score 14.4; DB 6; Length 32; 93.8%; Pred. No. 1e+04;
                                                                                     1; Indels
Sequence 32 BP; 7 A; 10 C; 9 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Bcl-2/CRE hybrid antisense oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumourigenesis; hepatitis B infection; human.
                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory proteins or for diagnostic assa:
Bcl-2/CRE hybrid antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 25; 78pp; English
                                                                                                                                                                                                                                                                                                ABK90294 standard; DNA; 34 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-2002; 2002WO-US001967.
                                                                                                                                     23
                                                                                                                                                                                32 AGCGTGCGCCATGGTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2001; 2001US-0263244P
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                     8 AGCGTGCGCCATGGGG
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-590754/63.
                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENT-) GENTA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200257480-A2
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                              ABK90294;
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60.0%; Score 14.4; DB 6; Length 34;

Query Match

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The invention relates to a hybrid oligomer comprising a cyclic AMP response element (CRE) sequence and a sequence that hybridises to the bcl 2-pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of cancer cells in vitro, which comprises contacting the growth of cancer cells in vitro, which comprises contacting the cancer cells with a tybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; the pharmaceutical composition of the invention is useful for carrier. The pharmaceutical composition of the invention is useful for preventing or treating cell-proliferative disorders e.g., cancer, hyperplasia or tumourigenesis and also bacterial infection, viral infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and catching candidate transcription factors or other molecules e.g., gene requilatory proteins or for diagnostic assays. The present sequence is a screening candidate transcription assays. The present sequence is a Bcl-2 antisense oligomulectide
                                                                                                                                                                                                                                                                                                                      Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE; cAMP response element; bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic; autoimmune disorder; parasitic infection; virucide; hyperplasia; tumourigenesis; hepatitis B infection; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid oligomer comprises a cyclic AMP response element sequence and sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-prollferative disorders e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                      Bcl-2-targeting antisense oligonucleotide BKl-PS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 58; 78pp; English
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                                                                                                                                                                            ABK90296 standard; DNA; 34 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2002; 2002WO-US001967.
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                                           21
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/*tag≃ a
                                                                                                                                                                                                                                                     (first entry)
                                                                               13 ccascerececeáre
                                           6 CCAGCGTGCGCCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENT-) GENTA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200257480-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
modified_base
                                                                                                                                                                                                                                                     21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                               ABK90296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klem RE;
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Gaps

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Indels

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Pred. No. 1e+04;

93.8%;

Mismatches

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15; Conservative

Matches

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bcl-2 antisense oligomer are also useful for preventing or treating hepatitis B virus infection. The hybrid oligomers can also be used for screening candidate transcription factors or other molecules e.g., gene regulatory proteins or for diagnostic assays. The present sequence is a Bcl-2/CRB hybrid antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybrid oligomer comprises a cyclic AMP response element sequence and a sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                          Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE; cAMP response element; bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic; autoimmune disorder; parastic infection; virucide; hyperplasia; tumourigenesis; hepatitis B infection; human.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyperplasia or tumourigenesis and also bacterial infection, viral
                                                                            ö
                                     60.0%; Score 14.4; DB 6; Length 34; 93.8%; Pred. No. 1e+04; ive 0; Mismatches 1; Indels
G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             Bcl-2/CRE hybrid antisense oligonucleotide BK7-DE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 58; 78pp; English.
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(၄)
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                                                                                                                                                 ccadcdrdddcdcarrd 28
                                                      llarity 93.8%;
Conservative
                                                                                                                 CCAGCGTGCGCCATGG 21
                                                                                                                                                                                                                                               ABK90352 standard; DNA; 34
                                                                                                                                                                                                                                                                                                                       (first entry)
   Sequence 34 BP; 6 A; 12
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                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENT-) GENTA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                       Query Match
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                                                                              Matches
                                                                                                                                                                                                            RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a peptide acting as agonist, antagonist or inverse agonist on a target receptor. Specifically, it comprises transformation of endocrine cell lines originating from mammalian hypothalamus and pancreatic islets, culturing the transformant and contacting with cells expressing the target receptor. The identification of those cells with a response reaction can be used for selecting a transformant cell line with the appropriate target activity that is expressing the novel transformed DNA. Accordingly, the present invention describes novel cell lines that are applicable in expression cloning systems of bioactive peptide precursor applicable in expression cloning systems of bioactive peptide precursor and in screening GPCR ligands for use as drugs including agonists, antagonists and inverse agonists i.e. activators and inhibitors. Such cell lines can provide a highly sensitive and convenient GPCR ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel method for obtaining a DNA that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bioactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kishimoto K, Kunitomo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrine cell lines originated from mammalian hypothalamus and pancreatic islet, applicable in expression cloning systems of bioactipeptide precursor genes, and in screening G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assay system. This oligonucleotide sequence is a PCR primer used amplify human GPCR cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 14.4; DB 10; Length 34; 75.0%; Pred. No. 1e+04; ive 0; Mismatches 6; Indels C
                                                                                                                                                                                                                                                               human, PCR; primer, ss; transformation, endocrine cell line, expression cloning system; bioactive peptide; GPCR ligand.
                                                                                                                                                                                                                               PCR primer used to amplify human GPCR G2A cDNA (SeqID 138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34 BP; 8 A; 14 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshizawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 22; SEQ ID NO 138; 316pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saeki S,
                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2003; 2003WO-JP004840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-2002; 2002JP-00113030.
                               28
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 75.0%;
Conservative
                                                                                                                         ADF50458 standard; DNA; 34
                                 13 ccagcerececarre
                                                                                                                                                                                            12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miura K,
Obinata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-833737/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                          WO2003087366-A1
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki K,
9
                                                                                                                                                          ADF50458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligands
                                                                                                          ADF50458/c
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Matches
                                                                                       RESULT 39
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DB 6; Length 34;

Score 14.4;

60.08;

Query Match

Seguence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;

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AAC88236;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for detecting gene polymorphisms of a gene that encodes cytochrome P450. The method involves using an oligonucleotide and/or a primer selected from those having sequences with at least 13 bases, including the base at position-21 in the base sequences represented by the oligos of 40.41 base pairs, or their complementary sequences, provided in the specification. The method is applicable in obtaining gene information, evaluation of drugs including safety and therapeutic efficacy, and screening drug candidates. This polymucleotide sequence represents one of the 40.41 base pair long oligos used in the gene polymorphism detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                            cytochrome P450- encoded gene obtaining gene information,
                                                                                              polymorphism; cytochrome P450; drug evaluation; safety; single nucleotide polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                         Cytochrome P450 gene polymorphism detecting oligo, SEQ ID No 27.
                                                                                                                                                                                  /standard_name= "Single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41 BP; 12 A; 13 C; 11 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                           Detecting gene polymorphism particularly of cytock with specific oligonucleotides, applicable obtaini evaluation of drugs and screening drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.4; DB 1
Pred. No. 1e+04;
0; Mismatches
                                                                                                                                                                                                                                                                                                                  Saito S;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 27; 144pp; Japanese
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human SNP oligonucleotide #7160.
ADK17713/c
ID ADK17713 standard; DNA; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                              replace (21, T)
                                                                                                                                                                                                                                                  29-MAY-2003; 2003WO-JP006750.
                                                                                                                                                                                                                                                                       30-MAY-2002; 2002JP-00158237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGTCCAGCGTGCGC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGATCCAGCGTGCGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%;
93.8%;
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                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                 Sekine A,
                                                                                                                                                                                                                                                                                                                                       WPI; 2004-043114/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                            (RIKE ) RIKEN KK
                                                                                                gene
                                                                                                        screening;
                                                                                                                                                                                                       WO2003102181-A1
                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                 Nakamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2002
                                                    06-MAY-2004
                                                                                                                                                                                                                            11-DEC-2003
                                                                                              detection;
                                                                                                                                                             variation
                              ADK17713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                              Ношо
                                                                                                         drug
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, cytochromes, the present sequence is one such oligonucleotide. The oligonucleotides and the preteins encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune of diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, concerned the concerned of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein, cytokome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; lineage restricted precursor cell; neuron-restricted precursor; NRP; glial-restricted precursor; GRP; mouse neural tube; transplantation; antibody; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine lineage-restricted precursor cell population PCR primer #14
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                                                                                                                               multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50 BP; 8 A; 24 C; 13 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 3440; 4143pp; English.
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27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2000; 2000WO-US035498
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-465210/50.
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les 18; Conser
                                                                                                                                                                                                                                                                                                        WO200147944-A2.
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2001
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its acid probes including one of 2,018,500 fully defined sequences, or its that of earlies match, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring can eatie and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid probes in situ hybridisation, in Southern, Northern or dottobe and solid sation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by communications of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA to genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence. Then
              New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New array of nucleic acid probes, useful for in situ hybridization, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.2%; Score 14.2; DB 9; Length 25; Best Local Similarity 84.2%; Pred. No. 1.2e+04; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human microarray DNA oligonucleotide SEQ ID NO 94301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                  Claim 1; SEQ ID NO 94919; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GTCCAGCGTGCGCCATGGG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-567953/53.
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                                                                                                                                                                                                                                                                                                                                                                                             New pure populations of neuron- or glial-restricted precursor cells and neuroepithelial stem cells from mouse neural tubes or embryonic stem cells for developing new drugs or techniques that enhance survival of transplanted cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides populations of lineage-restricted precursor cells from mouse neural tube and mouse embryonic stem cells. These populations are of neuron-restricted precursor cells (NRPs) and glial-restricted precursor cells (GRPs). These cell populations are useful in the development of new transplant techniques, for transplantation in diseases where neuronal or glial degeneration has occurred, in the identification of drugs which enhance the survival and proliferation of transplanted cells, to identify genes specific to selected stages of development, and in the generation of cell-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.2e+04;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Page 22; 37pp; English.
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                                                                                                                                    05-MAY-2000; 2000WO-US012446.
                                                                                                                                                                                          99US-0133159P
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                                                                                                                                                                                                                                             (UTAH ) UNIV UTAH RES FOUND
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hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-species comparison
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                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-024863/03
                                                                                                                                                                                                                                                                                                      Mujtaba T, Rao MS;
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                            WO200068359-A1
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                                                                                                                                                                                             07-MAY-1999;
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                                                                                  16-NOV-2000
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IID AC19

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Gaps

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, or nanalysis of genetic variation or in hybridisation to a DNA library, or monounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more compounds are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring come expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes in situ hybridisation, in Southern, Northern or dotonce containing sequence or specific containing sequence presented is one of the containing sequence presented is one of the containing acid that have been containing sequence presented is one of the containing acid probes in screening of the microarray. Note: The sequence containing acid probes in sequence of the sequence presented is one of the containing acid probes in serventing of the microarray. Note: The sequence containing acid probes in serventing of the microarray. Note: The sequence containing acid probes in serventing of the microarray. Note: The sequence containing acid probes in serventing the propes in serventing of the sequence or secured in the microarray. Note: The sequence containing sequence or securing the sequence or sequence containing sequence or sequence and presented in the microarray. Note: The sequence containing sequence or sequence containing sequence or sequence containing sequence and sequence containing the sequence or sequence containi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/sequence.html
Northern or dot-blot hybridization to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human N-acteylglactosamine transferase NGalNAc-T1 PCR primer #3
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(AMSH ) AMERSHAM BIOSCIENCES KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.2%; Scor.
84.2%; Pred. No. ...
                        of any gene.
                                                                 Claim 1; SEQ ID NO 94301; 9pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GTCCAGCGTGCGCCATGGG 22
                        sequence or specific mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK43158 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GICCACTGTGCTCCATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             betal-4 linkage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004016790-A1.
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  Southern,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 45
ADK43158
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New isolated protein having specified amino acid sequence for enzyme used in producing oligosaccharides.

Sato T;

Gotoh M,

Narimatsu H,

WPI; 2004-203801/19.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capsule containing packaging cells that produce viral vectors for gene therapy - used as replaceable implants in treatment of cancer, atherosclerosis etc., providing localised, long-term vector delivery.
                                                                 protein. The protein is useful for enzyme used in producing oligosaccharides. The inventive isolated protein has the activity of transferring N-acetylgalactosamine to N-acetylglucosamine via betal-4 linkage. The present sequence represents human N-acteylglactosamine transferase, NGalNAc-T1, PCR primer.
                                                 The invention relates to an isolated N-acteylglactosamine transferase
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bcl-2 gene; anti-apoptotic gene; prevention; cell death; treatment; neurodegenerative disease; disease; Huntingdon's; Parkinson's; Alzheimer's; retroviral vector; LNXS; LNCX; live packaging cell; blocompatible capsule; release; viral vector; implant; gene therapy; tumour; PCR primer; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //note= "Kozak sequence which enhances translation
effeciency of bcl-2"
                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                     Length 31;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                   Sequence 31 BP; 4 A; 12 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer 1 used in RT-PCR to amplify bcl-2 cDNA.
                                                                                                                                                                                                   59.2%; Score 14.2; DB 12;
84.2%; Pred. No. 1.2e+04;
ive 0; Mismatches 3;
                 Example 1; SEQ ID NO 16; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 33; 45pp; English.
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/note= "Kozak
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                                                                                                                                                                                                                                                                                                                                                                              AAV05322/c
ID AAV05322 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-1998 (first entry)
                                                                                                                                                                                                 Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-018231/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAV05322;
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                                                                                                                                                                                                                                                                                                                                                              RESULT 46
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The vectors are used to transfect live packaging cells which form the core of a biocompatible capsule. These packaging cells are able to secrete a viral vector which includes a heterologous gene (in this case bcl-2) encoding a biologically active compound e.g. antisense sequence, blood coagulation factor, or an enzyme. The biocompatible capsules are surrounded by a jacket of permeable material with a porosity that allows calease of the viral vector. The biocompatible capsules are implanted, e.g. into the central nervous system, for use in gene therapy, particularly where the active compound is useful in the treatment of tumours, cancers and other cell proliferative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transfection; recombinant protein; vector; B-cell lymphoma 2; bcl-2; reverse transcriptase PCR; RT-FCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vector system comprising cistrons encoding a transactivator gand an apoptosis-protective protein, useful for transfecting and expressing recombinant polypeptide in mammalian cells.
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                     59.2%; Score 14.2; DB 2; Length 33; 84.2%; Pred. No. 1.2e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamster B-cell lymphoma 2 (bcl-2) cDNA cloning primer 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38 BP; 12 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                  Sequence 33 BP; 7 A; 10 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; SEQ ID NO 36; 119pp; English.
                                                                                                                                                                                                                                                                                                                               CCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                    ccascerrcscaracters 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEB55627 standard; DNA; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.2'
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-cell lymphoma 2 (bcl-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-506766/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-2005
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Score 14.2; DB 14; Length 38; Pred. No. 1.2e+04;

59.2%;

Best Local Similarity

Query Match

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The invention relates to the use of a polynucleotide comprising a sequence of 3977, 2441 or 3410 base pairs, fully defined in the specification, its fragment or complement, foor diagnosis or treating conizophrenia. The invention also claims a method for screening for a compound regulating the expression of the polynucleotide comprising: (a) bringing a test compound into contact with a cell capable of expressing the polynucleotide, whose expression is desired to be controlled; (b) detecting the expression of the polypeptide in the cell; and (c) detecting the expression of the polypeptide in the cell; and (c) controlled; conpared to a control. The polynucleotides and polypeptides are useful for diagnosing schizophrenia, and for identification of subjects who are predisposed to schizophrenia, and for identification of subjects who are predisposed to schizophrenia, and for evaluating the efficacy of drugs for such disorder, and monitoring the progress of patient symptoms involved in clinical trials for the progress of such disorder. This sequence corresponds to a hybridization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for diagnosing schizophrenia, and for identifying a compound modulating the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of such disorder. This sequence corresponds to a nyprimizar probe for the gene for the rat voltage-gated potassium channel Kv3.3.
Gaps
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                                                                                                                                                                                                                                                                 Rat voltage-gated potassium channel Kv3.3 DNA hybridization probe.
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Indels
                                                                                                                                                                                                                                                                                                  diagnosis; schizophrenia; potassium channel; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45 BP; 8 A; 16 C; 14 G; 7 T; 0 U; 0 Other;
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
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                                   6 CCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MITS-) MITSUBISHI PHARMA CORP.
                                                                                                                                                             BP.
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                                                                  24 ccadcrrgagccardgrgg
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus.
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16;
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                                                                                                                                                                                              ADY31048;
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ADY31048/
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                                                                                                                                                                                                                                                                                                                                      This antisense oligonucleotide is complementary to the translation initiation site of the human bcl-2 mRNA. The Bcl-2 antisense oligonucleotides are phosphorothicate derivatives and can straddle strategic sites such as the translation initiation site, donor and acceptor splicing sites, or sites for transportation or degradation. Blocking translation at such strategic sites prevents the formation of a functional bcl-2 gene product. These oligonucleotides may be used for treating cancers associated with high levels of bcl-2 gene expression, especially lymphomas and some leukaemias. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                            Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful for treating cancers, e.g. lymphoma(s) and some leukaemia(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
                                                                             Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
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Pred. No. 1.5e+04;
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100.0%; Pred. No. ...
                                                         Human bcl-2 antisense oligonucleotide 6.
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14; Conservative
                             (revised)
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                                                                                                                     Homo sapiens.
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Homo sapiens
                                                                                                                                                                                24-MAR-1994;
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21-FEB-1992;
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12-JUN-1998
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                                                                                          cancer; ss.
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          AAV19660;
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treating cancers, e.g. lymphoma(s) and some leukaemia(s).
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                                                                                                                       88US-00288692.
92US-00840716.
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Best Local Similarity 100.
Matches 14; Conservative
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AA906151 0362b01 8
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AA550951 Arabidops
AA571412 OP92C11.8
AB8937412 OP92C11.8
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AA370405 GC9188832
AA55406 O3188832
AA971412 OP92C11.8
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CL521622 SAL3H08 F
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                                                                February 15, 2006, 18:07:43 ; Search time 1596.3 Seconds (without alignments) 703.434 Million cell updates/sec
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ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 50) AUTHORS Strauk; Y. Taira, H. Teunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites JOURNAL EMBO Rep. 2 (5), 388-393 (2001)	PUBMED 11375929  COMMENT Contact: Yutaka Suzuki Contact: Yutaka Suzuki Department of Virology Department of Medical Science, University of Tokyo Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yeuzuki@ims.u-tokyo.ac.jp Suzuki.Y., Yoshiromo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). FEATURES Location/Qualifiers Source 150 /organiem="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:966" /clone="LNG15924" /clone="LNG15924"	Query Match         62.5%; Score 15; DB 1; Length 50;           Best Local Similarity 78.3%; Pred. No. 7.3e+04;           Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;           Qy         2 GGGTCCAGCGTGCGCATGGGGG 24           Db         5 GGGCCAGCGCTCGGCATGGGGG 27	RESULT 2 AU107436 LOCUS LOCUS LOCUS LOCUS AU107436 AU107436 AU107436 LOCUS AU107436 AU2044 ADDSE00456, mRNA sequence. AU107436 AU10743 AU107436 AU1	Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minacku, Tokyo 108-6639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full. length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). FEATURES 150 /organiem="Homo sapiens" /mol_type="mRNA"
AZ473927 1M0290M03 H92936 yt92e04.r1 CL520163 \$AA3D11 F CN757601 IDDAAA1DC CV933354 PMpcm_104 AQ02554B BF(X)1587 AA630952 nq76e01.05 AA630952 nq76e01.8 AA630952 nq76e01.8 AA630954 AG0561 BB046304 603626308	DM047185 G03627544  CD530897 08102 Ara  CN973499 20998 45-  BX121239 DANIO FEF  CL213837 M042B03 G  C20871 HUMGS000493  AZ81213 200079M19  AU103440 AU103440  AU103445 AU103445  AU106643 AU106643  AU106655 AU106655  AU106655 AU106655  AU107016 AU107016  AZ323931 1M0045F09  AA909237 0108C04.8  CZ474839 Q075012.x  A1287864 QW70412.x  A1357706 QW77901.x	CG718745 1119054C1 AA868659 ak4980C3.8 AI2625L2 qk44f11.x AB082692 Drosophil AL462237 T. brucei AZ784718 2M0027K01 AL93116 Arabidops CV064406 WNEL1061 DN652373 S383 cDNA	AU256510 AU256510 BG292849 G02388872 AJ59761 Arabidops AL760976 Arabidops AL94456 Arabidops AA840456 Arabidops AA878864 off84905.s BE296536 G01174028 AA680935 UmPrAm057 AA509356 V918809.r BH626517 1007110D0 A142399 E156403.x BG86682 G02785673 BX620428 BX620428 NA74151 Yy89c10.s1 CZ194596 PSTACOPS BH16609 SALK 0509 AA847140 od48D4.s AA867748 VALGa12.r A1793579 fc51d05.x	50 bp mRNA linear EST 28-JAN-2004 ns cDNA library Homo sapiens cDNA clone
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/organism="Cyprinus carpio"
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AJ796516.1 GI:51111844
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Antirrhinum majus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
Antirrhinum.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Saedder,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
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   /db xref="taxon:9606"
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MPI fuer Zuechtungsforseblung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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Homo sapiens
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                                                                                                        1 Similarity
18; Conserva
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Best Local Similarity
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Best Local
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AA878878/c
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AJ796516
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E 1 (bases 1 to 46)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

U Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mil.nih.gov
unknown library type
Trace considered overall poor quality
Trace considered overall Error: 0.00
Insert Length: 315 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on Oct 7, 2003 this sequence version replaced gi:37558281.
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 72B
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 34 row: a column: 07
Seq primer: Triplex 5' LD (5'-CTCGGGAAGCGCCCATTGTTTGTTGTTGTT-3')
High quality sequence stop: 47
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/clone lib="NCI CGAP Li5"
/note="Torgan: liver: Vector: pCMV-SPORT4; Site_1: Sall;
Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 0.8 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 bp mRNA linear EST 28-JUL-;
CCLM09a34a07£1 Carp muscle library 1 Cyprinus carpio cDNA clone
34a07 5', mRNA sequence.
CF661152
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                                                                                                                                                                                                                                                                                                                             1. .46
/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="t-axon:9606"
/clone="IMAGE:1437461"
/tissue_type="hepatic adenoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTCCAGCGTGCGCCATGGGGG 24
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EST 20-AUG-1998

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/note=_Organ: liver; Vector: pumils S-FL3; Site_1: DraIII (CACTGTGTG); ist trand cDNA was primed with an oligo(dr) primer [ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG] digested and cloned into distinct DraIII sites of the pWHSIS-FL3 vector (5' site CACTGTGTG, 3' site CACTGTGT). XhoI should be used to isolate the CDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 49)
Marram M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marram M., Hillier, L., Allen, M., Bowles, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
ristitute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                             AI098584 140 mRNA linear EST 20.

ALGSBACY, XI Sugano mouse liver mlia Mns musculus cDNA clone
IMAGE:1481821 3' similar to SW.A2HS MOUSE P29699
ALPHA-2-HS-GLYCOPROTEIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.7%; Score 13.6; DB 1; Length 49; 80.0%; Pred. No. 2.9e+05; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1481821"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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                             33 CCTTCCTGCGCCATGGGGG 15
  24
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  6 CCAGCGTGCGCCATGGGGG
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                      /sex="Male & female"
/tissue_type="Muscle"
/dev_stage="Mault"
/dev_stage="Adult"
/lab host=="coli Blectromax DH10B"
/lab host=="coli Blectromax DH10B"
/lab host=="coli Blectromax DH10B"
/note="Vector: pTriplEx2; Site 1: Sfil GGCCATTACGGCC; Site 2: Sfil GGCGCCTCGGCC; Serially subtracted cDNA
library prepared from muscle of warm, cold and hypoxia challenged animals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA993146 49 bp mRNA linear EST 03-JUN-1
ot77a10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
IMAGE:1622778 3' similar to SW:FBRL_HUMAN P22087 FIBRILLARIN ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.
1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP from Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Pred. No. 1.6e+05;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1622778"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
'db xref="taxon:7962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                4 GTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                             47 GTCCAGAGAGTGCCATGGG 29
                        clone="34a07
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Best Local Similarity 84.2
Matches 16; Conservative
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ACCESSION

VERSION KEYWORDS

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REFERENCE AUTHORS JOURNAL PUBMED

COMMENT

TITLE

FEATURES

ORIGIN

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/note="PCN varies" in the DNA of primary transformants of Orysa sativa plants. The DNA fragment (s) resulting of PCN were directly sequenced from the left border to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed Information to order the corresponding mutant line and a link to a database providing a graphical display is available from june 2004 at http://genoplante.info.infobiogen.fr/oryzatagline/.

This sequence has been generated in the framework of the French plant genomics program Genoplante (http://www.genoplante.org and http://genoplante.org and http://genoplante.info.infobiogen.fr)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procuremen: Christopher Moskaluk, M.D., Ph.D., Michael R..

Tissue Procuremen: Christopher Moskaluk, M.D., Ph.D., Michael R..

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NIT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Jases 1 to 40)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone lib="rlanking Sequence Tag of Oryza sativa T-DNA insertion lines"
                                        TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE Tel: 33467615629 Fax: 33467615605 Fax: 33467615605 Easil: emmanuel.guiderdoni@cirad.fr Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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UMR PIA Biotrop program
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 73.9
hes 17; Conservative
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ORGANISM
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AUTHORS
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

E (bases 1 to 37)

S sallaud,C., Gay.C., Larmande,P., Bes,M., Piffanelli,P., Piegu,B.,

Droc,G., Regad F., Bourgeois,E., Meynard,D., Perin,C.,

Ghesquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.

High throughput T-DNA insertion mutagenesis in rice: A first step

towards in silico reverse genetics

Contact: Guiderdoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Virology
Institute of Madical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-ength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CL517576 1anking Sequence Tag of Oryza sativa T-DNA insertion lines Oryza sativa (japonica cultivar-group) genomic, genomic survey
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                                                                                                                                             EST 28-JAN-2004
                                                                                                                                                    AU102746
AU102746 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Jogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="twanon:9606"
/db_xref="twanon:9606"
/clone="cAs09562"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.6; DB 1; Length 50;
Pred. No. 2.9e+05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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      GGTCCAGTGTCCCCCATGTG 27
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                                                                                                                                                                                                              CAS09562, mRNA sequence
                                                                                                                                                                                                                                                                      AU102746.1 GI:13552267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.7
Best Local Similarity 80.0
Matches 16; Conservative
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CL517576
      46
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CL517576/c LOCUS

RESULT 9

ò 셤 ORGANISM

ACCESSION

VERSION KEYWORDS

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Gaps

Gaps

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Length 43; Indels

us-09-669-187a-81.szlm50.rst

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(http://www.nbaroures/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ434579 33 bp DNA linear GSS 03-OCT-2000 IM0221I10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0221I10 F, genomic survey sequence.
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo. "
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
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/lab host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi; Muroidea; Muridae; Mus.
                                                                                                                                                       Score 13.4; DB 1;
Pred. No. 3.5e+05;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 0221 row: I column: 10
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0221110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 33.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                           1 GGGGTCCAGCGTGCGCCATGGGG 23
                                                                                                                                                                                                                                                                                                                                                                                       17 GGGGCCAGCGGTTCCCAGGGGG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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GSS.
                                                                                                                                                           55.8%;
                                                                                                                                           Query Match
Best Local Similarity 73.99
Matches 17, Conservative
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COMMENT
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AUTHORS
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                                                                               ORIGIN
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                           /mol_type="mRNM" saptems
/mol_type="mRNM"
/db_xref="taxon:9606"
/clone='mRNM:2219127"
/tissue type="top:"tissue type="to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R..

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA863355 43 bp mRNA linear EST 13-MAY-1998 oh04e09.sl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1456840 3' similar to SW:PRPB_HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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/clone lib="NCI CGAP Kid3"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; lst
strand cDNA was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector: mRNA
source: 2 pooled kidneys. Library went through one round
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 434)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.8%; Score 13.4; DB 1; Length 40; 73.9%; Pred. No. 3.5e+05; ive 0; Mismatches 6; Indels
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   'organism="Homo sapiens"
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'organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1456840"
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nes 17; Conservative
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Unpublished (1997)
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VERSION
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AUTHORS
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from the Jackson

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Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo.Nakagawa,K., Maruyama,K., Suyama,A. and
Suzuki,Y., Yoshitomo.Nakagawa,K., Maruyama,K., Suyama,A. and
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Hominidae, Homo.

Hominidae, Homo.

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Hominidae, Homo.

Homoses 1 to 50)

Suzuki, Y., Taira, H., Tsumoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Department of Vivologa
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.2%; Score 13; DB 1; Length 50; 76.2%; Pred. No. 5.18+05; Indels 5; Indels
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                                                                                                                           HEP06849, mRNA sequence
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Homo sapiens
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Matches 16; Conserv
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I (bases 1 to 38)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L (Dupblished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michael J. Brownstein (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.llh.gov

Plate: LLAMI1656 row: g column: 03

High quality sequence stop: 38.

Location/Qualifiers
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      adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                  Length 33;
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                                                                                                                                                              Score 13; DB 9; I
Pred. No. 5.1e+05;
0; Mismatches 5;
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76.2%;
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Best Local Similarity 76.2
Matches 16; Conservative
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Euteleostomi;

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50 bp mRNA linear EST 28-JAN-2004 AU107885 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HSI05714, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Vizology
Institute of Madical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Sataki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Sakaki, Y., Nakamura, Y., Suyama, A., and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 50)

Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yeuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleo.
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/mol_type="mRNA"
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EMBO Rep. 2 (5), 388-393 (2001)
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                  Email: yeuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU107884 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS03672, mRNA sequence.
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_tef="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="CAS03672"
/clone="CAS03672"
                                                                                                                                                                                                                                                                                                                                                                             54.2%; Score 13; DB 1; Length 50; 76.2%; Pred. No. 5.1e+05; tive 0; Mismatches 5; Indels
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AU107884.1 GI:13557406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                   ö
Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b4HB55y"
/note="Organ: brain; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Size: 2244
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 50)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Porest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                  /clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                     Length 50;
                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                  Score 13; DB 1; I
Pred. No. 5.1e+05;
0; Mismatches 5;
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Insert Length: 224 Std Error: 0.00
Seg primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Homo sapiens"
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/db xref="GDB:3827242"
                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:180595"
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                                                                                                                                                                                                                                                                         54.2%;
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602046279F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4195795 5',
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="INAGE:4195795"
/lab.host="DH10B (T1 phage-resistant)"
/lab.host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ompublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMSG31 row: n column: 20
High quality sequence stop: 34.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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76.2%; Pred. No. 5.1e+05;
tive 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="FVB/N"
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BF384787
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AUTHORS
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LOCUS

ACCESSION VERSION KEYWORDS SOURCE

RESULT 21 AI755616

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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/tissue_type="hypothalamus"
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/lab_host="DH10B"
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/clone_lip="hypothalamus"
/clone_lip="hypothalamus"
/clone_lip="hypothalamus"
/clones and
/constructed using the Cap-trapper method (Carninci, in
/constructed using the Cap-trapper method (Carninci, in
/constructed by M. Brownstein
/kimH/NHGRI, National Institutes of Health). Note: this is
                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

I (bases 1 to 38)

NH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michel J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michel J. Brownstein (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Llocation/Qualifiers

Llocation/Qualifiers
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Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
BIS97957 18 DP MRNA linear EST 07-SEP-2001
603249661F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5301590 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ683869 SEQRANO4 Sus scrofa cDNA clone C0001803_F11, mRNA
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                       Homo sapiens (human)
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Sus scrofa
                                                                mRNA sequence.
                                                                                                                                                                                                                       Homo sapiens
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AJ683869/c
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Contact: David Sibley, Ph.D.
WashU-Merck Eimeria tenella project
Unpublished (1999)
Contact: David Sibley, Ph.D.
WashU-Merck Eimeria tenella project
WashIngton University School of Medicine
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Contact David Sibley (toxocett@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /do_stage="Sportozoite"
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/lab_host="Soirs E. coli"
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/cloe="lib="Elimeria S5-2 Sporozoite stage"
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/note="Vector: Bluescript SK-; Site_1: EcoR1, Site_2:
/note="Vector: Bluescript SK-; Site_1: EcoR1, Site_2:
/note="Vector Sporozoites were obtained from in vitro sporulated
and excysted occysts of E. tenella grown in chickens.
cDMA was synthesized from poly mRNA using an oligo-dT
primer containing a XhoI site. Following second strand
synthesis, EcoR1 adapters were ligated to the cDNA and
products were size-selected on Sephacryl S500. cDNAs were
digested with EcoR1/XhoI and cloned into lambda Zap II
(Stratagene) . Clones were converted to phagemids by mass
excision using ExAssist helper phage and SOLR cells
(Stratagene) . Insert sizes range from 1.2-2.9 kb."
                                                                                                                                                                                                                                                 A1755616
37 bp mRNA linear EST 18-JAN-2000 ELESTea38h12.yl Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA 5' similar to TR:Q28583 Q28583 KAP5.4 KERATIN PROTEIN. ;, mRNA
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Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T.,
Liberator, P., Diaz, C., Tang, K., Steptoe, M., Theising, B.,
Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D.,
Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T.,
Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AI755616.1 GI:5149339
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                                                                              Roalin Institute
Roalin, Midlothian, EH25 9PS, UNITED KINGDOM
Roalin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass Sequencing. Bases called and trimmed with phred
Single pass Sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII (KS+) R. Sitel: EcoRI
R. Sitel: NotI S' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
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2M0285P03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0285P03 F, genomic survey sequence.
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NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 40)
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Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah
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embryo development in pigs and cattle Unpublished (2004)
Contact: Anderson SI Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0285 row: P column: 03
Seg primer: CGTTGTAAACGACGGCCAGT
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/mol_type="genomic DNA"
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High quality sequence stop: 40.
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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AZ998247/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gill #17321141gbl #AP1290T2.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 41)

S NIH-WGC http://mgc.nci.nih.gov/.

SNIH-WGC http://mgc.nci.nih.gov/.

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

CLone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL)

Flowd through the 1.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov

Plate: LLMM1752 row: j column: 15
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musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/lab_host="PDH10B"

/clone_lib="NIH_MGC_97"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oxifice at constant velocity. The sheared DNA was blunt end-repaired with 14 DNA polymerase and 14 polymcleotide kinase. Adaptor oligonucleotides were
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S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diamid inserts wouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, U
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1M0240A01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/note="Organ: testis; Vector: pBluescriptR (modified
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0240 row: A column: 01
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 44.
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/strain="C57BL/6J"
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94112, USA
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwn42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Dases 1 to 48)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rallam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Dlasmid inserts

Unpublished (2000)
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1M0355P08M Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clone_11b="Mouse 10kb plasmid UUGCNM library."
/note="Weetor: PWD42nry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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70.8%; Pred. No. 6.2e+05;
iive 0; Mismatches 7;
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Insert Length: 10000 Std Error: 0.0
Plate: 0355 row: P column: 08
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0355P08"
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Mus musculus
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Fax: 801 585 7177
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Matches 17; Conserv
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// Incomparism="Homo sapiens"

// Mol_type="mRNA"

// Ab_zref="Homos 19806"

// Lissue_type="pooled germ cell tumors"

// Lissue_type="pooled germ cell tumors"

// Lone_lib="NOI_CRAP GC4"

// Abobs="MIBN="NOI_CRAP GC4"

// Abobs="Wector: pT7T3D-pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3

vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo. "
polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 555 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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1 Similarity 70.8%;
17; Conservative C
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Best Local S
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TITLE
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ORIGIN

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BB616279 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4931436G19 5', mRNA sequence.
                                                                                                                                                                                                                                                                    50 bp mRNA linear EST 28-JAN-2004
AUJ06561 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
XAT03341, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Yr. Yoshitcom-Nakagawa,Kr. Maruyama,Kr. Suyama,A. and
Sugano,S. Construction and characterization of a full
Iength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae, Homo.

1 (bases Homo.)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Toda, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

ENBO Rep. 2 (5), 388-393 (2001)
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleo
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/db_xref="texon:9606"
/clone="xxr03341"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.3%; Score 12.8; DB 1; Length 50; Best Local Similarity 87.5%; Pred. No. 6.2e+05; Matches 14; Conservative 0; Mismatches 2; Indels
             Length 49;
Score 12.8; DB 1;
Pred. No. 6.2e+05;
                                                                0; Mismatches
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                                                                                                                   1 GGGGTCCAGCGTGCGCCATGGGGG
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          53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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             Query Match
Best Local Similarity 70.8<sup>†</sup>
Matches 17; Conservative
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24

1 GGGGTCCAGCGTGCGCCATGGGGG

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COMMENT

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/note="Site_1: XhoI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Taheda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Flat: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome_res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazakı,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
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/strain="C57BL/6J"
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FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfal14[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                               AZ982659 50 bp DNA linear GSS 27-APR-2001 2M0263J03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0263J03 R, genomic survey sequence.
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/lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42ry: Purified genomic DNA from M.
musculus C57BL/63 (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 0263 row: J column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0263J03"
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Location/Qualifiers
16 GCGGCCGTGCGGAGCCATGGCGG 39
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Fax: 801 585 7177
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Matches 17; Conserv
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KEYWORDS
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0; Gaps

53.3%; Score 12.8; DB 2; Length 50; 70.8%; Pred. No. 6.2e+05; ive 0; Mismatches 7; Indels

Query Match 53.3 Best Local Similarity 70.8 Matches 17; Conservative

ORIGIN

5

CL521622/c DEFINITION

à a ORGANISM

VERSION KEYWORDS SOURCE ACCESSION

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

FEATURES

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil 4732114 [gb|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xili0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus cDNA, clone:Y2G0137B14, strand:plus,
reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000040729, based
                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                               1 (bages 1 to 28)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.5%; Score 12.6; DB 9; Length 28; 78.9%; Pred. No. 7.5e+05; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: N column: 11
Seg primer: CACACAGGAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .28
/organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC2M0106N11"
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High quality sequence stop: 28.
Location/Qualifiers
                Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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KEYWORDS
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzae, Diliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza, Liliopsida; Poales; Poaceae;
Buhartoideae; Oryzae, Oryza, Liliopsida; Poales; Poaceae;
Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegu, B.,
Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,
High throughput T-DNA insertion mutagenesis in rice: A first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 French plant genomics program Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.genoplante.org and
http://genoplante-info.infobiogen.fr)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: emmanuel.guiderdoni@cirad.fr
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                            1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: TDNA tagged.
Location/Qualifiers
                                                                              32 GGGGTCCAGGCTTGGAGAGGGGGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant J. (2004) In press
Contact: Guiderdoni
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CL521622.1 GI:46148422
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AZ829200.1 GI:12999108
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AZ829200/c
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DEFINITION ACCESSION VERSION

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http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XE347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119098 row: 39
                                                       /clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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/clone_lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
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/cultivar="mixed background W23/A188/B73/K55"
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855 California Ave, Palo Alto, CA 94304, USA
TTE1: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.6; DB 9;
Pred. No. 7.5e+05;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Location/Qualifiers
                    http://baygenomics.ucsf.edu/
Unpublished (2001)
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 GGGCCCGCCTGCGCCATGG 11
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78.9%;
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Walbot, V.
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CG728115
CG728115.1 GI:3
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CG728115/c
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SOURCE
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                                                                                                                                                                                              Matahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,
Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,
Hayashizaki, Y. and Carninci, P.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Methods 1, 233-239 (2004)
2 (Dasses 1 to 45)
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N.,
Hori, F., Inocani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M.,
Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative Splicing Libraries (ASL8) are prepared by: Preparating of single-stranded DNA using a RNA template from full length CDNA libraries, hybridizating of single-stranded DNA, removing of remaining single-stranded DNA, aligneting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of r-shaped primers to isolated DNA hybrids with loop structures are isolated DNA hybrids with loop structures. PCR amplification of ligation products and their cloning into PFLCI vector. (Reference).
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/cell type="mixture of melanoma cell and melanocyte cell"
/cell type="mixture of melanoma cell and melanocyte cell"
/colore lib="alternative Splitcing Library L3"
/note="strand:plus, reference:ENSEMBL:Mouse-Transcript-
ENST:ENSMUST00000040729, based on BLAT search"
                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
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Mus musculus
                                                                   Mus musculus (house mouse)
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                         AK216071.1 (HTC; ASSETS.
                                                                                        Mus musculus
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ACCESSION
VERSION
KEYWORDS
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                           A1254752 ACI CGAP CO14 Homo sapiens CDNG Aclone IMAGE:1962469 3' similar to SW:WASP WOUSE P70315 WISKOTY-ALDRICH SYNDROME PROTEIN HOMOCLOG; contains element MSR1 repetitive element ;, mRNA sequence.
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ti45e03.x1 NCI CGAP Lyml2 Homo sapiens cDNA clone IMAGE:2133436 3'
similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ;, mRNA
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae, Homo.

1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality Insert Length: 764 Std Brror: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1.

    .49
    /organism="Homo sapiens"

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                                                             16 GGTGGAGCCTGGGCCATGG 34
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                                  3 GGTCCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
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Matches 15;
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/tissue type="leukocyte"
/tissue type="leukocyte"
/tissue type="leukocyte"
/lab hoste:"BH108"
/clone lib="NH MGC 118"
/clone lib="NH MGC 118"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EccRV
/destroyed; RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EccRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.rmdb.iastate.edu' and follow the links for RescueMu. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BHHIOB cells were transformed and then screened on LB plates with amplicillin."
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603062308F1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5211864 5',
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMIS31 row: o column: 01
High quality sequence stop: 48.
Location/Qualifiers
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1 (bases 1 to 48)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                  3 GGTCCAGCGTGCGCCATGG 21
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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us-09-669-187a-81.szlm50.rst

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/organism="Mus musculus"
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/strain="129 Sv"
/db_xref="taxon:10090"
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Mus musculus
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                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: capabs.remail.nih.gov.
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell"
/lab host="DH108"
/clone_lib="NCI_CGAP_Lym12"
/note="Organ_Iymph_node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
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cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2133436"
/tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n193910.sl NCI CGAP Co10 Homo sapiens CDNA clone IMAGE:1058274 3' similar to gb:003909 GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR (HUMAN);, mRNA sequence.
                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                               Hominidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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1. (Dases 1 to 6, 40 www. ncbi.nlm.nih.gov/ncicgap.
NCI-CBARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
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/organism="Homo sapiens"
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Homo sapiens (human)
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Best Local Similarity 78.2
Best Local 51 Conservative
                     Homo sapiens
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AA594397
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P070E01 GGTC Gene Trap Library GV18C05 Mus musculus cDNA clone P070E01, mRNA sequence.
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Bmail: info@genetrap.de
FlipROSACeoC42 gene trap. Sequence tag generated by 5'RACE.
Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web.new/databbase/result_clone.html?
'clone id=P070E01' ES cell line harboring insertion mutation of target gene is available at:
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Hansen, J., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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                                                                                                 Trace considered overall poor quality Insert Length: 1930 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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Location/Qualifiers
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                           CB221472.1 GI:28291986
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                                                           Bos taurus (cow)
Bos taurus
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Matches 15;
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Construction of a swine BAC library: application to the characterization and mapping of porcine type C endoviral elements Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
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             /sex="Male"
| Ceal type="Embryonic stem cell"
| Ceal type="Es cells [C57BL/6J x 129S6/SvEvTac] F1"
| Colone lib="GGTC Gene Trap Library GV18CO5"
| Note="Vector: FlipROSACeoC+2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 49)
Rogel-Gaillard, C., Bourgeaux, N., Billault, A., Vaiman, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 49)
Chardon, P., Iannuccelli, N., Roig, A., Dossat, C., Demars, J.,
Rogel-Gaillard, C., Roy, A., Schibler, L. and Milan, D.
A physical map of the swine genome
Unpublished
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/clone_lib="SBAB"
/note="Genoscope_sequence_ID_: IH0AAA28BF12FM1"
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                                                                                                                           52.5%; Score 12.6; DB 10; Length 49; 78.9%; Pred. No. 7.5e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                   linear
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GSS; Bac-end sequence BES; Genome Survey Sequence.
                                                                                                                                                                                                                                                                                                                   CR900779 49 bp DNA Sus scrofa BES, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="Large White"
/db_xref="taxon:9823"
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/clone="P070E01"
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                                                                                                                                 Query Match
Best Local Similarity 78.9
Matches 15; Conservative
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CR900779/c
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                                                                                                                          Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M.K. and Moore, S.S. Gene Expression Profiling of the Bovine Gastrointestinal Tract Gene Expression Profiling of the Bovine Gastrointestinal Tract Contact: Dr. Stephen Moore Beef Genomics Laboratory Dept of AFNS, University of Alberta 1410 Agrif, For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 50)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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/tissue_type="Simple columnar epithelial"
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/lone_lib="Bos taurus Duodenum #1 library"
/note="Gorgan: Intestine/duodenum yector: Uni-2ZAPXR;
Site_1: EcoRI; Site_2: Xho I"
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Uniublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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1 (bases I to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb
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llarity 78.9%; Pred. No. 7.5e+05;
Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: stephen.moore@ualberta.ca
Insert Length: 50 Std Error: 0.00
POLYA=No.
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FEATURES

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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adenocarcinoma, 3 pooled tumors"
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/note="Corgan: uterus, Vector: pCMV-SPORT6; Site_l: SalI;
/note="Corgan: uterus"
/cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmanila; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Murinae; Mus.
1 (bases it.o. 45)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                             Trace considered overall poor Insert Length: 2109 Std Erro Seq primer: -40UP from Gibco High quality sequence stop: 1 POLYA-NO.
                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11539-012"
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AZ434030
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /lan. interact. coil Birtain Ail-Ocold, 'l-Tesistant, F-" / (lone lib="Mouse lib") langia "E. (coil Birtain Ail-Ocold, 'l-Tesistant, F-" / (note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/64 (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwd4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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37 bp mRNA linear EST 07-MAR-2000 ty52a05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2282672 3' similar to TR:000599 000599 CON1. ;contains element MSRI repetitive
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Emall: gapbs.r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                           'sex="Male"
'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%; Score 12.4; DB 9; Length 23; 72.7%; Pred. No. 9.1e+05; ive 0; Mismatches 6; Indels
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Flate: 0451 row: E column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers
                                                                                                                                                                                                                                                       'organism="Mus musculus"
                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                 clone="UUGC1M0451E09"
                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           element ;, mRNA sequence.
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 72.7
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Best Local (
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AI619702/c
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TITLE
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ORIGIN

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/uctuaturem="aca mays"
/mol type="genomic DNA"
/cultivar="mixed background w23/A188/B73/K55"
/db xref="taxon:4577"
/tissue_type="leaf"
/fev stage="adult"
/lab_host="DH108"
/clone lib="1550 - RescueMu Grid M"
/clone lib="1550 - RescueMu Grid M"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: Bg11;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
RescueMu. Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamH1 and Bg111, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Tel: 650 725 8227
Email: walbotcstanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3590_1_301 column: 14
Class: transposon-tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                                      Gaps
                                                /cell_type="Embryonic stem cell"
/cell_line="ES cells 12952 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/noce="Vector: pTlbetageo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                               Query Match 51.7%; Score 12.4; DB 10; Best Local Similarity 72.7%; Pred. No. 9.1e+05; Matches 16; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Zea mays"
                                                                                                                                                                                                                                                                                                                            1 GGGGTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                                                                                                                                                                               36 édcerrecerrecedecaces 15
'clone="W126F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ585242.1 GI:27220303
                         /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 47)
Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
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KEYWORDS
SOURCE
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BZ585242
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                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                      Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-GG1d (Stratagene) cells and selected for ampicillin resistance."
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'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html?
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html'
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html'
Inhouse Sequence Identifier: 08571
Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL210842 46 bp mRNA linear GSS 22-MAR-2005 W126F07 GGTC Gene Trap Library GV03C04 Mus musculus cDNA clone CL210842
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1 (bases 1 to 46)
Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 9.1e+05;
0; Mismatches 6;
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Email: info@genetrap.de
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Best Local Similarity 72.7%;
Matches 16; Conservative
                                                              /sex="Male
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/Mol type="mRNA"
// (db xref="taxon:9606"
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/clone="IMAGE:1504849"
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/clone="IDH20B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries The pools consisted of I.M. AGE. Clones 297480-302087, 6826312-687239, 76408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.7%; Score 12.4; DB 1; Length 49; Best Local Similarity 72.7%; Pred. No. 9.2e+05; Matches 16; Conservative 0; Mismatches 6; Indels
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/organism="Homo sapiens"
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Yutaka Satou unpublished cDNA library (csef2)"
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (Dases 1 to 48)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona savignyi (Satou, Shin-i, Kohara, Satoh)
Unpublished (2004)
Contact: Yutaka Satou
Department of Zoology
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 2)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1605 Std Error: 0.00
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Bavignyi cDNA clone csef029n10 5', mRNA sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
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  2 GGGTCCAGCGTGCGCCATGGGG 23
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## ALIGNMENTS

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RESULT 1
US-08-617-874-1
US-08-617-874-1
Sequence 1, Application US/08617874
; Sequence 1, Application US/08617874
; APPLICANT: Jevnikar, Anthony M.
APPLICANT: M. Shengwu
APPLICANT: Stiller, Calvin R.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING
; TITLE OF INVENTION: INWINE RESPONSES IN MAWMALS
; NUMBER OF SEQUENCES: 10
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LOCATION: (1). [33)
OTHER INFORMATION: oligonucleotide used for RT-FCR amplification of Bcl2
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Sequence 11, Application US/09249585A

Patent No. 6417002

GRENAL INFORMATION:
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
CURRENT APPLICATION NUMBER: US/09/249,585A

CURRENT FILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 11

LENGTH: 33
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ADDRESSEE Burns, Doane, Swecker & Mathis, L.L.P.
STREET: George Mason Building, 699 Prince Street
CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: USA
Z19: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,874
FILING DATE: 21-MAY-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION COUNTRY: 30,427
REFERENCE/DOCKET NUMBER: 024916-002
TELECOMMUNICATION: INFORMATION:
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Pred. No. 6.6e+02;
); Mismatches 3;
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100.0%; Pred. No. 8e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA - primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66./.,
100.0%; Pr.
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                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 836-6620 TELEPRAX: (703) 836-2021 INFORMATION FOR SEO 1D NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 ccaecerececcares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.7
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.5
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OILER INFORMA.
US-09-249-585A-11
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US-08-410-804-13/C

Sequence 13, Application US/08410804

Sequence 13, Application US/08410804

GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Red, John C.
APPLICANT: Red, John C.
APPLICANT: Red, John C.
APPLICANT: REQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive. Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.2; DB 3;
Pred. No. 1.8e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                US-09-875-453B-69/c
; Sequence 69, Application US/09875453B
; Patent No. 6838556
                                                                                                                                                                      3 GGTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                 1 Grrccagccrrcgccargg 20
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                                                                 Query Match 63.3%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.3%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kim, Jungsuh P.
APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
APPLICANT: Laurance, Megan E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michelotti, Emil
Velligan, Mark D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: primer US-09-875-453B-69
, ORGANISM: mus musculus
US-09-396-196G-107962
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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               US-08-650-726-1/c

Sequence 1, Application US/08650726

Sequence 1, Application US/08650726

Patent No. 6027721

GENERAL INFORMATION:
APPLICANT: Hammang, Joseph P
APPLICANT: Aebischer, Patrick
ITLE OF INVENTION: DEVICE AND METHOD FOR ENCAPSULATED GENE
ITLE OF INVENTION: THERAFY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Ave. of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.8%; Score 15.8; DB 3; Length 33;
89.5%; Pred. No. 9.8e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US

ZIF: 10020-1104

COMPUTER 18ADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,726
FILING DATE: 20-MAY-1996
GIASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BILifi, Ivor R
REGISTRATION NUMBER: 39,529
REGISTRATION NUMBER: 32,239
REFERENCE/DOCKET NUMBER: CTI-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 21 596 9090
TELEFAX: 212 596 9090
TELEFAX: 212 596 9090
TELEFAX: 33 base pairs
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Patent No. 6821724
GENERAL INPORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 CCAGCGTGCGCCATGGGGG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 89.5
Matches 17; Conservative
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US-08-650-726-1
                                                                                                                                                                                                                                                                                                                                       STATE: N
COUNTRY:
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APPLICANT: Thomas, Rita L.

APPLICANT: Thomas, Rita L.

APPLICANT: Knoppachith, Ana

APPLICANT: Sheppard Liana T.

APPLICANT: Lim, Moon Young

APPLICANT: Lim, Moon Young

APPLICANT: Lim, Moon Young

TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION

TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION

FILE REPERENCE: 54600-8135.US00

CURRENT APPLICATION NUMBER: US/09/875,453B

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: US 60/209,549

FRIOR FILING DATE: 2000-06-06

NUMBER OF SEQ ID NOS: 246

SOOFWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 69
Score 15.2; DB 3; Length 25;
Pred. No. 1.8e+03;
0; Mismatches 3; Indels
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Gaps

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                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                     US-08-259-514-13/c
| Sequence 13, Application US/08259514
| Patent No. 25914
| Patent No. 3404
| Patent No. 3404
| APPLICANT: Reed, John C. APPLICANT: Reed, John C. APPLICANT: Sato, Takaaki
| APPLICANT: Sato, Takaaki
| TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
| NUMBER OF SEQUENCES: 22
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: CALHYN Campbell
| STREET: 4370 La Jolla Village Drive. Ste 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                         Score 15; DB 2; L. Pred. No. 2.2e+03; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           % Sequence 13, Application US/08858311

Patent No. 587639

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

APPLICANT: Resto, Takaaki

TILE OF INVERTION: FAS ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COKKENT AFPLICATION NUMBER: US/08/259,514
PILING DATE: 14-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: P-LJ 9954
TELECOMMUNICATION INFORMATION:
TELEFRONE: (619) 535-9001
TELEFRONE: (619) 535-9001
TELEFRONE: (619) 535-9001
TELEFRONE: (619) 535-901
TELEFRONE: (619) 535-8049
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDENDESS: single
                                                                                                            Query Match 62.5%; Sc
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
                                                                                                                                                                                                          6 CCAGCGTGCGCCATG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5
Best Local Similarity 100.
Matches 15; Conservative
nucleic acid
            ; STRANDEDNESS: sin
; TOPOLOGY: linear
US-08-607-269-8
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APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%; Score 15; DB 2; Length 27; 100.0%; Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
              SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR.1995
CLASSIFICATION DATA:
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
ATONEY/AGENT INPORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMUTION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 29
CORRESPONDICE ADDRESS:
CAMPAGE ASTO LA JOILA VIllage Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERNCK/OCKET NUMBER: P-LJ 9882
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPTCATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08607269
Patent No. 5702897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CCAGCGTGCGCCATG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-08-607-269-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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Gaps

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Score 15; DB 6; Lk
Pred. No. 2.2e+03;
0; Mismatches 0;
REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               62.5%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09866073A Patent No. 6723512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGTCCAGCGTGCGCCATGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 deerrccccccrccccarde 30
                                TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: PCR Primer US-09-258-689-5
                                                                                                                                                                                                                                                                                                                                6 CCAGCGTGCGCCATG 20
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                    linear
                                                                                                                                                                                    ;
PCT-US95-04600-8
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US-09-258-689-5
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; Sequence 8, Application PC/TUS9504600
GENERAL INFORMATION:
; TITLE OF INVENTION: Interaction of Proteins Involved in TITLE OF INVENTION: a Cell Death Pathway
inverse of Sequences: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: Campbell and Flores
ADDRESSES: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STRATE: California
COUNTRY: USA
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.5%; Score 15; DB 2; Length 27; 100.0%; Pred. No. 2.2e+03;
                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,311
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/410,804
FILING DATE: 12-MAR-1995
FILING DATE: 14-JUN-1994
ATTONEY/AGENT INFORMATION:
NAME: Campbell, Cathrin:
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
TELEPAK: (619) 535-9001
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 Dase pairs
LENGTH: 27 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04600
FILING DATE: 12-APR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: IMDXe, Richard J.
REGISTRATION NUMBER: 37,643
                     ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive. Ste 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.2.,
100.08; Pr.
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                                                                               STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                            San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                          ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-858-311-13
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Sequence 5, Application US/09258689
; Sequence 5, Application US/09258689
; Patent No. 6451527
; GENERAL INFORMATION:
; APPLICANT: Larocca, David
; APPLICANT: Baird, Andrew
; APPLICANT: Baird, Andrew
; APPLICANT: Baird, Andrew
; TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR
; TITLE OF INVENTION: SELECTING INTERNALIZING LIGANDS FOR GENE DELIVERY
; FILE REFERENCE: 760100, 430C3
; CURRENT APPLICATION NUMBER: US/09/258,689
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 10
; SSOTHARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Larocca, David
| APPLICANT: Baird, Andrew
| APPLICANT: Baird, Andrew
| APPLICANT: Rasener, Paul
| APPLICANT: Rasener, Paul
| APPLICANT: Rasener, Paul
| APPLICANT: Rasener, Paul
| TITLE OF INVENTION: DETECTING AND IDENTIFYING PROTEIN-PROTEIN
| TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERALIZATION
| TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING
| TITLE OF INVENTION: GENE DELIVERY VECTORS
| TITLE OF INVENTION: GENE DELIVERY VECTORS
| CURRENT APPLICATION OF SEQ 10 NOMBER: US/09/866,073A
| CURRENT FILLING DATE: 2001-05-24
| NUMBER OF SEQ 1D NOS: 18
| SEQ 1D NO 5
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Length 27;
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3 GGTCCAGCGTGCGCCATGG 21

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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 127, Application US/09830433A;
Fatent No. 6835384
GENERAL INFORMATION:
APPLICANT: AUJAME et al.
TITLE OF INVENTION: Ratrains of the Neisseria genius
TITLE OF INVENTION: Strains of the Neisseria genius
TITLE OF INVENTION: Extrains of the Neisseria genius
TITLE OF INVENTION: Strains of the Neisseria genius
TITLE OF INVENTION: Strains of the Neisseria genius
CURRENT APPLICATION NUMBER: US/09/830,433A;
CURRENT FILING DATE: 2001-04-26
FRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 129
SEG ID NOS: 129
SEQ ID NO IS: 29
LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Description of Artificial Sequence: primer US-09-830-433A-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rao, Mahendra S.
APPLICANT: Ralyani, Anjali J.
TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
FILE REFERENCE: T5530.CIP
CURRENT APPLICATION NUMBER: US/09/109,858
CURRENT APPLICATION NUMBER: US/09/109,435
EARLIER APPLICATION NUMBER: US 08/909,435
BARLIER FILING DATE: 1997-07-04
SOFTWARE: WordPerfect 8.0
SEQ ID NO 14
LENGTH: 19
                                                                                                                                                      Query Match 60.8%; Score 14.6; DB 3; Length 47; Best Local Similarity 81.0%; Pred. No. 3.2e+03; Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 14.4; DB 3; Length 29; 75.0%; Pred. No. 3.9e+03; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.2%; Score 14.2; DB 3; Length 19; Best Local Similarity 84.2%; Pred. No. 4.8e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                10 ĠĠĠŢŢĊĊĠĊĠŢĠĠĠĠĠĀŢĠĠ 30
                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                FEATURE:
COTHER INFORMATION: PCR Primer
US-09-866-073A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Rattus norvegicus
US-09-109-858-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.0
Best Local Similarity 75.0
Matches 18; Conservative
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US-09-109-858-14
LENGTH: 47
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                                                                                                                         Sequence 9, Application US/08217082A

Patent No. 5734033

GENERAL INFORMATION

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE

TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 224 Airport Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDES FOR INHIBITING THE TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT PAPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: FOATHRY, ANGREW D.
REGISTRATION NUMBER: 33.5.067-55 FWC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%; Score 14; DB 2; Le
100.0%; Pred. No. 5.8e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid DESCRIPTION: Synthetic DNA
GGTCCAGCATTTGCCATGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (408) 436-2075
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CCAGCGTGCGCCAT 19
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Best Local Similarity 100.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Jose
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-217-082A-9
                                                                                  RESULT 15
US-08-217-082A-9
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APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
ATTORNEY/AGENT INFORMATION:
NAME: POTINGY, Andrew D.
REGISTRATION NUMBER: 34,600
REGISTRATION NUMBER: 335-067-55 FWC
TELEPOMMUICATION INFORMATION:
TELEPHONE: (408) 436-2076
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid DESCRIPTION: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CCAGCGTGCGCCAT 19
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Patent No. 5734033

GENERAL INFORMATION:
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES:
ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
        CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%; Score 14; DB 2; Length 17; 100.0%; Pred. No. 5.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMFORTER: BATENIT Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/217,082A

FILING DATE: 24-MAR-1994

CLASSIFICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION NUMBER: US 07/288,692

PRIOR APPLICATION NUMBER: US 07/288,692

PRIOR APPLICATION NUMBER: US 07/288,692

PRILNG DATE: 22-DEC-1988

ATTORNEY/AGENT INPORMATION:

NAME: FORTHRY, ANGREY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: FORTHRY, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STARNDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ccaccarcccar 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                              CITY: San Jose
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 95110
                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-217-082A-10
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US-08-217-082A-17
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Gaps
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## Sequence 17, Application US/08465485A
## Patent No. 5831066
## GENERAL INFORMATION:
## APPLICANT: Reed, John
## TITLE OF INVENTION:
## CORRESPONDENCE 2
## CORRESPONDENCE 2
## ADDRESSEE: P.C.
## ADDRESSEE: P.C.
## STREET: 1755 S. Jefferson Davis Hwy., Suite 400
## COUNTY: U.S.A.
## COUNTY: U.S.A.
## COUNTY: U.S.A.
## Z1222
## COMPUTER READABLE FORM:
## MEDIUM TYPE: Floppy disk.
## ADDRESSEE: Ploppy disk.
             Length 18;
                                                                                                                                        Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,486A
FILING DATE: 05-UM-1995
CLASSIFICATION NUMBER: US/08/465,486A
FILING DATE: 05-UM-1995
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/846,592
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
RICH APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
RICH APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
ATTORNEY/AGENT: 1RFORMATION:
ANDER ATTORNEY/AGENT: NEFORMATION:
ANDER ATTORNEY/AGENT: ATTORNEY/AGEN
Query Match 58.3%; Score 14; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09080285
; Sequence 17, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DEC.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
; STATE: Virgina
; COUNTRY: U.S.A.
Last two internucleoside linkages are phosphorothioates
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                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE: 05-JUN-1995
FILING DATE: 05-JUN-1995
PRIOR APPLICATION NUMBER: US 08/465,485
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATFORDREY/AGENT INPORMATION:
NAMR: ROTHEN.
                                                                                                                      Query Match 58.3%; Score 14; DB 2; Le Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (408) 436-2070
                                                                                                                                                                                                                                       6 CCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ccaecerececar 18
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                           ) OTHER INFORMATION:
US-08-465-485A-24
      OTHER INFORMATION:
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Best Local Similarity
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US-09-080-285-17
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US-09-080-285-17
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| Sequence 24, Application US/08465485A |
| Patent No. 5831066 |
| GENERAL INPOWATION: |
| APPLICANT: Reed, John |
| TITLE OF INVENTION: Regulation of bc1-2 Gene Expression |
| NUMBER OF SEQUENCES: 29 |
| CORRESPONDENCE ADDRESS: 400 |
| COUNTRY: P.C. |
| STREET: 1755 S. Jefferson Davis Hwy., Suite 400 |
| CITY: Arlington |
| STREET: 1755 S. Jefferson Davis Hwy., Suite 400 |
| CITY: Arlington |
| STREET: 1755 S. Jefferson Davis Hwy., Suite 400 |
| COUNTRY: U.S.A. |
| ZIP: 22202 S.A. |
| COUNTRY: U.S.A. |
| SIP: 22202 S.A. |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: IBM PC compatible |
| OPERATING SYSTEM: PC-DOS/MS-DOS |
| SOFTWARE: Patent In Release #1.0, Version #1.25 |
| CURRENT APPLICATION DATA: |
| APPLICATION NUMBER: US/08/465,485A |
| FLING DATE: 20-JUN-1995 |
| FLING DATE: 20-SEP-1993 |
| PRIOR APPLICATION NUMBER: US 07/840,716 |
| FLING DATE: 20-SEP-1993 |
| PRIOR APPLICATION NUMBER: US 07/840,716 |
| FLING DATE: 20-SEP-1993 |
| ATPORTED PATE: 20-BC-1988 
                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                         58.3%; Score 14; DB 2; Lv
100.0%; Pred. No. 5.8e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REPERENCE/POCKET NUMBER: 3335-070-55 CONT
RELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Other nucleic acid; DESCRIPTION: Synthetic DNA ANTI-SENSE: YES FEATURE:
                           TELEPHONE: (408) 436-2070
TELEPAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (408) 436-2075
INFORMATION FOR SEQ 1D NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                6 CCAGCGTGCGCCAT 19
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                                                                                                                                                                                                                                                                                                                      Query Match 58.3:
Best Local Similarity 100.
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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LOCATION:
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APPLICANT: WRIGHT, Jim A.
APPLICANT: WRIGHT, Jim A.
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Alping H.
TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
FILE REFERENCE: 032396-040
CURRENT APPLICATION NUMBER: US/09/249,730
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 220
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Sequence 1. Application US/09118220

Fatent No. 6140051

GENERAL INFORMATION:

APPLICANT: Brown. Lauren R.

APPLICANT: APPLICANT: AND METHODS RELATED THERETO

TITLE OF INVENTION: AND METHODS RELATED THERETO

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Pred. No. 5.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATION SYSTEM: Windows SOFTWARE: Fast-SEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/118,220
                                                                                                                                                                                                                                                                                                                58.3%; Sco...
100.0%; Pred. No. ...
'.. 0; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BARTfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: GENT
TELECHONICATION INFORMATION:
TELECHONE: 619-235-8550
TELEPHONE: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PE: Diskette
IBM Compatible
svsTEM: Windows
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-118-220-1
                                                                                                                                                                                                                                                                    ) ORGANISM: Human
US-09-249-730-218
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COUNTRY: U.
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-118-220-1
                                                                                                                                                                                                                                                   TYPE: DNA
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                                       LOCATION: 16..17
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3335-070-55 CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NUMBER: CALLON NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid,
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: FOTUREY, ANGTEW D.
RECISTRATION NUMBER: 34,600
REFERENCE, DOCKET NUMBER: 3335-
TELECOMMUNICATION INFORMATION:
TELEFRONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR EGG ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified_base
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                              ZIP: 22202
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              RESULT 21
US-09-080-285-24
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DB 3;

58.3%; Score 14;

Query Match

RESULT 22 US-09-249-730-218 ; Sequence 218, Application US/09249730

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; Sequence 45, Application US/08960774
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CCAGCGTGCGCCAT 18
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 14; Conservative
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US-09-286-098-104
                                                                        JS-09-286-098-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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APPLICANT: Krieg, Arthur M.

APPLICANT: Schwartz, David A.

TITLE OF INVENTION: UNBERFYLATED CPG DINUCLECTIDE IN THE TREATMENT OF

TITLE OF INVENTION: UNBERFYLATED DISORDERS

TITLE OF INVENTION: UNBERFYLATED DISORDERS

TITLE OF INVENTION: UNBERFYLATED DISORDERS

TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS

TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS

TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS

TITLE OF INVENTION UNBERF: US/09/030,701B

CURRENT APPLICATION NUMBER: 06/039,405

PRIOR PILING DATE: 1997-02-28

NUMBER OF SEQ ID NOS: 65

SEQ ID NO 27

LENGTH: 18

LENGTH: 18
                                     Gaps
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                                                                                                                                                                                               Sequence 55, Application US/08738652B
Fatent No. 6207646
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7004 HCL
CURRENT PAPLICATION NUMBER: US/08/738,652B
CURRENT FILING DATE: 1996-10-30
EARLIER APPLICATION NUMBER: US 08/276,358
EARLIER PILING DATE: 1996-07-15
EARLIER FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 18
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
              Pred. No. 5.8e+03;
Mismatches 0;
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S8.3%; Score 14; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic oligonucleotide US-08-738-652-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-27
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100.0%; Fre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                        6 CCAGCGTGCGCCAT 19
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            Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity
                                                                                                                                                                                       US-08-738-652-55
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Sequence 51, Application US/09325193A

Patent No. 6406705

GENERAL INFORMATION:

APPLICANT: Bavis, Heather L.

APPLICANT: Schorr, Joachim

APPLICANT: Schorr, Joachim

APPLICANT: Schorr, Joachim

APPLICANT: Schorr, Joachim

APPLICANT: Maries, Arthur M.

TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant

TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant

FILE REFERENCE: C1039/7025/HCL

CURRENT APPLICATION NUMBER: US 09/154,614

PRIOR FILING DATE: 1998-09-16

PRIOR FILING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 98

SEQ ID NOS: 98

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.3%; Score 14; DB 3; L. 100.0%; Pred. No. 5.8e+03; tive 0; Mismatches 0;
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                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
                                                                                                                                             OPERATING SYSTEM: DOS 5.0
SOFTWARE: WORD PETFECT
CURRENT APPLICATION NUMBER: US/09/078,954
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                             08/856,374
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: 1NEX.
TELEPONMICATION INFORMATION:
TELEPONMICATION INFORMATION:
TELEPONMICATION INFORMATION:
TELEPONMICATION INFORMATION:
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100.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 18
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Best Local Similarity 100.C
Matches 14, Conservative
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STRANDEDNESS: single
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Best Local Similarity
COUNTRY: USA
ZIP: 80443-5270
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APPLICANT: Scherrer, Peter
APPLICANT: Con, Gerald
APPLICANT: Zon, Gerald
APPLICANT: Zon, Gerald
APPLICANT: Debeyer, Dan
TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents in
TITLE OF INVENTION: Lipid Vesicles
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: PO BOX 5270
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ZIP: 92037

COMPUTRY: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION IDMER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION NUMBER: US. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION NUMBER: 38,347
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 619/678-5090
TELEFRANCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET N
                           GENERAL INFORMATION:
APPLICANT: Krieg et al.,
APPLICANT: Krieg et al.,
TITLE OF INVENTION:
INMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
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; Sequence 14, Application US/09078954
; Patent No. 6287591
; GENERAL INFORMATION:
APPLICANT: SEMPLE, Sean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harasym, Troy
Hope, Michael J.
Ansell, Steven M.
Cullis, Pieter
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Klimuk, Sandra K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGCGTGCGCCAT 19
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Best Local Similarity
Matches 14; Conserva
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                  Patent No. 6239116
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APPLICANT:
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APPLICANT:
APPLICANT:
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CITY: F1
STATE: (
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Query Match 58.3%; Score 14; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 45, Application US/09136080E

Patent No. 6518017

GENERAL INFORMATION:

APPLICANT: Riley, Timothy A.

APPLICANT: Brown, Bob D.

APPLICANT: Arnold, Lyle J.

TITLE OF INVENTION: COMBINATORIAL ANTISENSE LIBRARY

FILE REPERENCE: OASBIO.003A

CURRENT APPLICATION NUMBER: US/09/136,080E

CURRENT FILING DATE: 1998-08-18

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 45

LENGTH: 18
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100.0%; Pred. No. 5.8e+03;
iive 0; Mismatches 0;
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EARLIER APPLICATION NUMBER: US 08/960,774
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 08/738,652
EARLIER FILING DATE: 1996-10-30
EARLIER FILING DATE: 1995-02-07
EARLIER FILING DATE: 1995-02-07
EARLIER FILING DATE: 1995-02-07
EARLIER FILING DATE: 1995-02-07
SARLIER FILING DATE: 1995-02-07
SARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/690,921
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/FP00/02920
PRIOR PILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 09/301,829
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Patent No. 6544518
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Hermand, Philippe
TITLE OF INVENTION: Vaccines
FILE REFERENCE: B45181-1
                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-136-080E-45
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US-09-191-170-53
Sequence 53, Application US/09191170
Fatent No. 6429199
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: for Activating Dendritic Cells
FILE REFREENCE: C1039/7017
CURRENT APPLICATION NUMBER: US/09/191,170
CURRENT FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; 2ive 0; Mismatches 0; Indels
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Pred. No. 5.8e+03;
         0; Indels
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APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
FILE REPERENCE: 10412-024
CURRENT APPLICATION NUMBER: US/09/724,426
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 17
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
FILE REFERENCE: 10412-024
CURRENT APPLICATION NUMBER: US/09/724,426
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN version 3.0
      0; Mismatches
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100.0%; Pre
                                                                                                                                                                                                      Sequence 17, Application US/09724426
Patent No. 6414134
                                                  6 CCAGCGTGCGCCAT 19
                                                                                            5 ccaccerccccar 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.3
Best Local Similarity 100.
Matches 14; Conservative
      14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-426-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-426-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                          RESULT 31
US-09-724-426-17
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US-09-724-426-24
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LENGTH: 18
      Matches
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Gaps

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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
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                                                                                                                                                                                                        6 CCAGCGTGCGCCAT 19
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                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 14; Conservative
; SEQ ID NO 218
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
US-09-249-247-218
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Sequence 218, Application US/09249247

Batent No. 6593305

GENERAL INFORMATION:

APPLICANT: WRIGHT, Jim A.

APPLICANT: YOUNG, Alping H.

TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase

FILE REFERENCE: 032386-023

CURRENT APPLICATION NUMBER: US 60/023,040

EARLIER APPLICATION NUMBER: US 60/039,959

EARLIER RILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: US 60/039,959

EARLIER REPLICATION NUMBER: US 60/039,959

EARLIER APPLICATION NUMBER: US 60/039,959

EARLIER REPLICATION NUMBER: US 60/039,959

EARLIER PILING DATE: 1997-03-07

SEARLIER PLING DATE: 1997-03-07

NUMBER OF SEQ 1D NOS: 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Immunostimulatory oligonucleotide sequence comprising COTHER INFORMATION: one or more CpG motifs
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                           Score 14; DB 3; La
Pred. No. 5.8e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Friede, Martin
APPLICANT: Hermand, Philippe
TITLE REFERENCE: B45181
CURRENT FILION NUMBER: US/09/301,829A
CURRENT FILION DATE: 1999-04-29
PRIOR PILION DATE: 1999-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
      PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 9908885.8
PRIOR FILING DATE: 1999-04-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09301829A; Patent No. 6558670; GENERAL INFORMATION:
                                                                                                                                                                                                                58.3%; Scc.
100.0%; Pre
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 CCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                         CCAGCGTGCGCCAT 18
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                                                                                                                                                                                                                                                                                                                CCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-690-921-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 37
US-09-249-247-218
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GENERAL LINCKMALLIANI

J GENERAL LINCKMALLIANI

APPLICANT: Reed, John C.

TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
FILE REFERENCE: 04040/1200990-U57

CURRENT APPLICATION NUMBER: US/09/724,425

CURRENT FILING DATE: 2000-11-28

PRIOR PILING DATE: 1999-08-17

PRIOR PILING DATE: 1999-08-17

PRIOR PILING DATE: 1999-08-17

PRIOR PILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1995-06-18

PRIOR PILING DATE: 1995-02-20

PRIOR PILING DATE: 1993-09-20

PRIOR PILING DATE: 1993-09-20

PRIOR PILING DATE: 1993-09-21

PRIOR PILING DATE: 1993-09-21

PRIOR FILING DATE: 1993-02-21

PRIOR FILING DATE: 1993-02-21

PRIOR FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN VETSION 3.1
    MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 14; DB 3; Lf
100.0%; Pred. No. 5.8e+03;
tive 0; Mismatches 0;
                                                                                                         CUKKEN APPLICATION DAMAS

CUKASI APPLICATION NUMBER: US/09/654,373

FILING DATE: 01-Sep-2000

CLASSIFICATION S. CURKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/152,179

FILING DATE: SEPTEMBER 2, 1999

APPLICATION NUMBER: 09/078,954

FILING DATE: MAY 14, 1999

APPLICATION NUMBER: 08/856,374

FILING DATE: MAY 14, 1997

ATTORNEY/AGENT INFORMATION:

NAME: MAXINA T. LASSON

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: 32,038

REFERENCE/DOCKET NUMBER: 1NEX.P-007

TELECOMMUNICATION INFORMATION:

TELECHONE: (970) 468-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                        COMPUTER: IBM Compatible OPERATING SYSTEM DOS 5.0 SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09724425 Patent No. 6841541 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (970) 468-0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ccaecerececar 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-654-373-14
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CRGANISM: HOR
US-09-724-425-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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  nucleotide
OTHER INFORMATION: Description of Artificial Sequence: nucleotic OTHER INFORMATION: base sequence of PNA derivatives that bind to OTHER INFORMATION: viral and cellular targets
                                                                                                                                                                   ;
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; FATELL NO. 9022000;
; TUTLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF TITLE OF INVENTION: USE THEREOF;
; TILE REFERENCE: 0838.1003-001;
; CURRENT APPLICATION NUMBER: US/09/634,320;
; CURRENT FILING DATE: 1090-08-09;
; PRIOR PILING DATE: 1999-08-09;
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FREESEQ for Windows Version 4.0;
; SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipid
Vesicles and Method of Making Same
                                                                                                                Query Match 58.3%; Score 14; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.3%; Score 14; DB 3; Length 18; ilarity 100.0%; Pred. No. 5.8e+03; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-634-320-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedabl & Larson LLP
STREET: PO BOX 5068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SEMPLE, Sean C.
Klimuk, Sandra K.
Harasym, Troy O.
Dos Santos, Nancy
Ansell, Steven M.
Cullis, Pieter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 41
US-09-654-373-14
; Sequence 14, Application US/09654373
; Patent No. 6835395
; GENERAL INFORMATION:
CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09634320
Patent No. 6822086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hope, Michael J.
Scherrer, Peter
McIntosh, Deidre
Wong, Kim F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CO
COUNTRY: USA
ZIP: 80435-5068
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                        CCAGCGTGCGCCAT 18
                                                                                                                                                                                                             6 CCAGCGTGCGCCAT 19
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Best Local Similarity
....hes 14; Conserva
                                                                                                                                                                                                                                                                                                                                RESULT 40
US-09-634-320-7/c
                                                ; OTHER INFORM
US-09-835-370-21
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Gaps ö

Length 18; Indels

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Sequence 6, Application US/10002884A

Sequence 6, Application US/10002884A

Sequence 6, Application US/10002884A

Batchi No. 6867043

APPLICANT: Stein, Cy A

APPLICANT: Baniereskaya, Lyuba

APPLICANT: Guzzo-Pernell, Nancy

TITLE OF INVENTION: PEC-PECTEIN EXPRESSION IN CELLS

TITLE OF INVENTION: PRC-PECTEIN EXPRESSION IN CELLS

FILE REFERENCE: 0579/63293

CURRENT APPLICATION NUMBER: US/10/002,884A

CURRENT FILING DATE: 2001-11-02

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ching-Leou Teng and Greg Hardee IIVENTION: Compositions and Methods for the Delivery of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.3%; Score 14; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
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100.0%; Pred. No. 5.8e+03;
tive 0; Mismatches 0;
                                                                                                                 REGISTRATION NUMBER: «Unknown»
REFERENCE/DOCKET NUMBER: «Unknown»
TELEPHONE: «Unknown»
TELEPHONE: «Unknown»
TELEFAX: «Unknown»
TELEFX: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE US-10-002-884A-6
                                                                                                                                                                                                                                                                                                                                                                        ;; ATTI-SENSE: yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-895-480A-14
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 46
US-09-108-673A-34
Sequence 34, Application US/09108673A
Patent No. 6887906
GENERAL INFORMATION:
APPLICANT: Ching-Leou Teng and Gre
                CLASSIFICATION: <Unknown>
FILING DATE: 29-Jun-2001
                                                                   FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S CCAGCGTGCGCCAT 18
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Best Local Similarity 100.'
Matches 14; Conservative
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US-10-002-884A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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US-09-985-480A-14
US-09-985-480A-14
US-09-985-480A-14
US-08-98-140A-14
US-08-98-140A-14
US-08-98-15
USENERAL INFORMATION: High Efficiency Encapsulation of Charged Therapeutic
USENERAL TITLE OF INVENTION: High Efficiency Encapsulation of Larged Therapeutic
USENERAL TITLE OF LINVENTION: Lipid Vesicles
USENERAL TITLE OF LINVENTION: Lipid Vesicles
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                  Score 14; DB 3; Length 18;
Pred. No. 5.8e+03;
                                                      0; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,480A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 3; Le
Pred. No. 5.8e+03;
         58.3%; Sco. 100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Oppedahl & Larson LLP
STREET: PO Box 5068
CITY: Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.3%; Sco
Best Local Similarity 100.0%; P1
Matches 14; Conservative 0;
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ZIP: 80435
COMPUTER READABLE FORM:
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                                                                                            6 CCAGCGTGCGCCAT 19
         Query Match
Best Local Similarity 100.0
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-724-425-24
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US-09-724-425-24
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APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
APPLICANT: Hermann Wagner
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
TITLE OF INVENTION: CpG-BASED IMMUNO-AGONIST/ANTAGONIST
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 110, Application US/09672126B
; Ratent No. 6949520
; GENERAL INFORMATION:
APPLICANT: Hartmann, Gunther
; APPLICANT: Brataler, Robert L.
APPLICANT: Methods Related to Immunostimulatory;
TITLE OF INVENTION: Methods Related to Immunostimulatory;
TITLE OF INVENTION: Nucleic Acid-Induced Interferon;
FILE REFERENCE: C1039/7044
CURRENT APPLICATION NUMBER: US/09/672,126B
CURRENT FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FRSLSEQ for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 18
                                                                                                       Query Match 58.3%; Score 14; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.8e+03;
tive 0; Mismatches 0;
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US-09-954-987B-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-01-23
PRIOR FILING DATE: 2001-01-23
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PSESEQ for Windows Version 3.0
SSOFTWARE: PSESEQ for Windows Version 3.0
SEQ ID NO 115
       ; OTHER INFORMATION: of PNA targeting CMV US-09-835-371-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 115, Application US/09954987B Patent No. 6943240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                          5 CCAGCGTGCGCCAT 18
                                                                                                                                                                                                                                               6 CCAGCGTGCGCCAT 19
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Best Local Similarity 100.
Matches 14; Conservative
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US-09-954-987B-115
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Sequence 21, Application US/09835371

Patent No. 6905820

GENERAL INFORMATION:

APPLICANT: ULLMANN: Eugen

APPLICANT: WILL, David W

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND

TITLE OF INVENTION: PROCESSES FOR PREPARING THEM

TITLE OF INVENTION: PROCESSES FOR PREPARING THEM

TITLE OF INVENTION: PROCESSES FOR PREPARING

CURRENT APPLICATION NUMBER: US/09/835,371

CURRENT ELLING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 21

LENGTH: 18
                                   NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Oligonucleotides Via the Alimentary Canal 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          COMPUTRY: USA

ZIP: 1910

COMPUTRY: USA

COMPUTRR READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: DEM FS/2

FILING DATE: DEM FS/2

FILING D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 20-SEP-1994
; PUBLICATION DATE: 30-MAR-1995
US-09-108-673A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Matches 14; Conservative
       TITLE OF INVENTION:
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                                                                                                                                                                                                                                               USA
                                                                                                                                                                           CITY: Phil
STATE: PA
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US-09-634-320-8

is Sequence 8, Application US/09634320

j Patent No. 6822086

igneral information:
    APPLICANT: Papisov, Mikhail, I.
    APPLICANT: Papisov, Mikhail, I.
    TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: USE THEREOF

CURRENT APPLICATION NUMBER: US/09/634,320

CURRENT FILING DATE: 1909-09

PRIOR APPLICATION NUMBER: US 60/147,919

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 8

IENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

PEATURE:

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Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels
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; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCGTGCGCCAT 18
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Search completed: February 15, 2006, 21:14:18 Job time : 57.9504 secs

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Sequence 35445, A Sequence 55179, A Sequence 87299, A Sequence 165784, Sequence 773179, Sequence 5, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 21, Appli Se

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US-10-719-900-91312

US-10-098-263B-3445

US-10-098-263B-3445

US-10-098-263B-3745

US-10-098-263B-87293

US-10-719-900-765784

US-10-719-900-765784

US-10-719-900-765785

US-10-719-900-765785

US-10-151-204-5

US-10-151-204-1

US-10-151-204-1

US-10-10-11-204-1

US-10-10-11-204-1

US-10-10-11-31-1

US-10-10-10-10-1

US-10-053-645A-3

US-10-19-900-345119

US-10-11-900-345119

US-10-11-900-345119

US-10-719-900-345119

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Sequence 200562,
Sequence 240612,
Sequence 827644,
Sequence 69, Appl
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96172, A
                                                      February 16, 2006, 01:43:22 ; Search time 348.298 Seconds (without alignments) 569.815 Million cell updates/sec
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cgn2_6/ptodata11/pubpna/US08_PUBCOMB.seq:*
cgn2_6/ptodata11/pubpna/US08_PUBCOMB.seq:*
cgn2_6/ptodata11/pubpna/US09B_PUBCOMB.seq:*
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         GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-112-653-75
US-10-113-4578-81
US-10-813-4578-81
US-10-813-4578-81
US-10-81-178-81
US-10-19-956-318311
US-10-19-956-318311
US-10-956-318311
US-10-956-318311
US-11-036-317-240612
US-11-036-317-240612
US-11-036-317-827644
US-09-875-453-69
US-09-776-479-90
US-10-112-653-384
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Maximum Match 100%
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                                        nucleic search, using sw model
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Sequence 127, Applisequence 3, Applisequence 35, Applisequence 35, Applisequence 35, Applisequence 14, Applisequence 14, Applisequence 94919, A Sequence 91541, A Sequence 91541, A Sequence 91541, A Sequence 879335, Sequence 879335, Sequence 879335, Sequence 546955, Sequence 546955,

Sequence 2, Apl Sequence 59, A Sequence 104, Sequence 7, Apl

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. LOCATION: (0)...(0) ...(0) ...(1) CTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends US-09-888-326-440
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APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
FRIOR APPLICATION NUMBER: US/09/776,479
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR PILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 81
LENGTH: 24
                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 24; DB 3; Length 24; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 24; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTHARE: PASLSEQ for Windows Version 3.0
ESEQ ID NO 440
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 81, Application US/09776479; Publication No. US20030087848A1; GENERAL INFORMATION:
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Sequence 19, Appl
Sequence 36, Appl
Sequence 4669, Ap
Sequence 554810,
Sequence 654807,
Sequence 499977,
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Sequence 40, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 3636, Ap
Sequence 150730,
Sequence 582207,
Sequence 693873,
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Sequence 202207,
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Sequence 203319,
Sequence 210932,
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Sequence 19, Appl
Sequence 10, Appl
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Sequence 82043, A
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Sequence 406309,
Sequence 534861,
Sequence 544751,
Sequence 844731,
Sequence 814163,
Sequence 932297,
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Sequence 40,
                      Sequence 2
Sequence 7
Sequence 2
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US-09-976-740-40
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                  US-10-053-645A-2

US-10-812-2165-7

US-10-914-18-2

US-10-148-953A-20

US-10-714-310-19

US-10-714-310-36

US-10-713-956-54807

US-10-719-956-54807

US-10-719-956-54807

US-10-719-916-49977

US-10-809-189-55452
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US-10-482-956-10
US-10-098-263B-96171
US-10-719-956-82043
US-10-719-956-470890
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Query Match 100.0%; Score 24; DB 3; Length 24; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 24; Conservative 0; Mismatches 0; Indels
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; Sequence 81, Application US/009706790289
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Fouron, Yve8
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; CURRENT APPLICATION NUMBER: US/09/776,479
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US-09-776-479-81
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APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REFERENCE: C1039/7052 (AWS)

; Sequence 440, Application US/0988326; Publication No. US20030026801A1; GENERAL INFORMATION:

RESULT 1 US-09-888-326-440

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REFERENCE: C01039/70060(AWS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT PILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 75
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-017-995-81

Sequence 81, Application US/10017995

Publication No. US2003005014A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

ITTLE OF INVENTION: Inhibituch of Angiogenesis by Nucleic Acids

FILE REFERENCE: C1037/JO25 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/017, 995

CURRENT FILING DATE: 2001-12-18

PRIOR PILING DATE: 2001-12-14

NUMBER OF SEQ ID NOS: 1093

SEQ ID NO SI

LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-75
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 81
LENGTH: 24
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                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Sequence US-09-776-479-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGTCCAGCGTGCGCCATGGGGG 24
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ORGANISM: Artificial Sequence
                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-10-112-653-75
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sequence 81, Application US/10831778

publication No. US20040235774A1

sequence 81, Application No. US20040235774A1

septicant: No. US20040235774A1

septicant: Brataler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Processor Septicant Of Septican
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100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          100.0%; Score 24; DB 5; Length 24; 100.0%; Pred. No. 1.7; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation No. US2003012026A1

j Sequence 81, Application US/10314578

publication No. US2003012026A1

j Publication No. US2003012026A1

j Publication No. US2003012026A1

j APPLICANT: Krieg, Arthur M.

APPLICANT: Krieg, Arthur M.

APPLICANT: Vollmer, Jorg

j TITLE OF INVENTION: Immunostimulatory Nucleic Acids

FILE REFERENCE: C1039/7035 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/314,578

CURRENT FILING DATE: 1999-09-25

PRIOR APPLICATION NUMBER: US 60/156,113

PRIOR FILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1990-09-27

PRIOR PILING DATE: 1900-09-27

PRIOR PILING DATE: 1900-09-27
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), OTHER INFORMATION: Synthetic Sequence US-10-017-995-81
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ORGANISM: Artificial Sequence
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                                                                                                                                           Query Match
Best Local Similarity 100.v
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TYPE: DNA
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                                                                                                                                                                                                             RESULT 8
US-10-005-073-1
; Sequence 1, Application US/10005073
; Publication No. US2002090371A1
; GENERAL INFORMATION:
    APPLICANT: Jevnikar, Anthony M.
    APPLICANT: Jevnikar, Anthony M.
    Stiller, Calvin R.
    Stiller, Calvin R.
    TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING IMMUNE RESPONSES IN MAMMALS
. TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING IMMUNE RESPONSES IN MAMMALS
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                                       100.0%; Score 24; DB 8; Length 24; 100.0%; Pred. No. 1.7; 0; Indels iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P. STREET: George Mason Building, 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/005,073
FILING DATE: 07-Dec-2001
CLASSIFICATION: cluknown>
PRIOR APPLICATION NUMBER: US/17,874
FILING DATE: 21-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: REA, TEACES STANCK
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 024916-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: /desc = "DNA - primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                       1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                               1 GGGGTCCAGCGTGCGCCATGGGGG 24
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
                                    Query Match
Best Local Similarity 100.0
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7.
Local Similarity 85.7.
Conservative
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US-10-831-778-81
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Sequence 368311, Application US/10719956 Publication No. US20040146910A1 GENERAL INFORMATION:

US-10-719-956-368311/c

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RESULT 11

US-10-956-157-200607/C

US-10-956-157-200607/Application US/10956157

Sequence 200607, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Worth

APPLICANT: Worth

APPLICANT: Worth

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: UNABER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SEQ ID NO 200607
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR PILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASEESEQ for Windows Version 4.0
SEQ ID NO 107962
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                         Query Match 64.2%; Score 15.4; DB 7;
Best Local Similarity 94.1%; Pred. No. 7.4e+03;
Matches 16; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 107962, Application US/10809189; Publication No. US20050048531A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GITCCAGCCTTCGCCATGGG 20
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                                                                                                                                                                                                                                                                                                ; ORGANISM: Rattus norvegicus US-10-719-956-368311
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Matches 17; Conservative
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US-10-809-189-107962
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Query Match
Best Local Similarity
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APPLICANT:
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; Sequence 240612, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT APPLICATION NUMBER: US 60/536,639
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR APPLICATION UNMER: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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; Sequence 827644, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REPRESNCE: 36654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.3%; Score 15.2; DB 10; Length 25; Best Local Similarity 85.0%; Pred. No. 9e+03; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                       Length 25;
                                                                                                                                                         3; Indels
                                                                                                       Score 15.2; DB 9;
Pred. No. 9e+03;
0; Mismatches 3;
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                                                                                                            63.3%;
85.0%;
                                                                                                              Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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Matches 17; Conservative
; LENGTH: 25
; TYBE: DDA
; ORGANISM: Probe Sequence
US-10-956-157-200607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                     RESULT 12
US-11-036-317-240612/c
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Weiner, George
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REPERENCE: C1039/7052 (AWS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 533
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 35;
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bruice, Thomas W. TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2; DB 3;
Pred. No. 8.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic oligonucleotide NAME/KEY: misc feature LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 4600-0135.30
CURRENT APPLICATION NUMBER: US/09/875,453
CURRENT FILING DATE: 2001-06-06
FRIOR APPLICATION NUMBER: US 60/209,549
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 533, Application US/09888326; Publication No. US20030026801A1; GENERAL INFORMATION:
Sequence 69, Application US/09875453
Publication No. US20030027320A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTCCAGCGTGCGCCATGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 GGGTCCAGCCGGAGCCATGG 9
                                                                                                                                                                                                                         Latour, Derek R.
Thomas, Rita L.
Kongpachith, Ana
Sheppard, Liana T.
Lim, Moon Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                                                                                                     Laurance, Megan E
                                                                      APPLICANT: Kim, Jungsuh P.
APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
                                                                                                                                                                            Michelotti, Emil
Velligan, Mark D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: primer US-09-875-453-69
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62.5%; Score 15; DB 3; Length 16; 100.0%; Pred. No. 1.2e+04;

Gaps

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0; Indels

0; Mismatches

15; Conservative

Matches

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Query Match
Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
                       US-10-112-653-84
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Publication No. US20040067902A9;
Publication No. US20040067902A9;
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Bretzler, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
ITILE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the FILE REFERENCE: C1037/7013 (HCL/MAT);
CURRENT APPLICATION NUMBER: US/09/776,479;
CURRENT FILING DATE: 2000-02-03;
NUMBER OF SEQ ID NOS: 1093;
SOUTHARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 90;
LENGTH: 16
                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Brataler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fourcon, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%; Score 15; DB 3; Length 16; 100.0%; Pred. No. 1.2e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%; Score 15; DB 3; Length 16; 100.0%; Pred. No. 1.2e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 90
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic Sequence US-09-776-479-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic Sequence US-09-776-479-90
                                                                                                           RESULT 16
US-09-776-479-90
; Sequence 90, Application US/09776479
; Publication No. US20030087848A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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5 TCCAGCGTGCGCCAT 19
                                            1 rccaccarccar 15
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Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                                               APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATWENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REFERENCE: C01039/70060(AWS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: PASLSEQ for Windows Version 3.0
SOFTWARE: PASLSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-017-995-90

i Sequence 90, Application US/10017995

j Sequence 90, Application US/10017995

j Publication No. US20030055014A1

i GENERAL INFORMATION: Robert L.

j TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

j FILE REPERENCE: C1037/7025 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/017,995

CURRENT FILING DATE: 2000-12-18

j PRIOR APPLICATION NUMBER: US 60/255,534

pRIOR PLIANG DATE: 2000-12-14

j NUMBER OF SEQ ID NOS: 1093

j SOFTWARE: PastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%; Score 15; DB 5; Le
100.0%; Pred. No. 1.2e+04;
iive 0; Mismatches 0;
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Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Sequence 84, Application US/10112653
Publication No. US20030050268A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-314-578-90
, Sequence 90, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Sccilarity 100.0%; Pr
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Gaps
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OTHER INFORMATION: Oligonucleotide
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotides, linkages between positions
OTHER INFORMATION: to 18 are phosphorothioates, linkages between
OTHER INFORMATION: positions 18 to 26 are phosphodiesters
OTHER INFORMATION: positions 19 to 29 carry 2'-OCH3 modified ribosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09817387
Patent No. US20010039263A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 101195-24
CURRENT APPLICATION NUMBER: US/09/817,387
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: DE 197 20 151.2
PRIOR PILING DATE: 1997-05-02
NUMBER OF SEQ 1D NOS: 29
SOFTWARE: PATENT VET. 1997-05-02
SOFTWARE: PATENT VET. 1997-05-02
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                PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 96172
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 62.5%; Score 15; DB 3; Length 29; Local Similarity 100.0%; Pred. No. 1.1e+04; ns 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-LIC/15/2900-91312.
Sequence 91312. Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Kue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
FILE REFERENCE: 3228.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT PILING DATE: 2003-11-20
FRICA APPLICATION NUMBER: 60/427,808
FRICA REPLICATION STELL 2002 11 20
FRICA FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: residues INFORMATION: linkages between positions 26 to 29 INFORMATION: phosphorothioates
                                                                                                                                                                                                                                              62.5%; Score 15; DB 5; I
78.3%; Pred. No. 1.1e+04;
tive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                       1 GGGGTCCAGCGTGCGCCATGGGG 23
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  2003-01-08
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                                                                                                                                                                                                                                                   Query Match 62.55
Best Local Similarity 78.33
Matches 18; Conservative
                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-96172
  CURRENT FILING DATE:
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US-09-817-387-12
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LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%; Score 15; DB 8; Length 16; Best Local Similarity 100.0%; Pred. No. 1.2e+04; Matches 15; Conservative 0; Mismatches 0; Indels
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REPERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
FRIOR APPLICATION NUMBER: US 60/156,113
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR APPLICATION NUMBER: US 60/227,436
FRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FRAEKEQ for Windows Version 3.0
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Publication No. US20030104410A1
GENERAL INFORMATION Michael
TITLE OF INVENTION: Human Microarray
FILE REPERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic Sequence US-10-831-778-90
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                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 16
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LENGTH: 16
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Best Local Similarity
Matches 17; Conserv
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; Sequence 55179, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitchan, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT PILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; RIOR FILING DATE: 2001-03-16
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
                                                                                                                           61.7%; Score 14.8; DB 8; Length 25; 88.9%; Pred. No. 1.3e+04;
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81.0%; Pred. No. 1.6e+04;
ive 0; Mismatches 4; Indels
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81.0%; Pred. No. 1.6e+04;
ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mitthan, Michael
APPLICANT: Mitthan, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 35445
LENGTH: 25
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 91312
LENGTH: 25
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                                                                                                                                                               Mismatches
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; Sequence 35445, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
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                                                                                                                                            Local Similarity 88.9
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                                                                      ORGANISM: Mus musculus
US-10-719-900-91312
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CORGANISM: Homo sapien
US-10-098-263B-35445
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; ORGANISM: Homo sapien
US-10-098-263B-55179
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nes 17; Conserv
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Best Local Similarity
Matches 17; Conserv
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                                                       TYPE: DNA
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Sequence 87293
Sequence 87293, Application US/10098263B
Sequence 87293, Application US/10098263B
Sequence 87293, Application US/10098263B
CENERAL INFORMATION:
TITLE OF INVENTION: Human Microarray
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.118.12.100/098,263B
CURRENT FILING DATE: 2003-01-08
FRIOR RPLICKTION NUMBER: 60/276,759
FRIOR PILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 87293
LENGHAL: 25
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
    APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT PILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; RIOR RILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICAMT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REPRENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.8%; Score 14.6; DB 5; Length 25; larity 81.0%; Pred. No. 1.68+04; Conservative 0; Mismatches 4: Indels
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Pred. No. 1.6e+04;
0; Mismatches 4;
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Best Local Similarity 81.0%;
Matches 17; Conservative (
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US-10-098-263B-87293
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APPLICANT: BAIRCA, ADGREW
APPLICANT: BAIRCA, ADGREW
APPLICANT: BAIRCA, ADGREW
APPLICANT: RASENET. PAUL
TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR
TITLE OF INVENTION: DETECTING AND IDENTIFYING PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION
TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING
TITLE OF INVENTION: GENE DELIVERY VECTORS
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 17
SOFTWARE PATENTING OF SEQ ID NOS: 17
SOFTWARE PATENTION OF SEQ ID NOS: 17
SOFTWARE PATENTIAL VET. 2.0
SEQ ID NO 5
LENGTH: 47
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60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels
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Pred. No. 1.4e+04;
0; Mismatches 4; Indels
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US-10-735-592-52
; Sequence 52, Application US/10735592
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                                                 Sequence 5, Application US/09866073
Patent No. US20020068272A1
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81.0%;
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Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                               APPLICANT: Larocca, David
                                                                                        GENERAL INFORMATION:
               RESULT 32
JS-09-866-073-5
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; Sequence 773179, Application US/11036317
; Publication No. USZ0050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REPERENCE: 3664.1
; CURRENT PILING DATE: 2005-10-13
; PRIOR PPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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US-10-719-900-765785

Sequence 765785, Application US/10719900

PUblication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVERNION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528-1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

RIOR PELING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SEQ ID NO 765785

LENGTH: 25
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                                                                                                                  Length 25;
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                                                                                                                    Score 14.6; DB 8;
Pred. No. 1.6e+04;
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0; Mismatches 4
                                                                                                                      Query Match 60.8%; Score 14.6; DB 8; Best Local Similarity 81.0%; Pred. No. 1.6e+04; Matches 17; Conservative 0; Mismatches 4
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Best Local Similarity 81.0
Matches 17; Conservative
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                                      TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-765784
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Best Local Similarity
Matches 17; Conserv
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US-11-036-317-773179/c
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SEQ ID NO 765784
LENGTH: 25
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Art. Krieg
APPLICANT: Art. Krieg
APPLICANT: Alocy, Vollmer
TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
FILE REFERENCE: C1037.70038US01
CURRENT AFLING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 52
LENGTH: 18
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; Publication No. US2005026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
; TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVERTION: WHORER: US/10/719,900
; CURRENT APPLICATION NUMBER: 05/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; RIOR RILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 217604
; LENGTH: 25
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APPLICANT: Joerg, Vollmer
TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
FILE REFERENCE: C1037.700380S01
CURRENT PEPLICATION NUMBER: US/10/735,592
CURRENT FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 5:3
LENGTH: 18
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93.8%; Pred. No. 2.1e+04;
tive 0; Mismatches 1;
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; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-52
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Best Local Similarity 93.8°
Matches 15, Conservative
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Matches 15; Conservative
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US-10-719-900-217604
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 195172
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 2: 99174
SEQ ID NO 2: 9536
LENGTH: 25
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                                                                      DB 8;
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                                                                    Query Match 60.0%; Score 14.4; D
Best Local Similarity 75.0%; Pred. No. 2e+0
Matches 18; Conservative 0; Mismatches
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; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
                                                                                                                                                                 1 GGGGTCCAGCGTGCGCCATGGGGG 24
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Best Local Similarity 93.8'
Matches 15; Conservative
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Matches 15; Conservative
; ORGANISM: Mus musculus
US-10-719-900-217604
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US-11-036-317-195172
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US-11-036-317-228536
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US-11-036-317-228536
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2 GGGTCCAGCGTGCGCC 17
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US-11-036-317-874107
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Sequence 313397, Application US/11036317
BUNDIACATION NO. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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US-11-036-317-304181
; Sequence 304181, Application US/11036317
; Publication No. US2005021482341
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; PRIOR PELLOTATION NUMBER: US 60/536,639
; RIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SEQ ID NO 304181
; SEQ ID NO 304181
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US-11-036-317-531172/c
US-11-036-317-531172, Application US/11036317
; Sequence 531172, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Alan
    TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
    FILE REPRENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR PILING DATE: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
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93.8%; Pred. No. 2e+04;
iive 0; Mismatches 1;
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Best Local Similarity 93.8
Matches 15, Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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CORGANISM: Mus musculus
US-11-036-317-304181
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US-11-036-317-313397
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Publication No. US20050214823A1
Publication No. US20050214823A1
Publication No. US20050214823A1
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Wethod of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 874107
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NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 531172
LENGTH: 25
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Pred. No. 2e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                   60.0%; Score 14.4; DB 10;
93.8%; Pred. No. 2e+04;
tive 0; Mismatches 1;
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Pred. No. 2e+04;
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1. Similarity 93.8%;
15; Conservative C
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Best Local Similarity 93.8<sup>3</sup>
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus
US-11-036-317-874107
                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-531172
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Best Local Similarity
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RESULT 48
US-10-053-645A-35
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                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 32
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                                                                                                              Sequence 942273, Application US/11036317
Sequence 1022050214823A1
Sequence 10220650214823A1
SEQUENCE 10220650214823A1
SEREMEAL INFORMATION:
TATLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse TILE REFERENCE: 3654.
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR APPLICATION NUMBER: US 60/536,639
FRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 942273
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TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic TITLE OF INVENTION: Btrains of the Neisseria genius FILE OF INVENTION: Btrains of the Neisseria genius FILE REFERENCE: P07180U300/BAS.
CURRENT APPLICATION NUMBER: US/10/909,436
CURRENT APPLICATION NUMBER: FR 98 13 693
PRIOR FILING DATE: 1998-R. FR 98 13 693
PRIOR FILING DATE: 1998-R. FR 98 13 693
PRIOR FILING DATE: 1998-R. ER 98 13 693
SOFTWARE: PREDENTIN Ver. 2.1
SOFTWARE: PREDENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 60.0%; Score 14.4; DB 8; Length 29; Local Similarity 75.0%; Pred. No. 1.9e+04; nee 18; Conservative 0; Mismatches 6; Indels
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2e+04;
1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10297321; Publication No. US20040072342A1; GENERAL INFORMATION:
APPLICANT: Bothwell, Alfred L. M.; APPLICANT: Pober, Jordan S.
4 GCGTCCAGCGTGCGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 93.8
Matches 15; Conservative
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US-11-036-317-942273
                                                                                     RESULT 44
US-11-036-317-942273
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US-10-909-436-127
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Matches
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APPLICANT: Robert B. Klem
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
FILE REFERENCE: 10412-022-99
CURRENT PEPLICATION NUMBER: US/10/053,645A
CURRENT PEPLICATION NUMBER: 60/263,244
PRIOR FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 33
LENGTHRES 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 35, Application US/10053645A; Publication No. US20030176376A1; Publication No. US20030176376A1; GENERAL INFORMATION: APPLICANT: Robert E. Klem: APPLICANT: Robert E. Klem: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A: TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2;
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APPLICANT: Schechner, Jeffrey S.
APPLICANT: Zheng, Lian
TITLE OF INVENTION: Production and Use of Microvessels in a
TITLE OF INVENTION: Fibronectin-containing Gel
FILE REFERENCE: 44574-5074-WO
CURRENT APPLICATION NUMBER: US/10/297,321
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: US 60/208,931
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5, end
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; OTHER INFORMATION: Bcl-2 cDNA
US-10-297-321-3
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. Sequence 33, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Matches 15; Conservative
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US-10-053-645A-41
                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense; OTHER INFORMATION: Oligionucleotide
US-10-053-645A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 41, Application US/10053645A

Publication No. US20030176376A1

GENERAL INFORMATION:

APPLICANT: Robert E.

TITLE OF INVENTION: GELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS.

TITLE OF INVENTION: ANTIENSE OLIGOMERS, AND HYBRID OLIGOMERS.

TITLE OF INVENTION: ANTIENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF

TITLE OF INVENTION: ANTIENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF

TITLE OF INVENTION: ANTIENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF

TITLE OF INVENTION: ANTIENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF

TITLE OF INVENTION NUMBER: 05/263,244

PRIOR PRIING DATE: 2001-01-22

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 41

LEMETH APPLICATION WINDOWS Version 4.0

SEQ ID NO 41

LEMETH APPLICATION WINDOWS VERSION 4.0
TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF FILE REFERENCE: 10412-022-99
CURRENT APPLICATION NUMBER: US/10/053,645A
CURRENT FILING DATE: 2002-01-22
PRIOR PRIOR PRICATION NUMBER: 60/263,244
PRIOR FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 34
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US-10-911-374-14
; Sequence 14, Application US/10911374
; Sequence 14, Application Wo. US20050003531A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Mahendra S
; APPLICANT: Kalyani, Anjali J
; TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
; FILE REFERENCE: T5530.CIP
; CURRENT APPLICATION NUMBER: US/10/911,374
; CURRENT APPLICATION NUMBER: US/09/109,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 14.4; DB 6; Length 34; 93.8%; Pred. No. 1.8e+04;
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Best Local Similarity
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US-10-053-645A-41
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## PRIOR FILING DATE: 1998-07-02
| PRIOR APPLICATION NUMBER: 08/909,435
| PRIOR APPLICATION NUMBER: 08/909,435
| PRIOR FILING DATE: 1997-07-04
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 14
| LENGTH: 19
| TYPE: DNA
| ORGANISM: Rattus norvegicus
| ORGANISM: Rattus norvegicus
| Ouery Match
| Best Local Similarity 84.2%; Score 14.2; DB 8; Length 19;
| Best Local Similarity 84.2%; Pred. No. 2.66+04;
| Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
| Organize Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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INFLAMMATORY DISEASES

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Query Match 100.0%; Score 24; DB 11; Length 24; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 24; Conservative 0; Mismatches 0; Indels
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FILLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039 70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: PatentIn version 3.2
LENGTH: 24
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Sequence 39338, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2005-03
NUMBER OF SEC ID NOS: 673904
SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 39338
LENGTH: 25
LENGTH: 25
LENGTH: 25
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Sequence 402269, Application US/10310914A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and ITTLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200. CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

SOFTWARE: Patent In version 3.3

SEQ ID NO 402269

LENGTH: 25
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85.7%; Pred. No. 4.5e+02;
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US-11-121-849-393938
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APPLICANT: Krieg, Arthur M. APPLICANT: Berg, Daniel J. TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

; Sequence 75, Application US/11127654; Publication No. US20050250726A1; GENERAL INFORMATION:

US-11-127-654-75

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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
TITLE OF INVENTION: Microarrays
FITLE OF INVENTION: Microarrays
FILLE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR PILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 235244
LENGTH: 25
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| Sequence 34498, Application US/10310914A
| Sequence 34498, Application US/20060003322A1
| GRNERAL INFORMATION:
| APPLICANT: Shiler, Kouzat
| TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %Sequence 84, Application US/11127654
; Sequence 84, Application US/11127654
; Sequence 84, Application No. US20050250726A1
; Sequence 84, Application No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TILLE OF INVENTION: INFLAMMATORY DISEASES
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039, 70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8; DB 11;
Pred. No. 6.6e+02;
0; Mismatches 2;
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                    US-11-121-849-235244/c
Sequence 225544/Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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Best Local Similarity 89.5%;
Matches 17; Conservative C
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Query Match
Best Local Similarity 85.07
Matches 17; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-235244
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ORGANISM: Human
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Sequence 2, Application US/11201322

Sequence 2, Application No. US2050272129A1

GENERAL INFORMATION:
GENERAL INFORMATION:
THE COLOR FOR INFORMATION:
TITLE OF INVENTION: THEREOF FOR IMPROVING BIOMASS PRODUCTION, SURVIVAL, LONGEVITY AN TITLE OF INVENTION: THEREOF FOR IMPROVING BIOMASS PRODUCTION, SURVIVAL, LONGEVITY AN TITLE OF INVENTION: THEREOF FOR IMPROVING BIOMASS PRODUCTION, SURVIVAL, LONGEVITY AN TITLE OF INVENTION: SISSTANCE OF FUNGI
FILE REFERENCE: 30302

CURRENT PILING DATE: 2005-08-11

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 2

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LENGTH: 30

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Sequence 11.1. Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 16; DB 11; Length 30; 100.0%; Pred. No. 5.4e+02; rive 0; Mismatches 0; Indels
                                                                                                           66.7%; Score 16; DB 7; Length 25; 70.8%; Pred. No. 5.4e+02; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Single strand DNA oligonucleotide US-11-201-322-2
                                                                                                                                                                                                                                                                                                                             1 GGGGTCCAGCGTGCGCCATGGGGG 24
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                       Query Match 66.7
Best Local Similarity 70.8
Matches 17; Conservative
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Matches 16; Conserv
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) ORGANISM: Human
US-10-310-914A-402269
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LENGTH: 22
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-201-322-2/c
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Sequence 46668, Application US/11121849
Sequence 46668, Application US/11121849
Sublication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE NEPERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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TITLE OF INVENTION: Microarrays
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TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: WIMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 05/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF EQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                 Indels
    78.3%; Pred. No. 1.4e+03;
tive 0; Mismatches 5;
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                                                                                                                                 2 GGGTCCAGCGTGCGCCATGGGGG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 gecencial description 3 secondescription 3 second
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                                                                                                                                                                                       25 GGCCCAGCGTCCACCTTGGTGG 3
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Best Local Similarity 78.3'
Matches 18; Conservative
                                            18; Conservative
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CORGANISM: Homo sapien
US-11-121-849-46869
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US-11-121-849-46868
    Best Local Similarity
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US-10-310-914A-45418/c
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US-11-121-849-46868
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Publication No. US20060003322A1
GENERAL INPORMATION:
GURRENT APPLICATION NUMBER:
GURRENT FILING DATE:
GOOD-12-06
NUMBER:
GOOD-13-06
SOFTWARE:
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded E TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
RATOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 23997
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%; Score 15; DB 11; I
100.0%; Pred. No. 1.4e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-84
PRIOR FILING DATE: 2002-03-29
PRIOR PEDLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SEQ ID NO 84
LENGTH: 16
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CORGANISM: Homo sapien
US-11-121-849-23997
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US-10-310-914A-94891/c
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US-11-121-849-23997/c
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ORGANISM: Human
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US-10-310-914A-650086/c
US-10-310-914A-650086/c
Sequence 650086, Application US/10310914A
Sequence 650086, Application US/20322A1
GENERAL INFORMATION.
GENERAL INFORMATION.
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TITLE REFERENCE: 06087-0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 650086
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$\text{Sequence 895311}, Application US/10310914A}$
$\text{Sequence 895311}, Application US/10310914A}$
$\text{Publication No. US20060003322A1}$
$\text{GENERAL INFORMATION:}$
$\text{GENERAL INFORMATION:}$
$\text{APPLICANT: Shiler, Kvuzat}$
$\text{APPLICANT: Shiler, Kvuzat}$
$\text{TITLE OF INVENTION: Uses thereof}$
$\text{TITLE OF INVENTION: Uses thereof}$
$\text{TITLE OF INVENTION: US/10.10,914A}$
$\text{CURRENT APPLICATION VMBER: US/10,310,914A}$
$\text{CURRENT FILING DATE: 2002-12-06}$
$\text{NUMBER OF SEQ ID NOS: 1388402}$
$\text{SOFTMARE: PatentIn version 3.3}$
$\text{SEQ ID NO 895311}$
$\text{LENGTH: 26}$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.6; DB 7; Length 26; Pred. No. 2.1e+03;
Query Match 60.8%; Score 14.6; DB 7; Length 24; Best Local Similarity 71.4%; Pred. No. 2.1e+93; Matches 15; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
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                                                                                                                   4 GTCCAGCGTGCGCCATGGGGG 24
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Best Local Similarity 81.0%;
Matches 17; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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US-10-310-914A-650086
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US-10-310-914A-895311
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Sequence 38276, Application US/10310914A
Sequence 38276, Application US/2066003322A1
Sequence 38276, Application No. US2066003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
SALILAY: Bentwich, Isaac
APPLICANT: Bentwich, Rvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                              APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUSOI.
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 45418
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Pred. No. 2.18+03;
0; Mismatches 4; Indels
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Best Local Similarity 81.0%;
Matches 17; Conservative
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                          APPLICANT: Bentwich, Isaac
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Best Local Similarity
Matches 15; Conserv
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US-10-310-914A-402274
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US-10-310-914A-38276
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; ORGANISM: Human
US-10-310-914A-38276
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ORGANISM: Human
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LENGTH: 21
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RESULT 21
US-10-658-947-14
US-10-658-947-14; Application US/1065894/
; Sequence 14. No. US2005025153A1
; Publication No. US2005025153A1
; GENERAL INFORMATION:
; APPLICANT: Inex Pharmaceuticals Inc.
; APPLICANT: Inex Pharmaceuticals Inc.
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
; Lipid Vesicles
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                                                                                                                                                                                           Length 18;
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                                                                                                                                                                      Score 14; DB 7; Len
Pred. No. 3.7e+03;
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ZIP: 80435
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.3%; Score 14; DB 7; Lk Best Local Similarity 100.0%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 0;
                                                                                                   FEATURE:
; OTHER INFORMATION: oligonucleotide-- G3139 Genta
US-10-918-638-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/895,480
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/ACENT INFORMATION:
NAME: «Unknown»
                                                                                                                                                                                        Query Match
58.3%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 3.7
Matches 14; Conservative 0; Mismatches
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OPERATING SYSTEM: DOS 5.0
SOFTWARE: WOLD POTFOL
SOFTWARE: WOLD PATA:
APPLICATION NUMBER: US/10/658,947
FILING DATE: 09-58p-2003
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedahl & Larson LLP
STREET: PO Box 5068
CITY: Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-658-947-14
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MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
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STRANDEDNESS: single
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                SEQ ID NO 24
LENGTH: 18
TYPE: DNA
ORGANISM: artificial sequence
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200,-CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ PURARE: PatentIn version 3.3
SEQ ID NO 721320
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Publication No. US20050249663A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Copharos
TITLE OF INVENTION: AND
TITLE OF INVENTION: AND
TITLE OF INVENTION: AND
CURRENT PEPLICATION NUMBER: US/10/918,638
CURRENT FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: US/10/246,300
PRIOR FILING DATE: 2002-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%; Score 14; DB 6; Length 18; 100.0%; Pred. No. 3.7e+03; Pred. o; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10994213
Publication No. US20060019911A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.3
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Best Local Similarity
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-721320
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US-11-127-654-1
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US-10-619-279-45
Sequence 45, Application US/10619279
SEQUENCE 100917030:
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: 0103/7023/HCL
CURRENT FILING DATE: 1039/7023/HCL
SPRIOR APPLICATION NUMBER: US 08/960,774
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
SOFTWARE OF SEQ ID NOS: 123
SOFTWARE FEASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%; Score 14; DB 7; Length 18; 100.0%; Pred. No. 3.7e+03; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-619-279-45
                                                                            Sequence 6, Application US/10469561
; Sequence 6, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Blis
TITLE NET FILLANT: Alan Peter Lewis
; TITLE REPERENCE: P64355USW
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT FILLIG DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; IRNOFEL 16
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100.0%; Pre
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ORGANISM: Artificial Sequence
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5 CCAGCGTGCGCCAT 18
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hes 14; Conservative
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ORGANISM: unknown
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LENGTH: 18
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## Sequence 1, Application US/11127654

## Sequence 1, Application US/11127654

## Sequence 1, Application No. US20050250726A1

## Sequence 1, Application No. US20050250726A1

## Septicant: Krieg, Arthur M.

## APPLICANT: Krieg, Arthur M.

## APPLICANT: Berg, Daniel J.

## TITLE OF INVENTION: INFLAMMATORY DISEASES

## TITLE OF INVENTION: UNMBER: US/11/127,654

## CURRENT FILING DATE: 2005-05-12

## PRIOR PPLICATION NUMBER: US 60/279,642

## PRIOR APPLICATION NUMBER: US 60/279,642

## PRIOR APPLICATION NUMBER: US 60/279,642

## PRIOR PILING DATE: 2001-03-29

## PRIOR PILING DATE: 2001-03-29
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APPLICANT: Kline, Joel N.
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TTITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7048 (AMS)
CURRENT PAPLICATION NUMBER: US/10/435,656
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR PILING DATE: 1994-07-15
PRIOR PILING DATE: 1995-02-07
PRIOR FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 18
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ilarity 100.0%; Pred. No. 3.7e+03;
Conservative 0; Mismatches 0;
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Sequence 55, Application US/10435656 Publication No. US20050277604A1 GENERAL INFORMATION:
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                                                                                                                           APPLICANT: Krieg, Arthur M.
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Best Local Similarity
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RESULT 26

RESULT 24

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Gaps
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APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
CURRENT APPLICATION NUMBER: US/11/031,460
FRIOR FILING DATE: 2005-01-07
FRIOR PILING DATE: 1994-07-15
FRIOR APPLICATION NUMBER: US 08/276,358
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR PILING DATE: 1995-02-07
FRIOR PILING DATE: 1995-02-07
FRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
                                        APPLICANT: Klinma, Dennis
APPLICANT: Klinma, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7048 (4MS)
CURRENT APPLICATION NUMBER: US/11/134,918
FRIOR APPLICATION NUMBER: US/09/818,918
PRIOR PILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 1994-07-15
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
PRIOR PLING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/738,652
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Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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APPLICANT: Krieg, Arthur M.
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Best Local Similarity
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     Sequence 85, Application US/11127654

publication No. US20050250726A1

GENERAL INPORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: INFLAMMATORY DISEASES

FILE REFERENCE: C1039.70060US01

CURRENT APPLICATION NUMBER: US/11/127,654

CURRENT APPLICATION NUMBER: US/11/127,654

PRIOR FILING DATE: 2005-05-12

PRIOR FILING DATE: 2002-03-29

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040

SOFTWARE: PACENTION NUMBER: US 60/279,642

NUMBER OF SEQ ID NOS: 1040

SEQ ID NOS: 1040

SEQ ID NO 85

LENGTH: 18
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Publication No. US20050261225A1

Publication No. US20050261225A1

APPLICANT: Stein, Cy A

APPLICANT: Benimetskaya, Lyuba

APPLICANT: Guzzo-Pernell, Nancy

TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR

TITLE OF INVENTION: PRC-PROTEIN EXPRESSION IN CELLS

FILE REFERENCE: 0575/63293

CURRENT APPLICATION WUMBER: US/11/081,140

CURRENT PILING DATE: 2005-03-15

PRIOR FILING DATE: 2001-11-02
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Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE
US-11-081-140-6
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US-11-134-918-55
; Sequence 55, Application US/11134918
; Publication No. US20050267064A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial sequence
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SOFTWARE: Patentin version 3.1
SEQ ID NO L
LENGTH: 18
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Best Local Similarity 100.
Matches 14; Conservative
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US-11-127-654-85
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Segurace 132, Application US/11099683
Sequence 132, Application US/11099683
Fublication No. US2006019916A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur
APPLICANT: Vollmer, Jose
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES
FILE REPERENCE: C1037.700470801
FILIS REPERENCE: C1037.700470801
CURRENT APPLICATION NUMBER: US/11/099,683
CURRENT FILING DATE: 2005-04-04
PRIOR FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.3
SEQ ID NO 132
LENGTH: 18
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; Sequence 8, Application US/10994213
; Publication No. US20060019911A1
; GENERAL INFORMATION:
; APPLICANT: Paplicov, Mikhail, I.
; TITLE OF INVENTION: DRUG-CARRIER
; TITLE OF INVENTION: USE THEREOF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERRENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/09/634,213
CURRENT FILING DATE: 2004-11-19
; PRIOR PILING DATE: 2006-09-09
; PRIOR PILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
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58.3%; Score 14; DB 11; I

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 14; Conservative 0; Mismatches 0;
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CTHER INFORMATION: c indicates an RNA base US-10-994-213-8
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US-10-994-213-9/c
'Sequence 9, Application US/10994213
'Publication No. US20060019911A1
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial sequence
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US-10-994-213-8
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APPLICANT: Krieg, Arthur
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: IMMUDATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES
TITLE OF INVENTION: IMMUDATION: MACHING IL-10 RESPONSES
CURRENT APPLICATION NUMBER: US/11/099,683
CURRENT FILING DATE: 2005-04-04
PRIOR PILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.3
SEQ ID NO 131
LENGTH: 18
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                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kineg, Archur M.
APPLICANT: Kline, Joel N.
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Schibberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7048 (AMS)
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US/09/818,918
PRIOR APPLICATION NUMBER: US/09/818,918
PRIOR PILING DATE: 1994-07-15
PRIOR FILING DATE: 1994-07-15
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1996-10-30
PRIOR FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 56
SOFWWARE: FastSEQ for Windows Version 3.0
LENGTH: 18
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58.3%; Score 14; DB 11; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 14; Conservative 0; Mismatches 0; Indels
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                                 US-11-067-587-55
; Sequence 55. Application US/11067587
; Publication No. US2060003955A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 14; Conservative
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Page 11

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof; TITLE OF INVENTION: uses thereof; FILE REFERENCE: 06087.0200.CPUS01; CURRENT APPLICATION NUMBER: US/10/310,914A; CURRENT FILING DATE: 2002-12-06; NUMBER OF SEQ ID NOS: 1388402; SOFTWARE: Patentin version 3.3; SOFTWARE: 220 ID NO 100840
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; Sequence 2, Application US/10994213
; Publication No. US20060019911A1
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: USE THEREOF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 0318.1003-001
; CURRENT APPLICATION NUMBER: US/10/994,213
; CURRENT PILING DATE: 2004-11-19
; PRIOR PILING DATE: 2000-08-09
; PRIOR PILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/10994213; Sequence 1, Application No. US2060019911A1; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail, I.; TITLE OF INVENTION: USE THEREOF; TITLE OF INVENTION: USE THEREOF; FILE REFERENCE: 0838.1003-001; CURRENT APPLICATION NUMBER: US/09/634,213; CURRENT FILING DATE: 2004-11-19; PRIOR APPLICATION NUMBER: US/09/634,320; PRIOR PELLING DATE: 2000-08-09; PRIOR FILING DATE: 1099-08-09; PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 22;
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Pred. No. 3.7e+03;
0; Mismatches 5;
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100.0%; Pred. No. 3.7e+03;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 23
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ilarity 77.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Human
US-10-310-914A-100840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 38
US-10-994-213-2/c
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Sequence 81, Application US/11127654

Publication No. US20050250726A1

Sequence 81, Application WS/11127654

Publication No. US20050250726A1

GENERAL INFORMATION:

APPLICANT: Edging, Arthur M.

TITLE OF INVENTION: INFLAMMATORY DISEASES

FILE REFERENCE: C1039-7006000501

CURRENT FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 60/279,642

NUMBER OF SEQ ID NOS: 1040

SOFTWARE: PatentIn version 3.2

SEQ ID NO 91

TEMBER OF SEQ ID NOS: 1040

SEQ ID NO 91
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                                                                                                                                                                APPLICANT: Papisov, Mikhail, I.
TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 0838.1003-001
CURRENT APPLICATION NUMBER: US/09/634,213
CURRENT FILING DATE: 2004-11.19
PRIOR APPLICATION NUMBER: US/09/634,320
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NOS: 1200-08-09
LEWARD 10 NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 14; DB 6; Length 19; 100.0%; Pred. No. 3.7e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%; Score 14; DB 11; I 100.0%; Pred. No. 3.7e+03; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: c indicates an RNA base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-310-914A-100840/c
; Sequence 100840, Application US/10310914A
; Publication No. US20060003322A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CCAGCGTGCGCCAT 19
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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Sequence 46867, Application US/11121849
publication No. US20050272080A1
publication No. Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
PILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR FILING DATE: 2005-03
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 46867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46870, Application US/11121849
Sequence 46870, Application US/11121849
Publication No. US20050272080A1
Sequence 46870, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT PILION DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILIOR DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 46870
LENGTH: 25
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; APPLICANT: Bentwich, Isaac; APPLICANT: Shiler, Kvuzat; APPLICANT: Shiler, Kvuzat; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 14; DB 11; Length 25; 77.3%; Pred. No. 3.7e+03; Live 0; Mismatches 5; Indels
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                                                     22 GGGGTCAGGTGTGGGACATGGG 1
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Best Local Similarity 77.3
Matches 17; Conservative
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Best Local Similarity 77.3
Matches 17; Conservative
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CORGANISM: Homo sapien
US-11-121-849-46867
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US-10-310-914A-1042200/c
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US-11-121-849-46870
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION:
BIOINFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT PELICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 903934

LENGTH: 23
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US-10-914A-989919/C

US-10-914A-989991/C

US-10-914A-98991/C

US-10-914A-98
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                                                                                                                                                                                                                                                                                                                                                     Length 23;
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                                                                                                                                                                                                                                                                                                                                                     58.3%; Score 14; DB 6; L. 100.0%; Pred. No. 3.7e+03; tive 0; Mismatches 0;
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Pred. No. 3.7e+03;
3; Mismatches 5;
                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                            OTHER INFORMATION: t = amino modified T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GCUCCAGCCUGGGGCAUGAGGG 23
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                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 14; Conservi
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US-10-310-914A-903934
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ORGANISM: Human
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                                           SEQ ID NO 2
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                                                                                                                                                                                                                                 FEATURE:
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Sequence 77551, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Rvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 775551
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1384402
SOFTWARE: Patentin version 3.3
SEQ ID NO 321695
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                                                    57.5%; Score 13.8; DB 7;
88.2%; Pred. No. 4.5e+03;
                                                                                                    Mismatches
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                                               Query Match
Best Local Similarity 88.2'
Matches 15, Conservative
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          US-10-310-914A-906465
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ORGANISM: Human
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ORGANISM: Human
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APPLICANT: Benevich, Isaac
APPLICANT: Biler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REPRENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 906465
LENGTH: 18
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## Sequence 19743, Application US/10939294A

## Publication No. US20S0266417A1

## Publication No. US20S0266417A1

## APPLICANT: Barany, Francis

## APPLICANT: Purmer, Daniel

## APPLICANT: Pingle, Manesh

## APPLICANT: Pingle (TRP D-2995-02)

## CURRENT APPLICATION NUMBER: US/10/939,294A

## CURRENT PILING DATE: 2004-09-10

## RIOR PILING DATE: 2003-09-12

## NUMBER OF SEQ ID NOS: 38895

## SOFTWARE: Patentin version 3.3

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TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1042200
LENGTH: 26
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ORGANISM: Human
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ORGANISM: Human
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Gaps ; 0

56.7%; Score 13.6; DB 7; Length 20; 70.0%; Pred. No. 5.5e+03; ive 2; Mismatches 4; Indels

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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 222305
LENGTH: 20
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Matches 14; Conservative
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ORGANISM: Human
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        APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded :
TITLE OF INVENTION: Microarrays
TILE REPERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 330122
LENGTH: 25
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APPLICANT: KAZUJABU OSATOH
APPLICANT: KAZUJABU NAKAMURA
APPLICANT: KAZUJABU UNKAMURA
APPLICANT: KAZUJABU UNKAMURA
APPLICANT: TOODIAGE SHINKAWA
APPLICANT: NOCKO YAMASKI
APPLICATION NUMBER: US/11/131,212
CURRENT APPLICATION NUMBER: US/09/971,773
PRIOR APPLICATION NUMBER: US/09/971,773
PRIOR FILING DATE: 2002-10-06
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR PILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 40
LENGTH: 45
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Pred. No. 4.4e+03;
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US-10-310-914A-222305
; Sequence 22305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Matches 15, Conservative
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CORGANISM: Homo sapien
US-11-121-849-330122
GENERAL INFORMATION
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US-11-131-212-40/c
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CQ846419
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AX135389 Sequence
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AR038395 Sequence
AR038395 Sequence
AR178131 Sequence
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                    GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 300 summaries
                                                                              nucleic search, using sw model
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38
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seg length: 50
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AR351569 Sequence AX492879 Sequence AX135021 Sequence AX068147 Sequence AR275619 Sequence	AR278099 Sequence AR409070 Sequence	AR616918 Sequence AX082449 Sequence	AX084800 Sequence	BD176640 Promoter.	AX248800 Sequence BD161889 K1 gene.	BD161898 Nonhuman	Seque	Arsussts nomo sapi AX686396 Sequence	BD161877 K1 gene.	AX306642 Sequence	A79823 Sequence 3 AR003558 Sequence	AR041144 Sequence	AR075338 Sequence	AR119903 Sequence	AR154200 Sequence	AR169478 Sequence	ARI7557 Sequence	BD134764 Thermoana	BD190485 AMPLIFICA	BD191470 Nucleic a	BD240946 Self-Cont BD249410 Electroni	125354 Sequence 3	AR195022 Sequence AR352409 Sequence	AR352438 Sequence	AR430589 Sequence	AR642//2 Sequence AR648091 Sequence	AX135666 Sequence	Z27179 H.sapiens r AR172768 Sequence	AR178712 Sequence	AR181283 Sequence	AR231912 Sequence	AR343387 Sequence	AR391176 Sequence	AR431619 Sequence	AR290084 Sequence	CO006807 Sequence	CQ009108 Sequence	L39584 Homo sapien	BD124012 Neuroprot	AR404019 Sequence	CS048086 Sequence	AX650583 Sequence	AX650584 Sequence	AX650585 Sequence	AX590776 Sequence	M23371 Mus musculu	AX766988 Sequence	AROZIOI4 Sequence ARO43429 Sequence	AR062344 Sequence
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VERSION AR088703.1 GI:10015467  KEYWORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 38) AUTHORS Nabel, G.Jan. TITLE Methods and compositions for treatment of diseases JOURNAL Patent: US 5990090-A 2 23-NOV-1999; FEATURES 1. 38 /organism="unknown" /mol_type="unassigned DNA"	Ouery Match 100.0%; Score 38; DB 6; Length 38;  Best Local Similarity 100.0%; Pred. No. 2.3e-05;  Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 GGGGACTTTCCGCTGGGGACTTTCC 38	RESULT 2 AX103956 LOCUS LOCUS LOCUS DEFINITION Sequence 148 from Patent W00122972. ACCESSION AX103956 VERSION AX103956. KEYWORD SOURCE	other sequence of the sequence	ORIGIN  Query Match  Query Match  Best Local Similarity 100.0%; Score 38; DB 6; Length 38;  Best Local Similarity 100.0%; Pred. No. 2.3e-05;  Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 GGGACTTTCCGCTGGGACTTTCCAGGGGACTTTCC 38	RESULT 3 AX355389 LOCUS DEPINITION Sequence 417 from Patent W00197843. ACCESSION AX555389.1 GI:18620057 KEYWORDS SOURCE S	other sequiple of the sequiple
AR183803 Sequence AR368186 Sequence B10784 PCR primer I38420 Sequence 5 AR053668 Sequence CQ918211 Sequence AR258603 Sequence AX513944 Sequence AX513944 Sequence AX513945 Sequence AX51357675 Sequence AX157675 Sequence AR157676 Sequence AR157676 Sequence SR157676 Sequence BD268660 Isolation	A43615 Sequence 5 AR288379 Sequence AR289545 Sequence AR290662 Sequence AR214693 Sequence AR2120586 Sequence CS120586 Sequence	AX1315359 Sequence AX233963 Sequence BD266036 Universal AX29330 Sequence AX23970 Sequence AX279570 Sequence AX279571 Sequence AX203132 Sequence AR108167 Sequence AR260321 Sequence CQ637928 Sequence	182400 Sequence 48 AR001104 Sequence 48 AR010134 Sequence AR401634 Sequence AR401634 Sequence AR60391 Sequence AR078082 Sequence AR078082 Sequence B3563 Detection of I76164 Sequence	AR61747 Sequence AR61747 Sequence L32494 Human (clon 182405 Sequence 55 182405 Sequence 56 A83621 Sequence 50 AR206162 Sequence AR595445 Sequence AX517555 Sequence AX517555 Sequence	182397 Sequence 44 AX538890 Sequence AX538891 Sequence S80775 gamma delta AX241782 Sequence CQ003473 Sequence CQ00574 Sequence	linear PAT 07-SEP-2000
33 6 AR183803 33 6 AR368186 37 6 E10784 38 6 138420 40 6 AR053668 40 6 AR258603 41 6 AR258603 41 6 AR364432 41 6 AR513944 41 6 AR51294 45 6 AR157675 45 6 AR157675 46 6 BD26866	ουυυυυυ	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	• • • • • • • • • • • • • • •	<b>υ υ υ υ υ υ υ υ υ υ υ υ</b> υ	<b>υνυυ</b> ωυυυ	ALIGNMENTS 38 bp DNA from patent US 5990090.
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RESULT 1
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Unknown...
Unclassified.

1 (bases 1 to 46)
Neininger, A.M.
Neininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a Sequence-specific detection of nybrids from non-perfect hybrids
hybrids from non-perfect hybrids
Patent: US 5871902-A 28 16-FEB-1999;
Location/Qualifiers
Location/Qualifiers
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Unclassified.
1 (bases 1 to 39)
Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and Pepinsky,R.Blake.
Tar-derived transport polypeptide conjugates
Patent: US 5747641-A 43 05-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.9%; Score 30; DB 6; Length 39; Best Local Similarity 86.8%; Pred. No. 0.061; Matches 33; Conservative 0; Mismatches 5; Indels
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 94.1%; Pred. No. 0.028;
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                                                     1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACT
                 0; Mismatches
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Sequence 28 from patent US 5871902.
AR035456
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 94.1
Matches 32; Conservative
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nes 32; Conserv
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KEYWORDS
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VERSION
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TITLE
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Weininger,S. and Weininger,A.M.
Weininger,S. and Weininger,A.M.
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 29 16-FEB-1999;
Location/Qualifiers
 1. .38
/organism="synthetic construct"
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide
/note="Synthetic oligonucleotide
chimeric phosphorcthioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
                                                                                                                                                                                          Gaps
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                                                                                                                                                       ch 100.0%; Score 38; DB 6; Length 38; Similarity 100.0%; Pred. No. 2.3e-05; 38; Conservative 0; Mismatches 0; Indels
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100.0%; Score 38; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 38; Conservative 0; Mismatches 0; Indels
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    .38
    forganism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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synthetic construct
other sequences; artificial sequences.
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Sequence 148 from Patent WO02053141.
AX547009
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AR035457
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/mol_type="unassigned DNA"
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                                                                                                                                                                        Local Similarity
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El (bases 1 to 39)

(S Frankel, A., Pabo,C., Barsoum,J.G., Fawell,S.E. and Pepinsky, R. Blake.

Tat-derived transport polypeptides

Tat-derived transport polypeptides

Location/Qualifiers
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and Pepinsky, R. Blake.
Tat-derived transport polypeptides
Patent: US 6316003-A 44 13-NOV-2001;
Location/Qualifiers
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78.9%; Score 30; DB 6; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.061;
Matches 33; Conservative 0; Mismatches 5; Indels
                                                    Score 30; DB 6; Length 39;
Pred. No. 0.061;
0; Mismatches 5; Indels
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 44 from patent US 6316003.
AR178132
/organism="unknown"
/mol_type="unassigned DNA"
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AR178131.1 GI:17921024
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                                                         Query Match 78.9%;
Best Local Similarity 86.8%;
Matches 33; Conservative
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Best Local Similarity 86.8<sup>†</sup>
Matches 33, Conservative
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AR178132/c
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AR178131
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and
Pepinsky, R. Blake.
Tat-derived transport polypeptides and fusion proteins
Patent: US 5804604-A 43 08-SEP-1998;
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and
Pepinsky, R. Blake.
Tat-derived transport polypeptides and fusion proteins
Patent: US 8804604-A 44 08-SEP-1998;
Location/Qualifiers
                                                    M. Unclassified.

Unclassified.

I (bases 1 to 39)

S Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and Pepinsky, R. Blake.

Tat-derived transport polypeptide conjugates

AL patent: US 5747641-A 44 05-MAY-1998;

Location/Qualifiers
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Pred. No. 0.061;
0; Mismatches 5; Indels
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Pred. No. 0.061;
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/mol_type="unassigned DNA"
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Sequence 43 from patent US 5804604.
AR038395
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/wol_type="unassigned DNA"
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                  GI:3966065
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86.8%;
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Best Local Similarity 86.8
Matches 33; Conservative
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AR038396/c
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Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and
Pepinsky,R.Blake.
Nucleic acid conjugates of tat-derived transport polypeptides
Patent: US 56706174 43 23-SEP-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 39)

Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and
Pepinsky,R.Blake.
Nucleic acid conjugates of tat-derived transport polypeptides
Patent: US 5670617-A 44 23-SEP-1997;
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and Pepinsky, R.Blake.
Fusion protein toomprising tat-derived transport moiety Patent: US 5674980-A 43 07-0CT-1997;
Location/Qualifiers
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Pred. No. 0.061;
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Pred. No. 0.061;
0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                   /organism="unknown"
/wol_type="unassigned DNA"
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Sequence 44 from patent US 5670617.
166590
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 43 from patent US 5674980.
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Best Local Similarity 86.8%;
Matches 33; Conservative
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Best Local Similarity 86.8%;
Matches 33; Conservative
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and
Pepinsky, R. Blake.
Nucleic acids encoding and methods of making tat-derived transport polypeptides
Patent: US 5652122-A 44 29-JUL-1997;
                                                                                                                                                               I (Dasses 1 to 39)
Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and
Pepinsky,R.Blake.
Nuclea encoding and methods of making tat-derived transport
polypeptides
Patent: US 5652122-A 43 29-JUL-1997;
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Sequence 44 from patent US 5652122.
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IS8472.1 GI:2477710
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/organism="unknown"
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Sequence 43 from patent US 5670617.
166589
                                 39 bp
Sequence 43 from patent US 5652122.
IS8471

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/organism="unknown"
/mol_type="unassigned DNA"

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PAT 20-DEC-2002

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Arntzen, C.J., Blake, M.E., Gutterman, J.U., Hoffmann, J.J., Jayatilake, G.S. and Bailey, D.T. Triterpene compositions and methods for use thereof Patent: US 6444233-A 9 03-SEP-2002; Research Development Foundation; Carson City, NV Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.4%; Score 29.8; DB 6; Length 44; Best Local Similarity 93.9%; Pred. No. 0.076; Matches 31; Conservative 0; Mismatches 2; Indels
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Haridas,V. and Gutterman,J.U.
Triterpene compositions and methods for use thereof
Patent: US 6689398-A 9 10-FEB-2004;
Research Development Foundation; Carson, NV
Location/Qualifiers
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Best Local Similarity 93.9%; Pred. No. 0.076;
Matches 31; Conservative 0; Mismatches
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Sequence 9 from patent US 6689398.
AR473523. GI:42711810
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PF 19-MAY-1999 JP 2000549243
PR 19-MAY-1998 US 60/085997,03-SEP-1998 US 60/099066 PI
CHARLES J ARNTZEN,MARY BLAKE TRACEY,JORDAN U GUTTERMAN,JOSEPH
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Arntzen,C.J., Tracey,M.B., Gutterman,J.U., Hoffmann,J.J.,
Bailey,D.T. and Jayatilake,G.S.
Triterpen compositions and methods for use thereof
Patent: JP 2002515430-A 9 28-MAY-2002,
RESEARCH DEVELOPMENT FOUNDATION
ON Artificial Sequence
PN JP 2002515430-A/9
PD 28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description of Artificial Sequence:SYNTHETIC PRIMER Location/Qualifiers
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                                                                                                                                                                                                                                               Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and Pepinsky, R.Blake.
Fusion protein comprising tat-derived transport moiety Patent: US 5674980-A 44 07-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism='Artificial Sequence'
Location/Qualifiers
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Pred. No. 0.061;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences, artificial sequences.
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Sequence 44 from patent US 5674980.
168237
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/mol_type="unassigned DNA"
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Best Local Similarity 86.8%;
Matches 33; Conservative
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Weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 23 16-FEB-1999;
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Weininger, S. and Weininger, A.M.
Weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids
Patent: US S871902-A 20 16-FEB-1999;
Location/Qualifiers
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hybrids from non-perfect hybrids
Patent: US 5871902-A 19 16-FEB-1999;
Location/Qualifiers
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                                                1. .45
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                      45 bp
Sequence 23 from patent US 5871902.
AR035451
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 20 from patent US 5871902.
AR035448
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity
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AR035451
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AR035448
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Weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
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Aggarwal, B.B. and Darnay, B.G.
Tumor necrosis factor receptor-I-associated protein kinase and methods for its use
Patent: US 5856161-A 12 05-JAN-1999;
Location/Qualifiers
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Arntzen, C.J. and Gutterman, J.U.
Arnterpene compositions and methods for use thereof
Patent: US 6746696-A 9 08-JUN-2004;
Research Development Foundation; Carson City, NV
Location/Qualifiers
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                  linear
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Pred. No. 0.076;
0; Mismatches 2;
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Sequence 12 from patent US 5856161.
AR027239
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Sequence 19 from patent US 5871902.
AR035447
AR035447.1 GI:5952115
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                AR542759 44 bp
Sequence 9 from patent US 6746696.
AR542759
                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
                                                                                                                                                                                                                                                           /organism="unknown"
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                                                               AR542759.1 GI:53935323
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Best Local Similarity 93.9%;
Matches 31; Conservative
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AR027239
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PAT 29-SEP-1999
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Weininger,S. and Weininger,A.M.
Sequence-specific detection of nucleic acid hybrids using a
Sequence-specific detection of nucleic acid hybrids molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 27 16-FEB-1999;
Location/Qualifiers
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Georgopoulos, K.
Ikaros: A T cell pathway regulatory gene
Patent: US 6228611-A 142 08-MAY-2001;
Location/Qualifiers
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Georgopoulos,K.
Ikaros polypeptides
Patent: US 5824770-A 142 20-OCT-1998;
Location/Qualifiers
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Pred. No. 0.2;
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Sequence 142 from patent US 5824770.
AR049839
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Sequence 142 from patent US 6228611.
AR149733 GI:15114324
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
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Best Local Similarity 93.8%;
Matches 30; Conservative 0
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weininger, S. and Weininger, A.M.

Sequence-specific detection of nucleic acid hybrids using a

BNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids

Patent: US 5871902-A 21 16-PEB-1999;

Location/Qualifiers
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1 (bases 1 to 46)
Weininger,S. and Weininger,A.M.
Weininger,S. and weininger,A.M.
Squence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 22 16-FEB-1999;
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                                                                                                                         46 bp | 1
Sequence 21 from patent US 5871902.
AR035449
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Sequence 27 from patent US 5871902.
AR035455
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Sequence 22 from patent US 5871902.
AR035450. GI:5952118
                                   7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
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AR035450
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BD081630 33 bp DNA linear PAT 27-AUG-2002 Inhibition of human immunodeficiency virus (HIV-1) replication. BD081630
             PAT 18-DEC-2003
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                                                                                                                      Unclassified.

1 (bases 1 to 32)
Traichlis.P.N.
Tpl2 transgenic knockout mice
Tpl2 transgenic knockout Tpl2 transgenic Knockout Tpl2 Tpl2 Transgenic Knockout Tpl2 Tpl2 Tpl3;
Thomas Jefferson University; Philadelphia, PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (barell to 32)
Tsichlis P.N.
Tpl2 transgenic knockout mice
Patent: US 6660906-A 11 09-DEC-2003;
Thomas Jefferson University; Philadelphia, PA;
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synthetic construct
other sequences, artificial sequences.
( Dases 1 to 3)
Suhadolnik, R.J., Adelson, M.E. and Iacono, K.T.
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Sequence 11 from patent US 6660906.
AR438118
             AR438116 32 bp
Sequence 9 from patent US 6660906.
AR438116
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    .32
/organism="unknown"
/mol_type="genomic DNA"

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/organism="unknown"
/mol_type="genomic DNA"
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                                                            AR438116.1 GI:40204578
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Unclassified.
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AR438118
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BD081630
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AR438116
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Weininger,S. and Weininger,A.M.
Sequence-specific detection of nucleic acid hybrids using a
Sequence-specific detection of season of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 38 16-FEB-1999;
Location/Qualifiers
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1 (bases 1 to 36)
Georgopoulos,K.
Georgopoulos,K.
Isolated antibody that binds to an Ikaros polypeptide Patent: US 6630141-A 142 07-OCT-2003;
The General Hospital Corporation; Boston, MA
                          Query Match 75.8%; Score 28.8; DB 6; Length 36; Best Local Similarity 93.8%; Pred. No. 0.2; Matches 30; Conservative 0; Mismatches 2; Indels
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                                                                                                              GGGACTTTCCGCTGGGGACTTTCCAGGGAGGC 35
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                                                                                            2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
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1 Similarity 93.8%; Pred. No. 0.2;
30; Conservative 0; Mismatches
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Seguence 142 from patent US 6630141.
AR404853
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/wol_type="unassigned DNA"
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Sequence 38 from patent US 5871902.
AR035466
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/mol_type="mRNA"
                                                                                                                                                                                                                                                       AR404853.1 GI:40153580
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Best Local Similarity 96.7%;
Matches 29; Conservative
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PAT 08-OCT-2004
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                         Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                         Hominidae, Homo.

1 (bases 1 to 35)

Fujihara, S.M. and Nadler, S.G.

Intracellular targeted delivery of compounds by 70 kD heat shock Patent: JP 2002530426-A 1 17-SEP-2002;

BRISTOL MYERS SQUIBE CO
OS Homo sapiens (human)

PN JP 2002530426-A/I

PP 17-NOV-1999 JP 2000583940

PR 24-NOV-1999 US 60/109872

PI SHERI M FUJIHARA, STEVEN G NADLER
                                                                                                                                                                                                                                                                                                                        A61P19/02,
C A61P29/00,A61P29/00,A61P35/00,C12N15/09,A61K37/02,C12N15/00
C A61P29/00,A61P29/00,A61P35/00,C12N15/09,A61K37/02,C12N15/00
Intracellular targeted delivery of compounds by 70 kD heat CC shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 35)
Fujihara, S.M. and Nadler, S.G.
Intracellular targeted delivery of compounds by 70 kD heat shock
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/organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.7%; Score 28; DB 6; Length 35; 100.0%; Pred. No. 0.44; ive 0; Mismatches 0; Indels
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Bristol-Myers Squibb Company; Princeton,
Location/Qualifiers
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Sequence 4 from patent US 6730302.
AR532727
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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    .35
    /organism="unknown"
    /mol_type="genomic DNA"

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     Homo sapiens (human)
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Best Local Similarity 100.
Matches 28; Conservative
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AR532727
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Intracellular targeted delivery of compounds by 70 kD heat shock
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PC
C12N1/15,C12N1/19,C12N1/21,C12N5/10//A61K35/76,C12N15/00,C12N5/ PC
Inhibition of human immunodeficiency virus (HIV-1) replication Defence: JP 2001520017-A 4 30-OCT-2001;
TEMPLE UNIVERSITY OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION OS Artificial Sequence
D Artificial Sequence
D 30-OCT-2001
PP 15-OCT-2001
PP 15-OCT-1998 JP 2000516047
PP 16-OCT-1997 US 66,061984
PI 16-OCT-197 US 66,061984
PI 16-OCT-197 US 67,061984
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                                                                                                                                                                                CC Description of Artificial Sequence: sense probe oligonucleotide CC corresponding to NF-kappa beta him:
FT Source
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/organism='Artificial Sequence'
Location/Qualifiers
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    .33
    forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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/organism="unknown"
/wol_type="unassigned DNA"
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ACTIVITION OF NF-kB PRECURSOR
Patent: WO 8908147-A 2 08-SEP-1989;
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BD249738
BD249738.1 GI:33059508
JP 2002530426-A/1.
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PAT 29-SEP-1999
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Weininger, S. and Weininger, A.M.
Weining molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids
Patent: US 5871902-A 24 16-FEB-1999;
Location/Qualifiers

    .35
/organism="synthetic construct"
/mol type="unassigned DNA"
/db zref="taxon:32650"
/noTe="Oligonucleotide probe for NF-KB (antisense)"

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9
Lipton, J. and Catania, A.
A uro-genital condition treatment system
Patent: Ep 1433485-A 10 30-JUN-2004;
Zengen, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 24 from patent US 5871902.
AR035452
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Best Local Similarity 96.6%;
Matches 28; Conservative C
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Best Local Similarity 96.6%;
Matches 28; Conservative
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AR589386/c
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      PAT 08-OCT-2003
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weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
Squence-specific detection of samply capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 26 16-FEB-1999;
Location/Qualifiers
                                                                                                                                       van Lint,C., Burny,A., Quivy,V. and Adam,E.
Method for obtaining the elimination of integrated and functional
viruses from infected mammal cells
Patent: WO 3053468-A 2 03-JUL-2003,
UNIVERSITE LIBRE DE BRUXELLES (BE)
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                                                                                                                                                                                                                                                                                                     /note="mutagenic oligonucleotide primer"
                                                                                                                                                                                                                                                      /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences; artificial sequences.
                                                                                                                other sequences; artificial sequences.
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Sequence 26 from patent US 5871902.
AR035454
AR035454.1 GI:5952122
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/mol_type="unassigned DNA"
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Sequence 10 from Patent EP1433485.
CQ846479
    AX798846 42 bp
Sequence 2 from Patent W003053468.
AX798846.1 GI:37604920
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synthetic construct
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Best Local Similarity
Matches 30; Conserval
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Unclassified.
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CQ846479/c
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AR035454
                      DEFINITION
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Catania, A.P. and Lipton, J.M.
Antimicrobial and anti-inflammatory peptides for use in human immunodeficiency virus
Patent: US 6803044-A 5 12-OCT-2004;
Zengen, Inc.; Woodland Hills, CA
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Lipton, J.M. and Catania, A.P.
Uro-genital condition treatment system
Patent: US 6800291-A 9 05-OCT-2004;
Zengen, Inc.; Woodland Hills, CA
Location/Qualifiers
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                        35 bp
Sequence 9 from patent US 6800291.
AR585153
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Sequence 5 from patent US 6803044.
ARS89385.1 GI:56636661
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Sequence 5 from patent US 6617171.
AR397504
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    /organism="unknown"
    /mol_type="genomic DNA"

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/organism="unknown"

    (bases 1 to 32)
    Faustman, D.L. and Hayashi, T.

                                                                     AR585153.1 GI:56628768
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Matches 27; Conservative
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AR397504
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RESULT 47
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Weininger,S. and Weininger,A.M.
Sequence-specific detection of nucleic acid hybrids using a
Sequence-specific detection of specific acid hybrids molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 25 16-FEB-1999;
                                           Gaps
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/mol type="taxon:38630"
/noTe="Oligonucleotide probe for NF-kB (sense)"
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            Score 27.4; DB 6; Length 44;
Pred. No. 0.81;
0; Mismatches 6; Indels
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Pred. No. 0.99;
0; Mismatches 3;
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A uro-genital condition treatment system
Patent: EP 1433485-A 9 30-JUN-2004;
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other sequences; artificial sequences.
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Sequence 25 from patent US 5871902.
AR035453. GI:5952121
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Sequence 9 from Patent EP1433485.
CQ846478
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             / Match 72.1%;
Local Similarity 83.8%;
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Matches 31
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CE 1 (bases 1 to 32)

RS Faustman, D.L. and Hayashi, T.

3 Methods for diagnosing and treating autoimmune disease

NAL Patent: US 6773705-A 1 10-AUG-2004;

General Hospital Corporation; Boston, MA

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/mol_type="genomic DNA"
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Methods for diagnosing and treating autoimmune disease
Patent: US 6617171-A 5 09-SEP-2003;
The General Hospital Corporation; Boston, MA
Location/Qualifiers
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/organism="unknown"
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Sequence 1 from patent US 6773705.
AR575406.1 GI:56576396
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Ado40441 NF-kappaB
Aeb34893 Oligonucl
Aaq73476 NF KB tra
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                           GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 Maximum DB seq length: 50
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                                                                                                                                                                                                                                                                         Sequence:
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О
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No.
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Adt34424 Primer fo Abb;94866 Fat regul Adv62240 FeLV p15E Adt35022 Human int Adv68320 Exprogen a Adv68320 Human mic Adv68320 Human ShP Adv75580 SR profei Adv75580 SR profei Adv68443 Sequence Adv6443 Fuman mic Adv62542 Human mic Adv62542 Human car Adv62542 HBV amber Adv62542 HBV amber Adv6309 Frimer #4 Abz05999 Human mic Adv36310 Optimized Add43631 Oligonuci Add3631 Oligonuci Add1823 Human Str Adv62591 Human Str Adv6269 Primer #4 Abz50114 Human Str Adv63631 Human Str Adv6363 Human Str Adv62694 Polypepti Adv65082 Oligonuci Adf18224 DNA-bindi Adf18224 DNA-bindi Adf18224 DNA-bindi Adf18224 DNA-bindi Adv604793 Oligonuci Abq01000 Oligonuci Abq000000000000000000000000000000000000	Abd12616 Oligonucl Add20950 Probe use Adx20950 Probe use Adx30159 Human bia Adi31159 Human sin Adj33097 rpsF prom Adh06015 Gene poly Adh06018 Gene poly Adh06018 Gene poly Adh06018 L-beta-me Adf90076 1-beta-me Adf80100 Primer us Abf601970 HBW amber Adv6275 HBW amber Adv62275 HBW amber Acc136290 WNW minus Acc09532 Necrosis Acc15644 HBW amber Acc15644 HBW amber Acc15644 HBW amber
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Acf57180 M. tuberc Adf11059 Mtb DNA P Ady50544 Novel nuc Adu04902 Composite Abn85235 Protein a Abk87815 Human Kai Aat13993 SI primer Aat19933 SI primer Aat61522 Mycobacte Aat63008 M. tuberc Aat61537 Mycobacte Aav71893 Mycobacte Aav71893 Mycobacte Aav74891 Novel str Aac64840 Novel str Aac65251 Allele-sp Aac65214 Novel str Aac65161 Novel str Aac65162 Novel str Aac65163 Novel str Aac6362 Novel str

Human BAC Specific Human SNP Human SNP Adt01206 Novel mut Aaz25681 Transcrip Adp48377 NF-kappaB Intronic

Kappa-B-PT sequence, NF-kappa-B; nuclear factor kappa B; adhesion; differentiation; phosphorothioate; treatment; immune disorder; inflammatory disease; cancer; viral infection; inflammatory disease; cancer; viral infection; cohardin kappa B sequence; rheumatoid arthritis; ischaemia; reperfusion injury; restenosis; transplant rejection; Crohn's disease; ulcarative colitis; psoriasis; glomerulonephritis; leukaemia; malanoma; sarcoma; lymphoma; HIV; HILV; herpes virus; poison ivy; poison oak; Kappa-B-PT sequence (SEQ ID 2), used to inhibit NF-kappa-B. 09-FEB-2000 (first entry)

Synthetic

Aa142267 Human pol Abs70875 Hepatitis Aabs4489 TRIM adap Abs60719 Human DNA Abz48598 Human N-m Abz48698 Human N-m Aaf65574 avec muta Aaf65534 avec muta Aa665534 avec muta Aa605545 S. avermi

Human mic Human mic Human mic Human pol Hepatitis TRIM adap

Aci09133 H Ack19148 H Aci55943 H

Aav06347 Phosphati Aaz36082 Forward P

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/bound_moiety= "NF-kappa-B"
Location/Qualifiers
                                     /mod_base= OTHER
                          ๙
                                                                                                            Д
              1. .10
                                                                                                             *tag=
 Key
modified_base
                                                             protein bind
                                                                                                 protein_bind
                                                                                                                                    protein_bind
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Adu28711 Knock-dow Abd82499 SpoIIB ge Abk87827 Interleuk Ady51614 Transcrip Aaf74484 Clone 179

Adc98706 Double-st Abt08597 Human nov

Ado09962 Human NOV

Adg83558 Streptomy Abz02656 Human leu Abz00443 Human leu

US5990090-A. 23-NOV-1999

96US-00607519. 27-FEB-1996;

(UNMI ) UNIV MICHIGAN. 20-SEP-1993; 

Nabel GJ;

WPI; 2000-022803/02.

Composition useful for the treatment of immune and inflammatory diseases, cancer and viral infections.

Claim 1; Col 4; 14pp; English.

This sequence represents the kappa-B-PT sequence (SEQ ID 2) which contains three immunoglobulin kappa-B sequences (AAZ12918) which are contains three immunoglobulin kappa-B sequences (AAZ12918) which are bound by activated NF-kappa-B (nuclear factor kappa-B). It can inhibit NF-kappa-B binding to endogenous kappa-B enhancer/promoter elements, thus inhibiting transcription of genes that comprise such elements. NF-kappa-B is involved in the induction of cell adhesion associated with NF-kappa-B confiderentiation or activation. For example, the human promyelotic leukaemia cell line (HL-60 cells) can be induced to differentiate into monocytoid cells with concomitant expression of the leukocyte adhesion of paper concomitant with phorbol esters. However, this cappace of muchant kappa-B-PT sequence (AAZ12920) had no effect on differentiation and adhesion compositions containing the kappa-B-PT sequence may be used for the treatment of immune and inflammatory diseases, cancer and viral infections. In particular it can be used to transplant rejection, Crohn's disease, ulcerative colitis, psoriasis, transplant rejection, Crohn's disease, ulcerative colitis, psoriasis, elliv, collicial per persential may be used for the beneaved a further addition and adhesion containing the kappa-B-PT sequence may be used for the treatment of immune and inflammatory diseases, cancer and viral infections. In particular it can be used to transplant rejection, Crohn's disease, ulcerative colitis, psoriasis, containing the kappa virus infections and reaction to poison ivy, poison oak and poison sumac

Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;

AAZ32919 standard; DNA; 38 BP RESULT 1

AAZ32919 AAZ32919 ID AAZ3 XX AC AAZ3 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

Angiogenesis inhibitory oligonucleotide #148.

(first entry)

13-DEC-2002

ABS77664;

ВЪ.

ABS77664 standard; DNA; 38

RESULT 3

diabetic retinopathy; retinopathy of prematurity; macular degeneration, corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granularion; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                            Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                           Gaps
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 38; DB 4; Length 38; llarity 100.0%; Pred. No. 2e-05; Conservative 0; Mismatches 0; Indels
   100.0%; Score 38; DB 3; Length 38; 100.0%; Pred. No. 2e-05;
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present seguence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                         GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
                                                                                1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                             Immunostimulatory nucleic acid #139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 101; Page 41; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vollmer J;
                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2000; 2000WO-US026383
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                                                                                                                                                                                                             AAF99023 standard; DNA; 38
                                                                                                                                                                                                                                                                                      (first entry)
                                           38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-273485/28
Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200122972-A2.
                                                                                                                                                                                                                                                                                        12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                     AAF99023;
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Best Local &
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(COLE-) COLEY PHARM GROUP INC.

14-DEC-2001; 2001WO-US048458. 14-DEC-2000; 2000US-025534P.

WO200253141-A2.

Synthetic.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeoals, osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
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100.0%; Pred. No. 2e-05;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 22; 276pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-566690/60.
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     Bratzler RL;
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Gaps

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1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38

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GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38

Local Similarity es 38; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                            Treating non-allergic inflammatory diseases, such as psoriasis, eczo allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 9; Length 38;
Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunostimulatory nucleic acid #139.
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 12; 229pp; English
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                                                                                                                     29-MAR-2001; 2001US-0279642P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-2001; 2001US-00776479
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                                                                                29-MAR-2002; 2002US-00112653
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Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bratzler RL, Petersen
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PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-657977/62.
                                                                                                                                                                                                                                                                          WPI; 2003-521815/49
                                                                                                                                                                                                                                  Krieg AM, Berg DJ;
                                                                                                                                                                (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOURON Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003087848-A1.
US2003050268-A1
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                                     13-MAR-2003
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(PETE/)
(FOUR/)
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ADB36525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, brain and central nervous system (CNS) cancer, breast cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynax cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, prostete cancer, rhabdomyosarcoma, skin cancer, testicular cancer, rhabdomyosarcoma, skin cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic coract dermatitis; latex dermatitis; latex inflammatory bowel disease; ulcerative colitis; Crohn's disease; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                  Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 38; DB 6; Length 38; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                        Immunostimulatory nucleic acid SEQ ID NO: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 201; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory nucleic acid #141.
                                                                                                                                                                                                                                                                                                                       22-JUN-2000; 2000US-0213346P
                                                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-US020154
                                                                                                                                                                                                                                                                                                                                                               (IOWA ) UNIV IOWA RES FOUND.
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(first entry)
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nes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developing cancer.
                                                                                                                                                                                        WO200197843-A2
  16-APR-2002
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                                                                                                                                                                                                                                     27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                           Weiner G,
                                                                                                                                                Synthetic
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Best Local S
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Matches

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ACD99455 RESULT

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                                                       The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-respondive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
nucleic acid alone or in combination with an asthma/allergy medicament
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; antiasthmatic; antiallergic; dermatological; antinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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                                                                                                                                                                                         100.0%; Score 38; DB 9; Length 38; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                             Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                 1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                              Allergic response suppressor oligonucleotide #148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fouron Y;
                             Disclosure; Page 7; 221pp; English
                                                                                                                                                                                                                                                                                                                                                          ADU89464 standard; DNA; 38 BP.
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02-FEB-2001; 2001US-00776479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-2005 (first entry)
                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 38, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BEAL/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-833006/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urricaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the method of the invention.

Disclosure; SEQ ID NO 148; 235pp; English.

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AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding cregion (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR) and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR95007), and an OSA. The assembly sequence and asymmetry sequence (see AAR95099) are selected from NF-kappa B, SPI, TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high acid sequence of specificity. The method can be used for detecting specific canded sequences, including those found in human calls, in HIV, HIV, and other nucleic acid containing systems, including bacteria and
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                                                                                                                                                                                                                                                                                                                                                                                                                    Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV B2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                                                                          Gaps
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0
                                                    Score 38; DB 13; Length 38; Pred. No. 2e-05;
                                                                                            Indels
              Seguence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
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                                                                                                                                1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                  1 deceactificecrecedentificadedecrifice 38
                                                                                          Mismatches
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                                                    100.0%; Sc
100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                  AAT30609 standard; DNA; 43
                                                                                                                                                                                                                                                                                                                                                                                  Target binding region #29.
                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-287199/29.
                                                                    Local Similarity
nes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                            19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                        AAT30609;
                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viruses
                                                                          Best Loca
Matches
                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                  AAT30609
X S
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6 GGGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40

ð 셤 BP.

AAQ58049 standard; DNA; 39

AAQ58049

(first entry)

Oligonucleotide NF1

(revised)

25-MAR-2003 23-SEP-1994

AAQ58049;

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AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR) and optionally a linker sequence, assembly sequence (See AAR95994-R95999), an asymmetry sequence (See AAR95007), and an OSA. The assembly sequence and asymmetry sequence (See AAR95099-R95999) are selected from NF-kapae. The NAR8 (See AAR95007), and an OSA. The assembly sequence and asymmetry sequence are responsible (For the foliding and association of the NAR8. THE NAR8 (See AAR95007). The foliding and association of the NAR8. THE NAR8 (See AAR95007) are selected from NF-kapae. S. S. TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HTV) LTR and Tat binding the NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequence (TNAA). The method is highly sensitive, and has a high acid sequences, including those found in human cells, in HTV, HPV, and other nucleic acid containing systems, including bacteria and
                                        ö
                                                                                                                                                                                                                                                                                                                                                                     Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                        Gaps
                                        ;
0
81.1%; Score 30.8; DB 2; Length 43; 94.1%; Pred. No. 0.015;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46 BP; 7 A; 10 C; 20 G; 9 T; 0 U; 0 Other;
          0.015,
2;
                                                                                                     6 GGGGACTITCCGCTGGGGACTTTCCAGGGAGGCT 39
                                                                               1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACT 34
                    Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 73; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US015944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-00353476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weininger AM;
                                                                                                                                                                                                               AAT30608 standard; DNA; 46
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                   Target binding region #28.
                                        32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE POOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-287199/29.
                  Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                              19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9617956-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weininger S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                       AAT30608;
    Query Match
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HIV; tat; transport; moiety; conjugate; cargo molecule; cytoplasmic delivery; nuclear delivery; cysteine-rich region; transactivation; disulphide aggregation; ss.

93WO-US007833.

19-AUG-1993; 21-AUG-1992;

03-MAR-1994.

WO9404686-A1

Synthetic.

Barsoum JG, Fawell SE,

(BIOJ ) BIOGEN INC.

WPI; 1994-083202/10.

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The sequences given in AAQ58049-50 form a double stranded DNA molecule which was used as the cargo moiety in the conjugate of the invention. This oligonuclectide fragment was linked to a peptide fragment of the HIV tat protein which was used as transport moieties. These conjugates are used as cargo molecules for the efficient cytoplasmic and nuclear molecules which are not inherently capable of entering a target cell. The tat basic region amino acid sequence carries cargo molecules by covalent attachment. The reduced size of the transport peptides minimises attachment, the shological activity of the cargo molecule. By virtue of the absence of the cyteline-rich region (residues 22-36) of the tat protein, problems of spurious trans- estivation and disulphide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                     Transport of cargo moieties into cells - using genetic fusions of chemical conjugates comprising a portion of HIV tat protein as transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggregation are solved. The reduced transport peptide size also enhances uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 2; Length 39;
Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 116; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 78.9%;
1 Similarity 86.8%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ58050 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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ID AAQ5
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장: 음
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Gaps

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Query Match 79.5%; Score 30.2; DB 2; Length 46; Best Local Similarity 91.4%; Pred. No. 0.026; Matches 32; Conservative 0; Mismatches 3; Indels

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91US-00636662.
92US-00934375.
93WO-US007833.
                                                                 95US-00450257
                                                                                     89US-00454450
                                                                                                                                93US-00158015
                                                                                                                                            94US-00235403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Conservative
                                                                                                                                                                                                                               WPI; 1997-392943/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                            cargo moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                25-MAY-1995;
                                                                                                 32-JAN-1991;
                                                                                                          21-AUG-1992;
                                                                                                                       19-AUG-1993;
                                                                                                                                24-NOV-1993;
                                                                                                                                           28-APR-1994;
                     US5652122-A
                                                                                       21-DEC-1989;
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20-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5670617-A.
                                           29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1997,
  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT88240;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT88240,
  à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAQS8049-50 form a double stranded DNA molecule which was used as the cargo molety in the conjugate of the invention. This oligonucleotide fragment was linked to a peptide fragment of the HIV tat protein which was used as transport moieties. These conjugates are used as cargo molecules for the efficient cytoplasmic and nuclear delivery of biologically active non-tat proteins, nucleic acids and other molecules which are not inherently capable of entering a target cell. The tat basic region amino acid sequence carries cargo molecules by covalent attachment. The reduced size of the transport peptides minimises interference with the biological activity of the cargo molecule. By virtue of the absence of the cysteine-rich region (residues 22-36) of the aggregation are solved. The reduced transport peptide size also enhances uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                              Transport of cargo moieties into cells - using genetic fusions of chemical conjugates comprising a portion of HIV tat protein as transport peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                          HIV; tat; transport; moiety; conjugate; cargo molecule;
cytoplasmic delivery; nuclear delivery; cysteine-rich region;
transactivation; disulphide aggregation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 2; Length 39;
Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV; tat protein; transport protein; cargo delivery; NF-kappa B binding site; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 deddactrircederddddactrirceaeddddactrire 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                      Pepinsky RB;
                                                                                                                                                                                                                                                                                                                                          Claim 21; Page 116; 153pp; English.
                                                                                                                                                                                      93WO-US007833
                                                                                                                                                                                                            92US-00934375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT84584 standard; DNA; 39
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 86.8 es 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF-kappa B binding site.
                                                                                                                                                                                                                                                     Barsoum JG, Fawell SE,
                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                    Oligonucleotide NF2
                                                                                                                                                                                                                                                                           WPI; 1994-083202/10
                                                                                                                                                                                                                               (BIOJ ) BIOGEN INC
                                                                                                                                          WO9404686-A1
                                                                                                                                                                                                            21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
16-DEC-1997
                    25-MAR-2003
                                23-SEP-1994
                                                                                                                                                                03-MAR-1994
                                                                                                                       Synthetic
 AAQ58050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT84584;
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This double-stranded DNA sequence, comprising oligonucleotides NF1 (sense strand) and NF2 (antisense strand). corresponds to the wild-type NF-kappa B binding site. It was used in the preparation of transport polyperide. DNA conjugates. Such conjugates, in which modified HIV tat protein is used as transport polypeptide, can be used to deliver cargo molecules to cells in vivo or in vitro. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                          New DNA constructs for transporting molecules to cells - encode a fusion protein comprising a modified HIV tat protein and a carboxy-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemical conjugate; transport polypeptide; tat protein; nucleic acid; delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis; spurious transactivation; HIV-1; disulphide aggregation; NF-kappaB; inhibition; NF2; human immundeficiency virus type 1; transcriptional activation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                             Frankel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%; Score 30; DB 2; Length 39; 86.8%; Pred. No. 0.03; 1ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF-kappaB transcriptional activation inhibitor NF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 38
                                                                                                                             Fawell SE,
(UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE. (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                             Pabo C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Col 97; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00450246.
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                                                                                                                         Pepinsky RB, Barsoum JG,
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AAT89779
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                                                                                                                                                                                                                                                                                                          polypeptide moiety consisting of at least residues 49-57 of human collypeptide moiety consisting of at least residues 49-57 of human collypeptide moiety consisting of at least residues 49-57 of human collypeptide moiety with (HIV) tat protein, but not residues 22-36 and 73-86, and a cargo moiety emprising a single or double stranded nucleic acid, e.g. the present sequence. The conjugate can be used to deliver cargo moieties into the cytoplasm and nuclei of cells for therapeutic, prophylactic and diagnostic applications. In an example conjugates to inhibit transcriptional activation by NF-kappab were prepared, the corresponding to the wild type NF-KB binding site, while NF2 and NF4 form a duplex corresponding to a muteant NF-KB binding site, while NF2 and NF4 form a duplex corresponding to a muteant NF-KB binding site. Traut modified NF1 was annealed with NF2, and Traut modified NF3 annealed with NF4. The DNA was the reacted with bismaledinidohexane activated tat 32-72. The products were tested as in Science 250, 997-1000 (1990) for inhibition of NF-KB transcriptional activation. The results showed that the tat cransport polypeptides minimises interference with the protein is readily taken up into cells and the cell nucleus. The reduced size of the transport polypeptides minimises interference with the absence of the cysteine rich region of the HIV tat protein, the transport collypeptides solve the protein in the ready molecule. In addition, by virtue of the cause of the cause of the cysteine rich region of the HIV tat protein, the transport of disulphide aggregation (Updated on 25-MR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                            Conjugate for intracellular delivery - comprising transport moiety having amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemical conjugate; transport polypeptide; tat protein; nucleic acid; delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis; spuritous transactivation; HV-1; disulphide aggregation; NF-kappaB; inhibition; NF,; human immunodeficiency virus type 1; transcriptional activation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                      Pabo C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 2; Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF-kappaB transcriptional activation inhibitor NF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                      Frankel A, Pepinsky RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gegeactriccecreedeactriccacedeacerric 2
                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
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                                                                                                                           INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                     Claim 3; Col 97-98; 77pp; English.
           89US-00454450.
91US-00636662.
92US-00934375.
93WO-US007833.
93US-00158015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT88239 standard; DNA; 39 BP
                                                                                   94US-00235403
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                                                                                                                                                                    Fawell SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                WPI; 1997-479523/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                            WHITEHEAD
                                                                                                                                                                                                                                                            acid cargo moiety.
                                                                                                               BIOGEN
                                                                                                                                                                       Barsoum JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
20-JAN-1998
                                                                                   28-APR-1994;
              21-DEC-1989;
02-JAN-1991;
                                                        19-AUG-1993
                                           21-AUG-1992
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                                                                                                             (BIOJ )
(WHED )
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A novel covalently linked chemical conjugate, comprises a transport conjugation of at least residues 49-57 of human immunodeficiency virus (HIV) tat protein, but not residues 22-36 and 73-68, and a cargo moiety comprising a single or double stranded nucleic acid, e.g. the present sequence. The conjugate can be used to deliver cargo moieties into the cytoplasm and nuclei of cells for therapeutic, prophylactic and diagnostic applications. In an example conjugates to inhibit transcriptional activation by NF-kappaB were prepared, the climbibit transcriptional activation by NF-kappaB were prepared, the oligomucleotides used were NF1-4 (AATSB239-42). NF1 and NF2 for a duplex corresponding to the wild type NF-KB binding site, while NF2 and NF4 form a duplex corresponding to a muteant NF-KB binding site, while NF2 and NF4 form a duplex corresponding to a muteant NF-KB binding site. Traut modified NF1 was annealed with NF2, and Traut modified NF3 annealed with NF4. The DNA was the reacted with bismaleimidohexane activated tat 32-72. The cransport polypeptide significantly enhanced that the tat cransport polypeptides minimises interference with the correct protein is readily taken up into cells and the cell nucleus. The reduced size of the transport polypeptides minimises interference with the collectivity of the cargo molecule. In addition, by virtue of the biological activity of the cargo molecule. In addition, by virtue of the cargo molecule. In a cargo molecule of the cargo molecule. In addition of the cargo molecule. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conjugate for intracellular delivery - comprising transport moiety having amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHITEHEAD INST BIOMEDICAL RES.
UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
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91US-00636662.
92US-00934375.
93WO-US007833.
93US-00158015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 86.8
hes 33; Conservative
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24-NOV-1993;
28-APR-1994;
                                             Homo sapiens.
                                                                                                                                                                                                                                                                               25-MAY-1995;
                                                                                                                US5670617-A
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Synthetic
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This oligonuclectide primer is used with AAR89779 to form a duplex corresponding to the wild type transcription factor NP-kappaB binding site which is used in the construction of a transport polypeptide-DNA conjugate. This conjugate is used in a novel method for delivery of biologically active cargo molecules into the cytoplasm and nuclei of eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-LY, SIV) is readily taken up into cells when present e.g. taracellularly and can be modified to covalently link to cargo proteins centracellularly and can be modified to covalently link to cargo proteins problems of spurious trans-activation and disulphide aggregation. These transport polypeptides also minimise interference with the biological activity of the cargo molecule. This is applicable for therapeutic, prophylactic or diagnostic intracellular delivery of small molecules and macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated on 25-MAR-2003 to correct
                                                                           Human Immunodeficiency Virus; HIV Type 1; Tat protein; cargo molecule; intracellular delivery; fusion protein; therapeutic; prophylactic; diagnostic; transport polypeptide; E2 repressor protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion proteins containing truncated HIV tat sequences - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 2; Length 39;
Pred. No. 0.03;
0; Mismatches 5; Indels
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                                         Franscription factor NF-kappaB oligonucleotide NF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intracellular delivery of viral repressor proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pepinsky RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGACTTTC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 17; Col 95-96; 77pp; English
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93US-00158015.
94US-00235403.
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92US-00934375.
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(first entry)
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Matches 33; Conservative
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FAWELL S E.
PEPINSKY R B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BARSOUM J G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PABO C.
                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1993;
24-NOV-1993;
28-APR-1994;
20-MAR-1998
                                                                                                                                                                                                                                                                                         25-MAY-1995;
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                                                                                                                                                                  Synthetic.
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FAWE/)
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This oligonucleotide primer is used with AAT89780 to form a duplex corresponding to the wild type transcription factor NP-kappaB binding site which is used in the construction of a transport polypeptide-DNA conjugate. This conjugate is used in a novel method for delivery of biologically active cargo molecules into the cytoplasm and nuclei of eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-1, SIV) is readily taken up into cells when present extracellularly and can be modified to covalently link to cargo proteins extracellularly and can be modified to covalently link to cargo proteins problems of spurious trans-activation and disulphide aggregation. These transport polypeptides also minimise interference with the biological activity of the cargo molecule. This is applicable for therapeutic, prophylactic or diagnostic intracellular delivery of small molecules and macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated on 25-MAR-2003 to correct
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                                                                              Human Immunodeficiency Virus, HIV Type 1, Tat protein, cargo molecule, intracellular delivery; fusion protein; therapeutic; prophylactic; diagnostic; transport polypeptide; E2 repressor protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intracellular delivery of viral repressor proteins
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                                         Franscription factor NF-kappaB oligonucleotide NF1
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92US-00934375.
93WO-US007833.
93US-00158015.
94US-00235403.
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20-MAR-1998 (first entry)
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les 33; Conservative
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FAWELL S E.
PEPINSKY R B.
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21-AUG-1992;
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(FAWE/)
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RESULT 16 AAT89780/C ID AAT89 XX AC AAT89 XX DT 25-MA

Matches

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This sequence is a phosphorothioate primer used in a method for the delivery of biologically active cargo molecules into the cytoplasm and muclei of cells, for therapeutic, prophylactic or diagnostic purposes.

This is accomplished by the presence of a small, basic section of the tat transport protein from human immunodeficiency virus (HIV) Type I. This is cused as it is this protein which is observed to cause human cells in culture to take up HIV. The method involves the use of a cargo moiety in combination with a transport moiety usually in the form of a fusion combination with a transport moiety usually in the form of a fusion combination with a transport moiety usually in the form of a fusion cretains its biological activity after delivery into a target cell and where the transport moiety is one of following HIV tat protein fragments cretains its biological activity after delivery into a target cell and where the transport moiety is one of following HIV tat protein fragments concertify proposed into cells at high concentrations due to use of specific peptides into cells at high concentrations due to use of existing transporters. Previous methods of delivery include bombardment and transforming, which only allow a fraction of the cell population to be infected and can additionally damage cells as they cause physical companing of the cell walls/membranes to allow entry. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV tat-derived transport fusion proteins - used to deliver biological active molecules e.g. peptide(s) or nucleic acids, specifically into cytoplasm or nuclei of cells.
                                                                                                             TAT protein; cargo molecule; therapy; diagnosis; transport protein; fusion protein; human papillomavirus B2 repressor; target cell; phosphorothioate; primer; ss.
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                                                                        NF-kappaB binding site phosphorothioate primer NF2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pepinsky RB, Pabo C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WHED ) WHITEHEAD INST BIOMEDICAL RES. (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 2;
Pred. No. 0.03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 17; Col 97-98; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93WO-US007833.
93US-00158015.
94US-00235403.
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91US-00636662.
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86.8%;
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                            (first entry)
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les 33; Conservative
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  (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOJ ) BIOGEN INC. (WHED ) WHITEHEAD IN
                                                                                                                                                                                                                                                                                                                                                                         25-MAY-1995;
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25-MAR-2003
24-NOV-1998
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                                                                                                                                                                                                                                                                           US5804604-A
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                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD26647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a phosphorothioate primer used in a method for the delivery of biologically active cargo molecules into the cytoplasm and nuclei of cells, for therapeutic, prophlactic or diagnostic purposes.

This is accomplished by the presence of a small, basic section of the transport protein from human immunodeficiency virus (HIV) Type I. This is used as it is this protein which is observed to cause human cells in culture to take up HIV. The method involves the use of a cargo moiety is combination with a transport moiety usually in the form of a fusion protein. The cargo moiety is a human papillomavirus E2 repressor that retains its biological activity after delivery into a target cell and where the transport moiety is a human papillomying HIV tat protein fragments of a a 47-58, (b) as 47-62, (c) 38-72, (d) as 38-58, (e) as 37-58, (f) as 12-1 and 38-72, (g) as 47-62 or as 38-62. The proteins allow delivery of specific peptides into cells at high concentrations due to use of existing transporters. Previous methods of delivery include bombardment and transforming, which only allow a fraction of the cell population to be infected and can additionally damage cells as they cause physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV tat-derived transport fusion proteins - used to deliver biological active molecules e.g. peptide(s) or nucleic acids, specifically into cytoplasm or nuclei of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                             TAT protein; cargo molecule; therapy; diagnosis; transport protein; fusion protein; human papillomavirus E2 repressor; target cell; phosphorothioate; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
                                                      NF-kappaB binding site phosphorothioate primer NF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOJ ) BIOGEN INC.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
(UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Col 95-96; 83pp; English.
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93WO-US007833.
93US-00158015.
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     24-NOV-1998 (first entry)
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19-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                       25-MAY-1995;
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28-APR-1994;
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Frankel A;

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Gaps

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AAD26647 standard; DNA; 39 BP

AAD26647;

SXS

AAV56616 AAV56616/c ID AAV5661 XX AC AAV5661 XX

RESULT 18

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DB 2; Length 39; 5; Indels

Query Match

Matches

us-09-669-187a-148.szlm50.rng

AAD26648 standard; DNA; 39 BP

AAD26648/C

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The invention relates to a method for delivering a biologically active cargo molecule of interest into a cell. The method comprises presenting to the cell an extracellular fusion protein or a covalently linked conjugate consisting of a cargo moiety and a transport moiety having amino acids 49-57 of human immunodeficiency virus (HIV) transactivator (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein. The method is useful for delivering a molecule of interest such as polypeptides, antigen, monoclonal antibody, single- or double-stranded conclete acid, a therapeutic, prophylactic and diagnostic molecule to a cell in vitro or in vivo. The method delivers proteins or peptides, including regulatory factors, enzymes, drugs or toxins into the cytoplasm of cell nucleus. The method is useful for diagnostic, prophylactic or therapeutic intracellular delivery of small and macro molecules. The present sequence is a phosphorothiate oligonucleotide used for generating nuclear factor kappa B (NFKB) wild type binding site used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Delivering biologically active cargo molecules such as polypeptides, nucleic acids into cells by using transport polypeptides which comprise human immunodeficiency virus transactivator protein linked to cargo
                                                                                  Human immunodeficiency virus; HIV-1; tat; therapeutic; toxin; enzyme; regulatory factor; prophylactic; extracellular fusion protein; drug; NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
                                                  NF-kB wild type binding site generating NF1 phosphorothioate oligo.
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                                                                                                                                                                                                                                                                    /note= "Phosphorothioate backbone"
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(UYJO ) UNIV JOHNS HOPKINS SCHOOL MED]
(BIOJ ) BIOGEN INC.
                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                     OTHER
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92US-00934375.
93WO-US007833.
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                  26-MAR-2002 (first entry)
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                                                                                                                                                                                                Key
modified_base
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21-AUG-1992;
19-AUG-1993;
                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                         US6316003-B1
                                                                                                                                                                                                                                                                                                                                                                                28-APR-1994;
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                                                                                                                                                                                                                                                                                                                                             13-NOV-2001.
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The invention relates to a method for delivering a biologically active cargo molecule of interest into a cell. The method comprises presenting to the cell an extracellular fusion protein or a covalently linked conjugate consisting of a cargo moiety and a transport moiety having amino acids 49-57 of human immunodeficiency virus (HIV) transactivator (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein. The method is useful for delivering a molecule of interest such as polypeptides, antigen, monoclonal antibody, single- or double-stranded cucleic acid, a therapeutic, prophylactic and diagnostic molecule to a cell in vitro or in vivo. The method delivers proteins or peptides, including regulatory factors, enzymes, drugs or toxins into the cytoplasm and cell nucleus. The method is useful for diagnostic, prophylactic or herapeutic intracellular delivery of small and macro molecules. The therapeutic intracellular delivery of small and macro molecules. The cores present sequence is a phosphorothiate oligonucleotide used for generating nuclear factor kappa B (NFKB) wild type binding site used in the
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                                                                                                                                    Human immunodeficiency virus; HIV-1; tat; therapeutic; toxin; enzyme regulatory factor; prophylactic; extracellular fusion protein; drug; NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delivering biologically active cargo molecules such as polypeptides, nucleic acids into cells by using transport polypeptides which comprhuman immunodeficiency virus transactivator protein linked to cargo
                                                                                                   NF-kB wild type binding site generating NF2 phosphorothioate oligo.
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Pred. No. 0.03;
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                                                                                                                                                                                                                                                                                                                     /note= "Phosphorothioate backbone"
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                                                                                                                                                                                                                                              Location/Qualifiers
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/*tag= a
/mod_base= OTHER
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92US-00934375.
93WO-US007833.
93US-00158015.
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Best Local Similarity 86.8%;
Matches 33; Conservative
                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS
(BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                              modified base
                                                                                                                                                                                                            Unidentified
                                                                    26-MAR-2002
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Gaps

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33; Conservative

Matches

GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38 

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The invention relates to a mixture comprising one or more triterpene glycosides isolated from Acacia victoriae. The composition is used for the treatment of cancer, inhibiting the initiation and promotion of mammalian epithelial cells (such as skin, colon, uterine, ovarian, pancreatic, prostate, renal, lung, bladder or breast cells), for preventing the abnormal profileration of mammalian epithelial cells (such as crypt or colon cells), and/or regulating angiogenesis. The triterpene glycosides may also be used as solvent, an antioxidant, antifungal or antiviral agent, piscicide, molluscicides, contraceptive, antihelmintic, angiogenesis regulator, UV-protectant, expectorant, diuretic, anti-inflammatory agent, regulator of cholesterol metabolism, cardiovascular effecter, anti-ulcer agent, analgesic, sedative, immunomodulator, combating the effects of aging, increasing skin collagen, enhancing penile function and improving cognition and memory. The present sequence represents an integral of a contraction and improving cognition and memory. The present sequence represents and integral of a contraction and improving cognition and memory. The present sequence represents and contraction and improving cognition and memory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mixture containing triterpene glycosides, useful for treating variety of
                                                                                                                                                                                                                                                                                              Triterpene glycoside; antitumor; cytotoxic; antioxidant; contraceptive; antihelmintic; expectorant; diuretic; anti-inflammatory; cardiant; anti-inflammatory; cardiant; anti-inflammatory; cardiant; anti-inflammatory; cardiant; vascivolics; sedative; immunomodulator; antipyretic; cancer; vascivolics; Acacia victoriae; angiogenesis; antifungal; cholesterol; cardiovascular effecter; HIV; NP-kappaB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bailey DT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and improving cognition and memory. The present sequence repre
32P-labelled NP-kappaB oligo from HIV long terminal repeat use
electrophoretic mobility shift assay. (Updated on 15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29.8; DB 3; Length 44; pred. No. 0.037; 2; Indels 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;
39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 27; Page 199; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                     HIV LTR NF-kB oligonucleotide
                                                                                                      AAZ48474 standard; DNA; 44 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.4%;
93.9%;
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                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                         (revised)
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Jayatilake GS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1998;
                                                                                                                                                                                                               28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor cells.
                                                                                                                                                                                       15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1999
                                                                                                                                               AAZ48474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                              RESULT 21
                                                                                AAZ4847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a novel method for inhibiting inflammation which comprises administering a monoterpene composition that inhibits NFkappaB. The products of the invention have antiinflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic, antirhumatic, antiarthrilic, osteopathic, antiparkinsonian, nootropic, neuroprotective and antiparkinsonian activity. The method described can be used for treating inflammatory diseases, particularly premalignant inflammatory disease (e.g. Barretts esophagitis, inflammatory bowel disease, chronic pancreatitis, chronic prostatitis, familial polyposis and actinic keratosis), artherosclerosis, rheumatoriod arthritis, osteoarthritis, multiple sclerosis, Parkinson's disease and Alzheimer's disease. This sequence represents a 32P-labelled NPkappaB oligonucleotide used in an electrophoretic mobility shift assay
                                                                                                                                               NFkappaB; antiinflammatory; antiarteriosclerotic; antirheumatic; antiarthritic; osteopathic; antiparkinsonian; nootropic; monoterpene; neuroprotective; antiparkinsonian. Barretts esophagitis; osteoarthritis; inflammatory bowel disease; chronic pancreatitis; chronic prostatitis; familial polyposis; actinic keracosis; rheumatoid arthritis; multiple sclerosis; Parkinson's disease; Alzheimer's disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting inflammation used for treating e.g. osteoarthritis and multiple sclerosis comprises administering monoterpene composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detect the biological characteristics of active triterpenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGGACTITCCGCTGGGGACTITCCAGGGGGACT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 gegactriccecregegactriccaegeaeger 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.4%; Score 29.8;
93.9%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "32P labelled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 28; Page 349; 349pp; English.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibiting nuclear factor kappaB.
                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/mod_base= OTHER
              ABL61552 standard; DNA; 44 BP.
                                                                                                                                                                                                                                                                                 Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-2001; 2001WO-US043286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000US-0249710P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 93.9%;
Les 31, Conservative
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RERE-) RES DEV FOUND.
                                                                                                                   HIV-LTR NFkappaB DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-557793/59.
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200255016-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gutterman JU,
                                                                                                                                                                                                                                                                                                                                modified base
                                                                                  20-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2002
                                                   ABL61552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
ABL61552
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RESULT 23 AAT30599

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Gaps

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5, 34

Conservative

Local Similarity les 31; Conserv

Best Loca Matches

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GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCT 42 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACT

Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; AFTA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;

19-FEB-1997 (first entry)

rarget binding region #23.

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AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR) and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR95007), and an OSA. The assembly sequence and asymmetry sequence (see AAR95993-R95993) are selected from NF-kappa-B, SPI, TATA, human papillomavirus (HBV) E2. HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopetide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequences, including those found in human cells, in HIV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                          Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; TATR, human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 70; 172pp; English.
BP
                                                                                                                                                                                                                                                                                                                                                               95WO-US015944.
                                                                                                                                                                                                                                                                                                                                                                                                   94US-00353476
AAT30599 standard; DNA; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weininger AM;
                                                                      (first entry)
                                                                                                        Target binding region #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE POOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-287199/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weininger S,
                                                                                                                                                                                                                                                                                       WO9617956-A2
                                                                                                                                                                                                                                                                                                                                                             07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                   39-DEC-1994;
                                                                      19-FEB-1997
                                                                                                                                                                                                                                                                                                                             13-JUN-1996.
                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                    virus; ss
                                  AAT30599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viruses
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Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.

95WO-US015944. 94US-00353476.

WO9617956-A2

Synthetic. virus; ss

13-JUN-1996

Weininger S, Weininger AM;

WPI; 1996-287199/29.

(GENE-) GENE POOL INC.

09-DEC-1994; 07-DEC-1995;

Disclosure; Page 71; 172pp; English.

ANTIOSBI-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding cregion (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AARS95994-R95998), an asymmetry sequence (see AARS9599-R96006), a nuclear localisation signal sequence (see AARS9509).

CC ARS9599-R96006), a nuclear localisation signal sequences are responsible of the the OARS (see AARS96007), and an OSA. The assembly sequence and asymmetry sequence (see ARS9599) are selected from NF-Kappa B, SPI, TAPA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding cuits. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indiactor, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation as profice carded edgree of specificity. The method is highly sensitive, and has a high edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity and contraining systems, including bacteria and Query Match Best Loca Matches RESULT 25 AAX28079 ò ö Gaps ; 0 Length 45; Indels Seguence 45 BP; 7 A; 12 C; 16 G; 10 T; 0 U; 0 Other; Score 29.2; DB 2; I Pred. No. 0.064; 0; Mismatches 3; 2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTT 35 7 degacitriccecredegacitriccaeeaeeeer 40 76.8%; 91.2%; 31; Conservative Local Similarity Query Match

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                                                              Gaps
                                                              ;
0
                           ch 76.8%; Score 29.2; DB 2; Length 45; 1 Similarity 91.2%; Pred. No. 0.064; 31; Conservative 0; Mismatches 3; Indels
Sequence 45 BP; 8 A; 11 C; 16 G; 10 T; 0 U; 0 Other;
                                                                                                               GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
                                                                                             2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
                                                                                                                                                                                                        AAX28079 standard; DNA; 45
                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                               Local Similarity
                                                                                                                                                                                                                                                                   17-OCT-2003
10-JUN-1999
                                                                                                                                                                                                                                      AAX28079;
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AAT30603 standard; DNA; 45 BP

RESULT 24
AAT30603
ID AAT30
XX
AC AAT30

Matches

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AAT30603

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a HIV-LTR oligonucleotide used to test the method of the invention. The method is for inhibition of activation of the NF-kappaB transcription factor (A), for treatment of toxic or septic shock or graft versus host reactions in humans, comprises administration of curcumin (I, diferiloylmethane). (I) is used to treat toxic or septic shock and graft versus host reactions in humans. (I) may be used to inhibit activation of (A) e.g. in cases of radiation damage, atherosclerosis, cancer and human immune deficiency virus (HIV) infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multiple myeloma; proliferation inhibition; apoptosis induction; curcumin; diferulcylmethane; chemotherapy potentiator; I-kappa-B kinase inhibitor; I-kappa-B-alpha phosphorylation suppressor; NF-kappa-B suppressor; I-kappa-B-alpha; Bcl-2; Bcl-XL; cyclin Di; interleukin-6; IL-6; cell cycle arrest; cytostatic; NF-kappa-B; HIV-1 LTR; long terminal repeat; electrophoretic mobility shift assay;
                                               Inhibitor; activator; NF-kappaB transcription factor; toxic shock; septic shock; graft versus host disease; curcumin; diferuloylmethane; radiation damage; atherosclerosis; cancer; HIV infection; HIV-LTR; ss.
                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting activation of NFkappaB with curcumin used for treatment of e.g. septic shock or guest versus host reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 76.8%; Score 29.2; DB 2; Length 45; Local Similarity 91.2%; Pred. No. 0.064; es 31; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-1 LTR NF-kappa-B sequence used as EMSA probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Col 5; 21pp; English.
                                                                                                                 Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                  96US-00712932
                                                                                                                                                                                                                                                    96US-00712932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
               HIV-LTR oligonucleotide
                                                                                                                                                                                                                                                                                     (RERE-) RES DEV FOUND
                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-253918/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004000229-A2
                                                                                                                                                                                                                    26-SEP-1996;
                                                                                                                                                                                                                                                    26-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-2004
                                                                                                                                                                                    06-APR-1999
                                                                                                                                                                                                                                                                                                                       Aggarwal BB
                                                                                                                                                  US5891924-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH1217
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The invention relates to a method for inhibiting the proliferation of, and inducing apoptosis in multiple myeloma cells comprising and inducing apoptosis in multiple myeloma cells comprising cadministration of curcumin (diferuloy)methane). The invention also relates to a method for increasing the cytotoxic effects of a chemotherapeutic agent (e.g., vincristine, bichloroethylnitrosourea, chemotherapeutic agent (e.g., vincristine, prediisone or dexamethasone) against multiple myeloma cells (preferably CD138+ plasma cells) comprises administration of the chemotherapeutic agent against increases the cytotoxic effects of the chemotherapeutic agent against increases the cytotoxic effects of the chemotherapeutic agent against cultiple myeloma cells. It suppresses constitutive I-kappa-B-alpha chemothar constitutive I-kappa-B-alpha constitution of I-kappa-B-rapha activity, and convergulates the expression of I-kappa-B-regulated gene products (e.g. culpression of proliferation and arrest of cells at the GI/S phase of the cell cycle. The methods of the invention are used for the treatment of multiple myeloma. The present sequence represents an NF-kappa-B binding centuring myeloma. The present sequence represents an NF-kappa-B binding case a probe in electrophoretic mobility shift assay (EMSA) of NF-kappa-B in an example of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteopathic; osteogenesis; nuclear factor kappa B; cancer; breast tumor; myeloma; osteoporosis; Paget's disease; rheumatoid arthritis; head and neck tumor; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMSA probe for detecting NF-kappaB activation in curcumin treated cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                              Inhibiting proliferation of multiple myeloma cells comprises administering curcumin and optionally with vincristine, bichloroethylnitrosoures, melphalan, cyclophosphamide, adriamycin, prednisone or dexamethasone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.8%; Score 29.2; DB 12; 91.2%; Pred. No. 0.064; ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 degacrirccecrededacrirccadedacecer 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI
                                                                                                                                                                                                                                                                                                Example 3; SEQ ID NO 4; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADZ00136 standard; DNA; 45 BP
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24-JUN-2003; 2003WO-US019837
                                   24-JUN-2002; 2002US-0390926P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-2004; 2004US-00925608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 91.2%;
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2005 (first entry)
                                                                             (RERE-) RES DEV FOUND
                                                                                                                                                          WPI; 2004-156362/15
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                                                                                                                  Aggarwal B;
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Matches
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(AGGA/) AGGARWAL B

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                                                                                                                               The invention relates to a method of reducing or inhibiting osteoclast development induced by the receptor for activation of nuclear factor kappa B ligand (RANKL) by contacting the osteoclast or its precursor with compounds (I) comprising diferulcylmethane, guggulsterone, 1'-acetoxychavicol or their analogues. (I) is useful for reducing or inhibiting osteoclast development induced by RANKL, inhibiting the formation of osteoclast in an individual and reducing osteolytic activity and bone loss in an individual having breast cancer, multiple myeloma, post-menopausal osteoporosis, Paget's disease, rheumatoid arthritis or head and neck squamous cell carcinoma. The udierulcylmethane (curcumin) is safe to humans. This sequence corresponds to an electromobility shift assay (EMSA) probe used to analyze NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo from HIV long terminal repeat containing NF-kappaB binding site.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear factor-kappa B; NF-kappaB; NF-kappaB inhibitor; apoptosis stimulation; cancer; cytostatic; HIV long terminal repeat;
                                                 Use of compounds comprising diferuloylmethane, guggulsterone, 1'-acetoxycharicol or their analogues to e.g. reduce/inhibit osteoclast development induced by the receptor for activation of nuclear factor kappa B ligand.
                                                                                                                                                                                                                                                                       activation in curcumin-treated or untreated cells. The sequence is derived from the human immunoeficiency virus 1 long terminal repeat.
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                             Score 29.2; DB 14; Length 45; Pred. No. 0.064;
                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                        Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
                                                                                                                                                                                                                                                                                                                                                                                       10 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 43
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /bound_moiety= "NF-kappaB"
24. 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety= "NF-kappaB"
                                                                                                           Example 7; SEQ ID NO 1; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEA06160 standard; DNA; 45 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-2004; 2004WO-US036777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2003; 2003US-0517852P.
                                                                                                                                                                                                                                                                                                                               76.8%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Д
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.2
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aggarwal BB, Singh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RERE-) RES DEV FOUND.
                               WPI; 2005-295074/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005046708-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEA06160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
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The present invention relates to cell permeable nuclear factor (NF)-
kappaB, and specifically to polypeptides that selectively inhibit NF-
kappaB, and specifically to polypeptides that selectively inhibit NF-
comprises (i) a protein transduction domain of the p65 subunit of NF-
combinity and (ii) a protein transduction domain which is able to transport
comprises cell membrane. The protein transduction domain which is able to transport
comprises cell membrane. The protein transduction domain is
derived from a protein or domain selected from third helix of the
conformation or domain selected from third helix of the
conformation of disclosed is an isolated DNA encoding the
conformation. Also disclosed is an isolated DNA encoding the
inhibitor. Provided is a method of inhibiting the DNA binding activity of
conformation of increasing the level of apoptosis; and a method
conformation a cell with the inhibitor above, where the
inhibitor suppresses NF-kappaB binding to DNA. Activity is induced by an
coll comprises contacting a cell with the inhibitor above, where the
inhibitor suppresses NF-kappaB binding to DNA. Activity is induced by an
coll comprises contacting a cell with the NFADPOL myritytate accetate
contacting accordate death domain (TRADD), TNF receptor-associated factor-
coll (TNF, kappaB-inducing Kinase (NIK), or IkappaBalpha kinase (IKK).
The present sequence is a 45-mer double-stranded oligonucleotide from the
coll DNA-brotein complex to examine the specificity of binding of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                             New cell permeable nuclear factor kappaB inhibitor comprising a peptide fragment and a protein transduction domain, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29.2; DB 14; Length 45;
Pred. No. 0.064;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 gegacitriccecreeceacitriccaeceacecer 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                              Example 2; SEQ ID NO 1; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US015944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.8%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.4%,
-.hos 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weininger S, Weininger AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Target binding region #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE POOL INC.
WPI; 2005-372280/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9617956-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus; ss.
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invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence are responsible for the folding and association of the NARS. The NARS (see AAR95965-CC (BPV) E2. HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere viru NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high control acid sequence (TNA). The method can be used for detecting specific carded acquence including those found in human calls, in HIV, hum can obtain a method of the probe found in human calls, in HIV, hum can obtain a health of the probe of the hard of the probe of the AAT30581-T30614 represent target binding regions (TBR) of a probe of the Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV. HPV, and other nucleic acid containing systems, including bacteria and Disclosure; Page 72; 172pp; English. WPI; 1996-287199/29 Probe 

Sequence 46 BP; 8 A; 11 C; 17 G; 10 T; 0 U; 0 Other;

76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.077; ive 0; Mismatches 0; Indels 2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30 7 degactriccecrededactriccaeded 35 29; Conservative Query Match Best Local Similarity Matches 29; Conserva 셤

RESULT 30

AAT30602 standard; DNA; 46

AAT30602;

(first entry) 19-FEB-1997 Target binding region #22.

Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss AAT30602

AAT30602

AACT30602

AA

Synthetic.

WO9617956-A2

13-JUN-1996

95WO-US015944 07-DEC-1995;

94US-00353476 09-DEC-1994;

(GENE-) GENE POOL INC

Weininger AM;

Weininger S,

WPI; 1996-287199/29.

Probe nucleic acids, target binding assemblies, etc - for detection and

ART30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding convention. The probe of the invention contains a TBR, a booster binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AARS5994-R9598), an asymmetry sequence (see AARS5999-R96006), a nuclear localisation signal sequence (see AARS9993) are association of the NARs. The NARs (see AARS9607), and an OSA. The assembly sequence and asymmetry sequences are responsible (for the folding and association of the NARs. TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation as profice carpet nucleic acid sequence (TNA). The method is highly sensitive, and has a high charter acid sequences, including those found in human calls, in HIV, HPV, and other nucleic acid containing systems, including bacteria and localisation of specific nucleic acid sequences, esp. HIV and HPV. Disclosure, Page 71; 172pp; English. 

Sequence 46 BP; 8 A; 11 C; 17 G; 10 T; 0 U; 0 Other;

ö Gaps ö 76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.077; Indels ; 0 Local Similarity 100.0%; Pred. No. 0.0 (es 29; Conservative 0; Mismatches Query Match Best Loc Matches

2 GGGACTITCCGCTGGGGACTITCCAGGGG 30

RESULT 31

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Gaps .; 0

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AAT30601 standard; DNA; 46

AAT30601;

(first entry) 19-FEB-1997 Target binding region #21.

Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavitus; HPV; HPV E2; human immunodeficiency vitus; HIV LTR; human papillomavitus; HIV LTR; sequence; asymmetry sequence; HIV LTR; binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss. 

Synthetic.

WO9617956-A2

13-JUN-1996,

95WO-US015944 07-DEC-1995; 94US-00353476 09-DEC-1994;

(GENE-) GENE POOL INC.

Weininger AM; Weininger S,

WPI; 1996-287199/29.

Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.

Disclosure; Page 70; 172pp; English,

AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR) and optionally a linker sequence, an assembly sequence (see AAR5994-R95998), an asymmetry sequence (see AAR9599-R96006), an unclear localisation signal sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR9599-R96006), and an OSA. The assembly sequence and asymmetry sequence (see AAR95993) are selected from NF-kappa-B, SPI, TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indiactor, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequences. Including those found in human calls, in HIV, HV, and other nucleic acid containing systems, including bacteria and viruses 

Sequence 46 BP; 7 A; 11 C; 17 G; 11 T; 0 U; 0 Other;

Gaps ô 76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.077; ive 0; Mismatches 0; Indels 7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35 GGGACTITCCGCTGGGGACTITCCAGGGG 30 29; Conservative Query Match Best Local Similarity 유

AAT30600 standard; DNA; 46 RESULT 32

19-FEB-1997 (first entry) AAT30600;

Target binding region #20.

Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss. AAT30600
AAT3 AAT3
AXX
ACA AAT3
DE Targ
XXX
CW TARG
KW HALV
KW HALV
KW HALV
KW HOUCH
KW O'C
XX O'C
X

Synthetic.

WO9617956-A2

13-JUN-1996.

95WO-US015944 07-DEC-1995; 94US-00353476 09-DEC-1994;

Weininger S, Weininger AM; (GENE-) GENE POOL INC.

Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV. WPI; 1996-287199/29.

Disclosure; Page 70; 172pp; English.

AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding

region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR96007), comparing the NAR95999-R96006), a nuclear localisation signal sequence (see AAR96007), and and association of the NAR9. The NAR8 (see AAR95965-CC (HRV) EZ, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere with NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation of the probe. The probe can be cade sequence (TNA). The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific acid sequences, including those found in human calls, in HIV, HIV, and other nucleic acid containing systems, including bacteria and 

Sequence 46 BP; 7 A; 11 C; 18 G; 10 T; 0 U; 0 Other;

Gaps ö 76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.077; 0; Indels 100.0%; Pred. ... 29; Conservative Best Local Similarity Matches 29; Conserv Query Match

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RESULT 33 AAV67098

AAV67098 standard; cDNA; 36 BP. AAV67098;

(first entry)

14-JAN-1999

HIV LTR #2

CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease; ss.

Human immunodeficiency virus 1. US5824770-A Synthetic. 

20-OCT-1998.

92US-00946233. 93US-00121438. 94US-00238212. 95US-00465590. 05-JUN-1995; 14-SEP-1992;

(GEHO ) GEN HOSPITAL CORP. 02-MAY-1994;

14-SEP-1993;

Georgopoulos K;

WPI; 1998-582621/49

Ikaros poly:peptide(s) - useful for treating disorders of immune system or corpus striatum

Disclosure; Col 27; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFKB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of

a delta A element, an NFKB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFKB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides, bind to delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides, competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements and/or Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding of Ikaros-responsive elements and/or inhibit protein-protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. AAV6655 to AAV67118 represent oligonucleotides given in the present invention 

Sequence 36 BP; 6 A; 9 C; 14 G; 7 T; 0 U; 0 Other;

Gaps ö 75.8%; Score 28.8; DB 2; Length 36; 93.8%; Pred. No. 0.088; ive 0; Mismatches 2; Indels GGGACTTTCCGCTGGGGACTTTCCAGGGAGGC 35 2 GGGACTITCCGCTGGGGACTITCCAGGGGGAC 33 1 Similarity 93.8%; 30; Conservative Best Local Similarity Matches 30; Conser Query Match g

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BP. AAQ61543 standard; cDNA; 37

AAQ61543;

(first entry) (revised) 25-MAR-2003 21-OCT-1994 HIV long terminal repeat sequence comprising Ikaros binding site.

Ikaros; zinc finger; protein; immune disorder; therapy; treatment; corpus striatum; regulatory gene; enhancer; regulatory element; gene expression; HIV; human immunodeficiency virus; ss.

Human immunodeficiency virus.

WO9406814-A1

31-MAR-1994

93WO-US008743. 14-SEP-1993; 92US-00946233. 14-SEP-1992;

(GEHO ) GEN HOSPITAL CORP.

Georgopoulos K;

WPI; 1994-118387/14.

I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders.

Disclosure; Page 29; 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in a therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is at risk for an immune disorder. It is of particular use in treating a disorder of the corpus striatum. Heterologous genes may be expressed by placing them under the control of an Ikaros responsive control element and contacting the element with an Ikaros protein. Potential high affinity binding sites 

AAT30615-T30634 represent probe nucleic acids of the invention. The probe of the invention contains a target binding region (TBR), a booster binding region (BBR), and an optional support or attachment (GSA). The target binding assembly (TBA) recognised by the TBR (see AAT30581-T30614) of the probe, contains at least one nucleic acid recognition unit (NAR), of the probe, an asymmetry sequence, an assembly sequence (see AAR96007), and an OSA. The assembly captured and asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequences are responsible for the folding and sequence and asymmetry sequences are responsible for the folding and sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR function, but provides stability and control over the spacing of the NAR function, capt the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for ö for the Ikaros proteins were found in the enhancer and promoter regions of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma genes, the SL3 and HIV long terminal repeat and in the regulatory domains of other T cell restricted antigens. Related sequences to the Ikaros motif were also found in the purine boxes of the IL2 gene in the in the HIV purp site of the TDT promoter as well as in the NFkB variant sites of the HIV long terminal repeat. See also AAQ61504-Q61543. (Updated on 25-MAR-2003 to correct PN field.) Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; human papillomavirus; HIV LTR; acquence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV. Gaps ö 2; Length 37; 1; Indels Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other; Score 28.4; DB Pred. No. 0.13; 0; Mismatches 31 4 GGGACTTTCCGCTGGGGACTTTCCAGGGAG 33 2 GGGACTITCCGCTGGGGACTITCCAGGGGG Disclosure; Page 76; 172pp; English AAT30615 standard; cDNA; 37 BP 95WO-US015944. 94US-00353476. 74.7**%**; 96.7**%**; Query Match
Best Local Similarity 50...
Best Local Similarity 50...
Conservative Weininger S, Weininger AM; 21-FEB-1997 (first entry) Probe nucleic acid PNA1. (GENE-) GENE POOL INC. WPI; 1996-287199/29. WO9617956-A2 07-DEC-1995; 09-DEC-1994; 13-JUN-1996 virus; ss. Synthetic. AAT30615; RESULT 35 AAT30615 8888888888888 ð

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The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific nucleic acid sequences, including those found in human cells, in HIV, HPV, and other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This oligonuclectide from the HIV long terminal repeat was identified as a potential high affinity binding site for Ikaros (see AAW70963-71). It partially includes a core motif GGGAA found in consensus recognition sites of murine Ikaros isoforms mIk-1, mIk-2 and mIk-3 (see AAV52830-32). High affinity binding sites for Ikaros have been found in enhancer and promoter regions of the regulatory domains of the TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal repeat and in the regulatory domains of other T cell restricted antigens (see AAV45358-402) by gel retardation assay. Ikaros is involved in early differentiation of lymphocytes, The invention provides Ikaros incleic acids (see AAV42805-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and AAV42840) and polypeptides, vectors and host cells. These are used to treat T and B cell diseases, to control expression of heterologous genes placed under control of an Ikaros-responsive element, to treat nervous system diseases and to modulate cell division, amplification or
detecting or localising a specific target nucleic acid sequence (TNA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ဌ
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and control cell differentiation.
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                               Length 37;
                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikaros, mIK; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; HIV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differentiation, especially in haematopoietic cells
                                                                                                                                         containing systems, including bacteria and viruses
                                                                                                                                                                                                                Sequence 37 BP; 7 A; 9 C; 13 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                               Score 28.4; DB 2;
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGGACTTTCCGCTGGGGACTTTCCAGGGGG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGACTTTCCGCTGGGGACTTTCCAGGGAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 39; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV LTR binding site for Ikaros.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV45402 standard; DNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-00711417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97CA-02194256.
                                                                                                                                                                                                                                                                           74.7%;
96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                     29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-378292/33.
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georgopoulos K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA2194256-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV45402;
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV45402 JA AAV5602 JA AAV5
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DB 2; Length 37;

74.7%; Score 28.4;

Query Match

Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

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The invention relates to an animal with a structurally intact Tp12 gene but functionally disrupted endogenous Tp12 (a protooncogene which encodes continually disrupted endogenous Tp12 (a protooncogene which encodes consistance to lipopolysaccharide induced endocoxin shock or tumour careaistance to lipopolysaccharide induced endocoxin shock or tumour can do Tp12 protein. Tp12 is useful for treating thematoid cartifitis. TNRalpha-mediated inflammatory diseases. Tp12 protein current in Tp12 is useful for treating rheumatoid arthritis. TNRalpha-mediated inflammatory diseases or LpS induced carbotoxin shock, may be treated by transfecting bone marrow derived cells invitro with a DNA construct which encodes sequences that interferes with the expression of function of the endogenous Tp12 in the cells and administering the cells to an animal. The knock out animals and the constructs used to generate the animals are useful in the development of compositions and methods of treating inflammation. Tp12 agonist and antagonist are useful as targets for the development of novel the novel cagnits which eliminate the functional role of Tp12 and as research tools confict and protein interactions involved in inflammatory disorders. Tp12 polymucleotide sequences facilitate the discovery and development of antice endotoxin shock and/or antinflammatory compounds. The present sequence is human immunodeficiency virus LTR NF-kB-specific (funclear factor kappa in interaction in the exemplification of the
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knock-out animal resistant to lipopolysaccharide-induced endotoxin shock and tumor necrosis factor alpha-mediated inflammatory disease, comprises a functionally disrupted endogenous Tpl2 gene.
                                                                                                                                                                                                                                                                                                                                                           Tpl2; serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB; inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock; research tool; LPS; lipopolysaccharide; nuclear factor kappa B; HIV;
                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus LTR NF-kB-specific double-stranded oligo.
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                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
                       1;
  0.13;
                       0; Mismatches
                                                          2 GGGACTTTCCGCTGGGGACTTTCCAGGGGG 31
                                                                                              4 GGGACTTTCCGCTGGGGACTTTCCAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28;
Pred. No.
  No.
    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 55; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus; ds
                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.7%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2001; 2001WO-US007588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2000; 2000US-00522775.
96.78;
                                                                                                                                                                                                    AAD17457 standard; DNA; 32
                                                                                                                                                                                                                                                                                (first entry)
                       29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-582266/65.
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Best Local Similarity
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200166559-A1.
                                                                                                                                                                                                                                                                                  10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rsichlis PN
                                                                                                                                                                                                                                          AAD17457;
    Best Local
                       Matches
                                                                                                                                                          RESULT 37
                                                                                                                                                                               AAD17457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an animal with a structurally intact Tp12 gene but functionally disrupted endogenous Tp12 (a protooncogene which encodes a cytoplasmic serine threonine protein kinase). The animal has increased resistance to lipopolysaccharide-induced endotoxin shock or tumour and DNA are useful for identifying compounds that agoinse or inhibit the cumour of Tp12 in useful for treating rheumatoid arthritis. TNFalpha-mediated inflammatory diseases Tp12 protein arthritis. TNFalpha-mediated inflammatory diseases or LPS induced arthritis. TNFalpha-mediated but ansisfecting bone marrow derived cells invitro with a DNA construct which encodes sequences that interferes with the expression of function of the endogenous Tp12 in the cells and constructs used to generate the animals are useful in the development of compositions and methods of treating inflammation. Tp12 agonist and constructs used to generate the animals are useful in the development of compositions and methods of treating inflammation. Tp12 agonist and an animal animals are useful in the development of compositions and methods of treating inflammation. Tp12 and as research tools to facilitate the elucidation of the mechanistic action of the novel constructs and protein interactions involved in inflammatory disorders. Tp12 protein interactions involved in inflammatory disorders. Tp12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide sequences facilitate the discovery and development of antiendotoxin shock and/or antinflammatory compounds. The present sequence is an oligonucleotide used for generating nulcear factor kappa B (NF-kB) DNA binding site probe used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knock-out animal resistant to lipopolysaccharide-induced endotoxin shock and tumor necrosis factor alpha-mediated inflammatory disease, comprises a functionally disrupted endogenous Tpl2 gene.
                                                                                                                                                                                                                                                                      Tpl2, serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB; inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock; research tool; LPS; lipopolysaccharide; nuclear factor kappa B; ss.
 Gaps
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                                                                                                                                                                                                                                         Nuclear factor kappa B binding site probe generating oligo #1.
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
 ö
Mismatches
                               29
                                                            ggactriccicricidadentriccades 32
                               GGGACTITCCGCTGGGGACTITCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Page 50; 98pp; English
 ö
                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2000; 2000US-00522775.
                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2001; 2001WO-US007588
                                                                                                                                            AAD17455 standard; DNA; 32
                                                                                                                                                                                                          (first entry)
 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       WO200166559-A1
                                                                                                                                                                                                          10-DEC-2001
                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rsichlis PN;
                                                                                                                                                                            AAD17455;
                               0
 Matches
                                                                                                          RESULT 38
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nev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear factor kappa B inhibitor complex; HIV enhancer; immunoglobulin kappa light chain enhaner; transcription factor; ds.
                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                   Primer; PCR; amplification; HIV-1; genome; vector; inhibition; replication; gene expression; infection; probe; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replication and the subsequent infection of neighbouring cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.7%; Score 28; DB 2; Length 33; 100.0%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33 BP; 7 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                          HIV probe corrsponding to NF-kappaB binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vectors for inhibiting HIV replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 100.0%; Pred. No. 0.1
Conservative 0; Mismatches
5 GGGACTTTCCGCTGGGGACTTTCCAGGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGACTTTCCGCTGGGGACTTTCCAGGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Part of the kappa light chain enhancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iacono KT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 25; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
                                                                                                                                ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US021880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0061984P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suhadolnik RJ, Adelson ME,
                                                                                                                                AAX34336 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN90922 standard; DNA; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UTEM ) UNIV TEMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9919496-A1
                                                                                                                                                                                                                    06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2004
25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                           AAX34336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAN90922;
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                                                                                        RESULT 39
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Gaps ö

73.7%; Score 28; DB 5; Length 32; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.0
Matches 28; Conservative

us-09-669-187a-148.szlm50.rng

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The present invention provides assays for identifying compounds which modulate NF-kappaB. NF-kappaB, along with IgNF-A, IgNF-E and IgNF-B, i lymphoid cell nuclear factor which regulates the transcription of the immunoglobulin genes. The modulators are useful in the control of activation of host cells
                                                                             DNA
                                                                          Identifying an NF-kappa B modulator, useful for analyzing protein DNA interactions in cells or in identifying transcriptional regulatory factors by detecting NF-kappa B or IKB DNA binding activity level or cytoplasmic localization.
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        necrosis factor kappa B; NF-kappaB;
transcriptional regulatory DNA element; immunoglobulin;
transcription enhancer; immunoassay; IgNF-B; HIV enhancer; ds.
   Lenardo MJ;
                                                                                                                                                                                                                                                                                                     73.7%; Score 28; DB 4; Length 34; 100.0%; Pred. No. 0.18; O; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          Seguence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
   Baeuerle PA, Lebowitz JH,
                                                                                                                                                                                                                                                                                                                                                                 2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                                                                                    Disclosure; Fig 14; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV enhancer NF-KB binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86US-00917441.
86US-00946365.
88US-00162680.
88US-00180173.
89US-00341436.
91US-00791898.
95US-00464364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-2002; 2002US-00037341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADT77252 standard; DNA; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
 Fan C, Maniatis TP,
Corcoran LM, Staudt 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEBOWITZ J H.
BALDWIN A S.
CLERC R G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORCORAN L M.
BAEUERLE P A.
LENARDO M J.
                                             WPI; 2001-060011/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHARP P A.
SINGH H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004214757-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-1986;
24-DEC-1986;
12-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2005
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21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1991;
06-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADT77252;
                                                                                                                                                                                                                                                                                                        Query Match
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(LEBO/)
(BALD/)
(CLER/)
(CORC/)
(BAEU/)
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SING/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SENR/
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymphoid cell nuclear factor; immunoglobulin gene transcription; Ig gene; IgNF-A; IgNF-E; IgNF-B; IgNF-B; IgNF-AppaB; PCR primer; ss.
                                                                                                                                                                                                                          Altering gene expression in a cell - by controlling dissociation of nuclear factor kappa B inhibitor complex to prevent or cause binding to an enhancer, e.g. HIV-dna.
                                                                                                                                                                                                                                                                                                                The sequence is part of the HIV LTR enhancer. Tag a and tag b represent binding sites for NF-kB. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                               Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clerc RG, Baltimore D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                          ch 73.7%; Score 28; DB 1; Length 34; I Similarity 100.0%; Pred. No. 0.18; 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lymphoid cell nuclear factor related sequence #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Singh H, Sen R, Baldwin AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGACTITCCGCTGGGGACTITCCAGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGACTTTCCGCTGGGGACTTTCCAGGG 33
                                                                                                                                                                (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE,
(MASI ) MASSACHUSETTS INST TECHNOLOGY,
(WHED ) WHITEHEAD INST.
                                                                                                                                                                                                                                                                                      Disclosure, Fig 1, 69pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86US-00817441.
86US-00946365.
88US-00155207.
88US-00162680.
88US-00280173.
89US-00318901.
89US-0031898.
91US-0071898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC66959 standard; DNA; 34 BP
                                                                                                      89WO-US000820
                                                                                                                                   88US-00162680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                               WPI; 1989-278306/38.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 28; Conserv
Homo sapiens
Unidentified
                                                                                                      01-MAR-1989;
                                                                                                                                   01-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                          WO8908147-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6150090-A.
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05-DEC-1988;
                                                                          08-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1989,
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13-NOV-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sharp PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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The invention describes an isolated nuclear protein NF-kappaB (I) which binds: in a sequence specific manner, to a transcriptional regulatory DNA clement of an immunoglobulin light or heavy chain genes, or both; in a sequence specific manner, to enhancer DNA sequences of the kappa light chain gene; or to DNA sequences in the upstream region of both mouse cheavy and kappa light chain gene promoters, and to DNA sequences of mouse cheavy chain gene enhancer. (I) is useful for enhancing the transcription of the gene enhancer, and for screening for expression of sequence specific binding protein. A polyclonal or monoclonal antibody (II) specific binding protein. A polyclonal or monoclonal antibody (II) specific manner, to a transcriptional regulatory DNA element of an immunoglobulin light or heavy chain gene, or both is useful in an immunoglobulin light or heavy chain gene, or both is useful in a cimmunoglobulin light or heavy chain gene. To both is useful in a biological fluid, where (II) is specifically reacts with light-BAPPAB or NF-kappaB. DNA (III) encoding the DNA binding domain of (I) is useful for specifically stimulating gene transcription comprising (III) linked to DNA encoding an activator of the RNA polymerase for the gene, and introducing the construct into the cell.
                                                                                                                                                                                                          Novel isolated nuclear protein NF-kappaB that binds in sequence specific manner to transcriptional regulatory DNA element of immunoglobulin light or heavy chain genes, or both, useful for enhancing transcription of gene
                                                                    Sharp PA, Singh H, Staudt L, Lebowitz JH; , Corcoran LM, Baeuerle PA, Lenardo MJ, Fan C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 53; 126pp; English.
                                                                 Sen R, S
Clerc RG,
(FANC/) FAN C.
(MANI/) MANIATIS T P.
                                                                                                                                                                 WPI; 2004-774818/76
                                                                 Baltimore D,
                                                                                             Baldwin AS,
Maniatis TP;
                                                                                                                                                                                                                                                                                           interest
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0
73.7%; Score 28; DB 13; Length 34; 100.0%; Pred. No. 0.18;
                                0; Indels
                   100.0%; Pred. No. 0.1 ive 0; Mismatches
                                                                  2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                        6 GGGACTTTCCGCTGGGGACTTTCCAGGG 33
                                    28; Conservative
                   Best Local Similarity
   Query Match
                                    Matches
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Gaps

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Electrophoretic mobility shift assay protein concentration primer #1
                                                                              Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection; autoimmune disease; inflammatory disease; cancer; vascular disease; primer; ss.
                AAA61055 standard; DNA; 35 BP
                                                 (first entry)
                                                 06-NOV-2000
                                                                                                                    Synthetic
                                  AAA61055;
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The present seguence is that of a primer corresponding to nucleotides 344 Use of deacetylase inhibitor combined with one or more compounds used in viral treatment, for manufacturing medicament for obtaining elimination of integrated, functional and pathogenic virus e.g. HIV-1 in mammal cell. Disclosure; Page 10; 56pp; English WPI; 2003-569183/53.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

24-NOV-1998;

99WO-US027244. 98US-0109872P

17-NOV-1999;

02-JUN-2000

WO200031113-A1

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shock protein, useful in the treatment of transplant rejection, autoimmune diseases and cancer.
                                                                                                                                                            The present sequence is a primer which was used to determine the concentration of a fusion protein in an electrophoretic mobility shift sasay. The fusion protein comprised the C-terminuus of the 70kD heat shock protein (HBp70), and the p50 subunit of transcription factor NF-kappaB. The fusion protein was created in order to determine the ability of the HBp70 sequence to direct other proteins into the cell. It was shown that HBp70 fragments are able to direct other proteins into the cell, a feature which can be used in the treatment of transplant rejection, autoimmune diseases such as rheumatoid arthritis, multiple
                                                                                                                                                                                                                                                                                                      sclerosis, diabetes, asthma, inflammatory bowel disease, psoriasis, hepatitis, Graves disease and viteligo, inflammatory diseases including osteoarthritis, pancreatitis and adult respiratory distress syndrome, cancer, vascular diseases (such as restenosis and atherosclerosis) and DNA and RNA viral replication diseases (including herpes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-1; long terminal repeat; virus elimination; PCR; primer; se.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 73.7%; Score 28; DB 3; Length 35; Local Similarity 100.0%; Pred. No. 0.18; nes 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35 BP; 5 A; 9 C; 13 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV-1 LAI long terminal repeat 5' PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGACTITCCGCTGGGGACTITCCAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 gegeacrircecriegedacrirceage 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adam E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
                                                                                                                                   Example 6; Page 21; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quivy V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2002; 2002WO-BE000197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-2001; 2001EP-00870289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ULBR ) UNIV LIBRE BRUXELLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACF05495 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
             Fujihara SM, Nadler SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burny A,
                                          WPI; 2000-400029/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003053468-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jan Lint C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACF05495;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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to 377 of the coding strand sequence of the HIV-1 LAI 5' long terminal repeat (LTR), and including an added KpnI restriction site. This was used as 5' primer, with the 3' primer given in ACF05496, to amplify a 186 bp fragment of the 5' LTR (nucleotides 345-531) for use in the plasmid construct pLTR(345-531)-luc. This plasmid was used to demonstrate the trichostatin-A (TSA) inducibility of HIV-1 LTRs and also to show that intact kappaB sites are required for maximal TSA inducibility of the HIV-1 promoter. The invention relates to the use of a deacetylase inhibitor (e.g. TSA) combined with one or more compounds used in a viral treatment for the manufacture of a medicament for obtaining elimination of integrated, functional and pathogenic viruses, e.g. HIV-1, in a mammal cell, including a human cell. This allows significant elimination and possible suppression of the presence of virus in a patient and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                        improves long-term control of viral infections in patients receiving highly active antiretroviral therapy (HAART) treatment
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Sequence 42 BP; 7 A; 11 C; 15 G; 9 T; 0 U; 0 Other;

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Gaps
                                     ;
73.7%; Score 28; DB 9; Length 42; 100.0%; Pred. No. 0.19; ive 0; Mismatches 0; Indels
                                                                         2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                                          15 GGGACTTTCCGCTGGGGACTTTCCAGGG 42
                                   28; Conservative
                    Best Local Similarity
 Query Match
                                     Matches
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AAT30606 standard; DNA; 45 BP. (first entry) Target binding region #26. 19-FEB-1997 AAT30606; 

Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss.

Synthetic.

WO9617956-A2

13-JUN-1996.

95WO-US015944. 94US-00353476 07-DEC-1995; 09-DEC-1994;

(GENE-) GENE POOL INC.

Weininger AM; Weininger S,

WPI; 1996-287199/29.

Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.

Disclosure; Page 72; 172pp; English.

AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR95994-R95998), an asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence sare responsible for the folding and association of the NARS. The NARS (see AAR95065-

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R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high andleic acid sequences, including those found in human cells, in HIV, HPV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                              72.6%; Score 27.6; DB 2; Length 45; 88.2%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                   Sequence 45 BP; 9 A; 11 C; 15 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                           35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GGGACTTTCCGCTGGGGACTTTCCAGAGGGGT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      88.28;
                                                                                                                                                                                                                                                                                                                                                                                              30; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                             viruses
                                                                                                                                                                                                                                                                                                                                                                                              Matches
         $$$$$$$$$$$$$$$$$$
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RESULT 46 AAA99616/c

AAA99616 standard; DNA; 35

AAA99616;

(first entry) 22-JAN-2001

NF-kB oligonucleotide #2.

NF-kB; alpha-melanocyte stimulating hormone; alpha-MSH; antibacterial; fungicide; virucide; antiinflammatory; vaginitis; cystitis; urethritis; balanoposthitis; toxic shock syndrome; sexually transmitted disease; probe; ss.

Homo sapiens.

WO200056353-A2

28-SEP-2000.

23-MAR-2000; 2000WO-US007846.

24-MAR-1999; 99US-0126233P.

(ZENG-) ZENGEN INC.

Catania A; Lipton J,

WPI; 2000-628219/60.

Treating uro-genital conditions, such as vaginitis, cystitis, urethritis, or balanoposthitis comprises using alpha-melanocyte stimulating hormone or a derivative of it. 

Example 9; Page 15; 37pp; English.

The present sequence is an oligonucleotide used to determine the level of NF-kB activity in human UI cells treated with alpha-melanocyte stimulating hormone (alpha-MSH). Alpha-MSH and its derivatives were shown to inhibit TNF-alpha induced NF-kB activation and binding. Alpha-MSH and its derivatives have potent antipyretic and antiinflammatory properties, yet they have extremely low toxicity. A uro-genital condition treatment system has been developed that complises a carrier and a polypeptide including a sequence derived from alpha-MSH. The system may be used to treat a uro-genital condition such as vaginitis, cystitis, urethritis, or balanoposthitis. It may also be used to prevent toxic shock syndrome and infection from sexually transmitted diseases, and to treat an antibiotic resistant microorganism. The polypeptides used in the treatment system

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RESULT 48
           AAT30604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the use of alpha-melanocyte stimulating hormone (MSH), its derivative, or both, to combat cancer and in inhibiting cancer cell proliferation by administering the above alpha-MSH to a patient with cancer. The alpha-MSH is useful for combating cancer and for inhibiting cancer cell proliferation, where the cancer is mesothelioma, and is selected from Hodgkin lymphoma, non-Hodgkin lymphoma, squamous cell carcinoma, breast cancer and colorectal cancer. Sequences ACC47365-366 represent positive and negative strands of NF-kappaB DNA binding assays for determining alpha-MSH inhibition of NF-kappaB in cancer cells
can reduce the viability of microbes, reduce the germination of yeast, kill microbes, treat inflammation associated with microbial infection, increase the accumulation of CAMP in microbes and inhibit replication and
                                                                                                                                                                                                                                                                                         MSH; alpha-melanocyte stimulating hormone; alpha-MSH; cancer; cytostatic;
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of alpha-melanocyte stimulating hormone to combat cancer and in
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.1%; Score 27.4; DB 10; Length 35; 96.6%; Pred. No. 0.32; ive 0; Mismatches 1; Indels (
                                                                           72.1%; Score 27.4; DB 3; Length 35; 96.6%; Pred. No. 0.32;
                                                                                                1; Indels
                                                     Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                    NF-kappaB DNA binding site negative strand
                                                                                                                       1 GGGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                                                                    GGGGACTTTCCGCTGGGGACTTTCCATGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibiting cancer cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 14; 27pp; English.
                                 expression of viral pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-2001; 2001US-0317514P.
                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-2002; 2002WO-US028257
                                                                                                                                                                                                   ACC47366 standard; DNA; 35
                                                                                                                                                                                                                                               (first entry)
                                                                                                  28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catania AP
                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIPT/) LIPTON J.
(CATA/) CATANIA A P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-290144/28.
                                                                                    Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                 WO2003020223-A2
                                                                                                                                                                                                                                                                                                       NF-kappaB; ss.
                                                                                                                                                                                                                                               11-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipton J,
                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                         ACC47366;
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                                                                            Query Match
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 8888888
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AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R85998), an asymmetry sequence, and an OSA. The assembly sequence and asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence are responsible for the folding and association of the NARs. The NARs (see AAR96007), and an OSA. The man immunodeficiency virus (HPV) E2, HPV LTR, human immunodeficiency virus (HPV) E2, HPV, and control over the Paget of the TBA. The method is nighly sensitive, and has a high degree of sepecificity. The method can be used for detecting specific nucleic acid sequences, including those found in human cells, in HIV, HPV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                           Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
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AAT30604 standard; DNA; 44
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ઠે 유 NF-kB; alpha-melanocyte stimulating hormone; alpha-MSH; antibacterial; fungicide; virucide; antiinflammatory; vaginitis; cystitis; urethritis; balanoposthitis; toxic shock syndrome; sexually transmitted disease;

22-JAN-2001 (first entry) NF-kB oligonucleotide #1. 23-MAR-2000; 2000WO-US007846.

WO200056353-A2.

28-SEP-2000.

Homo sapiens.

probe; ss.

99US-0126233P

24-MAR-1999;

Catania A;

Lipton J,

(ZENG-) ZENGEN

WPI; 2000-628219/60.

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Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; ATAR; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Lat binding unit; probe, assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                    Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
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                                                                                                                                                                                                                                                                                                Disclosure, Page 72; 172pp; English.
                                                                                                                                                                                             94US-00353476
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                                                                                                                                                                                                                                 Weininger AM;
                          (first entry)
                                           Target binding region #25.
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                                                                                                     virus; ss.
                                                                                                                     Synthetic.
        AAT30605;
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invention. The probe of the invention contains a TBR, a booster binding invention. The probe of the invention contains a TBR, a booster binding invention. The probe of the invention contains a TBR, a booster binding assembly, and an optional support or attachment (OSA). The target binding assembly (TBA) recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR95066), a nuclear localisation signal sequence (see AAR9507), and an OSA. The assembly sequence and asymmetry sequence are responsible for the folding and association of the NARS. The NARS (see AAR95965-CTC for the folding and association of the NARS. The NARS (see AAR95965-CTC FOY LOTE). THE NARS (HIV) LTR and Tat binding units. The linker sequence is an olisopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation of the probe. The probe can be caid sequence (TNA). The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific nucleic acid sequences, including those found in human cells, in HIV, and other nucleic acid containing systems, including bacteria and
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The present sequence is an oligonucleotide used to determine the level of NF-KB activity in human UI cells treated with alpha-melanocyte stimulating hormone (alpha-MSH). Alpha-MSH and its derivatives were shown to inhibit TMF-alpha induced NF-KB activation and binding. Alpha-MSH and its derivatives have potent antipyretic and antiinflammatory properties, yet they have extremely low toxicity. A uro-genital condition treatment system has been developed that comprises a carrier and a polypeptide including a sequence derived from alpha-MSH. The system may be used to treat a uro-genital condition such as vaginitis, cystitis, urethritis, or balanoposthitis. It may also be used to prevent toxic shock syndrome and infection from sexually transmitted diseases, and to treat an antibiotic resistant microorganism. The polypeptides used in the treatment system can reduce the viability of microbes, treat inflammation associated with microbial infection, increase the accumulation of cAMP in microbes and inhibit replication and

Treating uro-genital conditions, such as vaginitis, cystitis, urethritis, or balanoposthitis comprises using alpha-melanocyte stimulating hormone or a derivative of it.

Example 9; Page 15; 37pp; English.

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71.6%; Score 27.2; DB 2; Length 44; 90.6%; Pred. No. 0.39; ive 0; Mismatches 3; Indels

llarity 90.6%; Conservative

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GGGACTTTCCGCTGGGGACTTTCCGGGGAGGC 38 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33

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AAA99615 standard; DNA; 35

RESULT 50 AAA99615

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Sequence 35 BP; 6 A; 9 C; 11 G; 9 T; 0 U; 0 Other;

us-09-669-187a-148.szlm50.rni

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LOCATION: replace(1..38, "")
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OTHER INFORMATION: LINKING ANY OF THE NUCLEOSIDES MAY BE REPLACED
OTHER INFORMATION: WITH PHOSPHOROTHIOATE GROUPS, METHYL ESTER
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    ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                     COMPUTER RELABBLE FORD

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,519
FILING DATE: 20-FEB-1996
CLASSIFICATION 514
PRIOR APPLICATION NUMBER: US 08/123,188
FILING DATE: 20-SEP-1993
ATTONNEY/AGENT INFORMATION:
NAME: Oblon, No. 5990000man F.
REGISTRATION NUMBER: 24,618
REFRENCE/DOCKET NUMBER: 6042-001-68
TELEPRAK: (703) 413-3000
TELEFAX: (703) 413-3200
TELEFAX: 248855 OPAT UR
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 38; Conservative 0; Mismatches 0;
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MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: SYNTHETIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 38 base pairs
                                                                                                                   ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                      STREET: 1755 S. J
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
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Sequence 4564, Ap
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Sequence 90860, A
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Sequence 348, App
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33, Appl
33, Appl
18, Appl
36, Appl
56047, A
96049, A
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7, Appli
1, Appli
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Sequence 119899,
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Sequence 119901,
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Sequence 36,
Sequence 5,
Sequence 960,
Sequence 960,
Sequence 960,
Sequence 106,
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Sequence 4,
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Patent No. 51
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Sequence 1
Sequence 1
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Patent No. 5990090
GENERAL INFORMATION:
APPLICANT: NOBELICANT: METHODS AND COMPOSITIONS FOR TREATMENT
TITLE OF INVENTION: OF DISEASES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
US-08-661-507-5
US-09-396-196G-96047
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US-09-255-2018-924
US-09-255-2018-924
US-09-255-2018-924
US-09-277-418-19
US-09-277-431A-19
US-09-277-431A-19
US-09-277-431A-19
US-09-378-678D-10
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US-08-607-519-2
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Gaps

Gaps

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79.5%; Score 30.2; DB 2; Length 46; 91.4%; Pred. No. 0.0045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, Stephen B.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,257
FILING DATE: 28-MAY-1995
CLASSIFICATION 514
PRIOR APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-APR-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-APR-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-APR-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 12-DEC-1993
APPLICATION NUMBER: US 07/454,600
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 07/456,662
FILING DATE: 28-NOV-1993
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTCANEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (2212) 596-9000
                                                                                                                                                                                                                                                 1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
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Pred. No. 0.0052;
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10020
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43, Application US/08450257
Patent No. 5652122
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.9%;
86.8%;
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                                                                                                                                                                     32; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
3DNESS: single
                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
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                US-08-353-476-28
                                                                                                                                                                     Matches
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81.1%; Score 30.8; DB 2; Length 43;
Best Local Similarity 94.1%; Pred. No. 0.0025;
Matches 32; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/08353476

Setent No. 5871902.
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 degelerricegeregederrirecadegadeer 39
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRAMDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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MOLECULE TYPE: CDN;
HYPOTHETICAL: NO;
ANTI-SENSE: NO US-08-353-476-29
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: USA
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US-08-353-476-28
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APPLICANT: BARSOUM, James G.
APPLICANT: FAMELL, Stephen B.
APPLICANT: FAMELL, Stephen B.
APPLICANT: FAMELL, STEPHEN B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/450,246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGACTTTC 2
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llarity 86.8%; Pred. No. 0.0052;
Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/450,246
FILING DATE: 25-MAY-1995
GLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/235,403
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B170 CIP
                                                                                                          Sequence 43, Application US/08450246
Patent No. 5670617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haley Jr., James F. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                    RESULT 6
US-08-450-246-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-450-246-43
                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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5; Indels
                                                                                                                                                                                                                                                                                              APPLICANT: PAGO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: PAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
CORRESPONDENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTR:

ZIP: 10020
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/450,257
TLING DATE: 25-MAY-1995
TLING DATE: 25-MAY-1995
                                                                           1 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 38
                                              GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/454,60
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/456,662
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 18-DEC-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: AB-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) SGK-COACTTELEFORD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                      RESULT 5
US-08-450-257-44/c
; Sequence 44, Application US/08450257
; Patent No. 5652122
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
  33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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  Matches
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Gaps ö

Length 39; Indels

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                           APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: PAWELL, Stephen E.
APPLICANT: PARILL, Stephen E.
APPLICANT: PALICAN: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: INP PC compatible
SOFTWARE: PRECEDION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/934,450
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 20-JAN-1991
APPLICATION NUMBER: US 07/454,650
FILING DATE: 20-JAN-1991
APPLICATION NUMBER: US 07/454,650
FILING DATE: 21-DAG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION NUMBER: B170 CIP 2
TELECOMMUNICATION NUMBER: B170 CIP 2
TELECOMMUNICATION NUMBER: B170 CIP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 egegacrircecreegacrirceacegegacrire 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/08450098
Patent No. 5674960
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: PABO, Carl
APPLICANT: FAWELL, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-450-098-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
      FRANKEL, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 596-909
TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-450-098-44/c
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                                                                                                                   APPLICANT: PRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, James G.
APPLICANT: PEBINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: New YORK

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,246

FILING DATE: 25-MAY-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/25,403

FILING DATE: 21-MG-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-MG-1992

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-MG-1993

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-MG-1993

APPLICATION NUMBER: US 07/654,450

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DEC-1989

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DEC-1989

APPLICATION NUMBER: US 07/636,662

FILING DATE: 24-MOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

NAME: HALEY Jr., James F.

NAME: NAME: 27, James F.

NAME: NAME: NAME: 27, James F.

NAME: NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 2;
Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
TELERA: (212) 596-9090
TELERA: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: NUMBER: 27,794
                           Sequence 44, Application US/08450246; Patent No. 5670617; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-450-098-43
; Sequence 43, Application US/08450098
; Patent No. 5674980
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic)
US-08-450-246-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.8%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
US-08-450-246-44/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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APPLICANT: PARNKEL, Alan
APPLICANT: PARO, Carl
APPLICANT: PARSO, Carl
APPLICANT: PARBLL, Stephen B.
APPLICANT: PARNKELL, Stephen B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 2; Length 39;
Pred. No. 0.0052;
0; Mismatches 5; Indels
                                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SURREWT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,233

FILING DATE: 25-MAY-1995

CLASSIFICATION NUMBER: US 08/235,403

FILING DATE: 21-A06-1992

APPLICATION NUMBER: US 07/934,375

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,75

FILING DATE: 28-JUL-1993

APPLICATION NUMBER: US 07/098,766

FILING DATE: 28-JUL-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DC-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-AUG-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DC-1993

APPLICATION NUMBER: US 08/158,015

FILING DATE: 21-DC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Haley JT., James F.

RESTERENCE/POCKET NUMBER: B170 CIP 2

TELECOMMUNICATION NUMBER: B170

TELECOMMUNICATION NUMBER: B170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gegenerricescreeceaciriceacesegenerric 38
                                  Avenue of the Americas
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Patent No. 5747641
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 86.8%;
Matches 33; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELER: 14-8367
INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
   ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                 ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
               STREET: 1252 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                        STATE: Ne COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-451-233-43
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PEPINSKY, R. B.
VENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
                                                                                                                                                                                                                                                                                      CAMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-MAY-1995
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/934,078
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DRC-1999
APPLICATION NUMBER: US 07/454,650
FILING DATE: 21-DRC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DRC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DRC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DRC-1999
APPLICATION NUMBER: US 08/158,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 2
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Pred. No. 0.0052;
0; Mismatches 5
                                                        STREET: 1251 Avenue of the Americas STREET: 1251 Avenue of the Americas CITY: New York CUMTRY: USA ZIP: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: B170 CIP 2
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application US/08451233
Patent No. 5747641
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANKEL, Alan
PABO, Carl
BARSOUM, James G.
FAWELL, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 596-9000
TELEFA: (1212) 596-9090
TELEA: 14-8367
INPORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.9%;
ilarity 86.8%;
Conservative
                               TITLE OF INVENTION: TA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-450-098-44
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CORRESPONDENCE ADDRESS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FWHELL, Stephen B.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCES ADDRESS:
ADDRESSEE: FISH & NEAVE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,236
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1994
APPLICATION NUMBER: DC7/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 08/158,015
FILING DATE: 22-DAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTOCKNEY/AGENT INFORMATION:
NAME: Haley JT., James F.
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 deceacitricecreceacitriceaceceacitre 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44, Application US/08450236 Patent No. 5804604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-450-236-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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Patent No. 5804604

GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: FRANKEL, Alan
APPLICANT: FARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: FREINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.9%; Score 30; DB 2; Length 39; 86.8%; Pred. No. 0.0052; ive 0; Mismatches 5; Indels
          1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATME: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.9
Best Local Similarity 86.8
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-451-233-44
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US-08-450-236-43
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BAREOUM, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
CUNATY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PACENTIN PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGACTITICCGCTGGGGACTITICCACGGGGGACTITIC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 3;
Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                   FILING DATE: 21.AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY.AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
  US 07/934,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/08235403
Patent No. 6316003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-235-403-43
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Best Local Similarity 86.8%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 14-8367
INFORMATION FOR SEQ ID NO: 47
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-235-403-44/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PRBO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: FRANKLY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUTICATION INPORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEFAX: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                   PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: US 07/098,766

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DGC-1989

APPLICATION NUMBER: US 07/636,662

FILING DATE: 22-ANN-1991

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

ATTORNAY AGENT INFORMATION:

NAME: Haley JT., James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%; Score 30;
86.8%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEB: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
US/08/450,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/08235403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                     25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Conservative
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-08-235-403-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-450-236-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: BLAKE, MARY E.

APPLICANT: BLAKE, MARY E.

APPLICANT: GUTTERMAN, JORDAN U.

APPLICANT: HOFPWANN, JOSEPH J.

APPLICANT: BAILEY, DAVID T.

APPLICANT: JAYATILAKE, GAMINI S.

TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF;
FILE REFERENCE: CLFR.09/999,495

CURRENT FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 09/314,691

PRIOR APPLICATION NUMBER: 60/099,066

PRIOR PLING DATE: 1999-05-19

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19

SOFTWARE: PALENTIN VEY: 2.0

SOFTWARE: PALENTIN VEY: 2.0

SOFTWARE: PALENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BLAKE, MARY E.
APPLICANT: BLAKE, MARY E.
APPLICANT: GUTTERMAN, JOSEPH J.
APPLICANT: BLAKE, DAVID T.
APPLICANT: HOFFWANN, JOSEPH J.
APPLICANT: JAYATILAKE, GAMINI S.
APPLICANT: JAYATILAKE, GAMINI S.
TITLE OF INVENTION: TRITERENE COMPOSITIONS AND METHODS FOR USE THEREOF
FILE REFERENCE: CLFR.006
CURRENT APPLICATION NUMBER: US/09/992,837
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691
PRIOR PELING DATE: EARLIER FILING DATE: 1999-05-19
PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 9
LINGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.4%; Score 29.8; DB 3; Length 44; 93.9%; Pred. No. 0.0065; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.4%; Score 29.8; DB 3; Length 44; 93.9%; Pred. No. 0.0065; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACT 34
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             Sequence 9, Application US/0999495
Patent No. 6689398
GENERAL INFORMATION:
APPLICANT: ARNIZEN, CHARLES J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09992837
Patent No. 6746696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 93.9
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 31; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-999-495-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-992-837-9
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Matches
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US-09-314-691-9

Squence 9, Application US/09314691

Patent No. 6444233

GENERAL INFORMATION:

APPLICANT: BLAKE, MARY E.

APPLICANT: BLAKE, MARY E.

APPLICANT: BLAKE, MARY E.

APPLICANT: BAILEY, DAVID T.

APPLICANTON: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF

CURRENT APLICATION NUMBER: 60/099,066

EARLIER FILING DATE: 1998-05-19

MUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 9

LENGTH: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
78.9%; Score 30; DB 3; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.0052;
Matches 33; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GGGACTTTCCGCTGGGGACTTTCCAGGGAGCT 42
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APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTONEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECHONE: (212) 596-9000
TELECHONE: (212) 596-9000
TELECK: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 93.9
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-235-403-44
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US-09-999-495-9
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.2%;
Matches 31; Conservative
                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 45 base pairs
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STRANDEDNESS: both
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-580-988A-12
                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
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                                                                                                                                                                                       PARENAL NO. SPEZION:
APPLICANT: ARNTZEN, CHARLES J.
APPLICANT: BLAKE, MARY E.
APPLICANT: BLAKE, MARY E.
APPLICANT: GUTTERMAN, JORDAN U.
APPLICANT: HOFFMANN, JOSEPH J.
APPLICANT: BALLEY, DAVID T.
APPLICANT: JAYATILAKE, GAMINI S.
ITILE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF FILE REFERENCE: CLFR: 106
CURRENT PILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: BARLIER PRING DATE: 1999-05-19
PRIOR FILING DATE: BARLIER FILING DATE: 1998-09-03
PRIOR FILING DATE: BARLIER FILING DATE: 1998-09-03
PRIOR FILING DATE: BARLIER FILING DATE: 1998-09-03
PRIOR PLING DATE: EARLIER FILING DATE: 1998-09-03
PRIOR PLING DATE: EARLIER FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
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US-08-580-988A-12
US-08-580-988A-12
Sequence 12, Application US/08580988A
Sequence 12, Application US/08580988A
Fatent No. 5856161
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-000-720-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 0.0065;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGT 42
  2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACT 34
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MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macincosh
COMPATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
                                              10 GGGACTITCCGCTGGGGACTITCCAGGGAGGCT
                                                                                                                                                    ; Sequence 9, Application US/10000720
; Patent No. 6962720
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1 Similarity 93.9%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Texas
: USA
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                                                                                                             RESULT 19
US-10-000-720-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 9
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; Sequence 19, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
    APPLICANT: Weininger, Arthur M
    TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
    TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
    WINMER OF SEQUENCES: 117
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Saliwanchik & Saliwanchik
    STREET: 2421 N.W. 41st St., Suite A-1
    CITY: Gainesvile
    STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29.2; DB 2;
Pred. No. 0.011;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 43
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-2908
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 bp
TYPE: nucleic acid
STRANDEDNESS: double
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Gaps
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Jeanner 21, Application US/08353476

Patent No. 5871902

GENERAL INFORMATION:
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:
STREET: 2421 N.W. 41st St., Suite A-1

CITY: Gainesville
STATE: Florida

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29; DB 2; Length 46; Pred. No. 0.014;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.3%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.C Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGACTITCCGCTGGGGACTITCCAGGGG 30
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                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STRATE: Ploxida COUNTRY: USA ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
ATVORNEY/AGRAT INPORMATION:
NAME: BENERAL ON VUMBER: 35,746
REFERENCE/COCKET WUMBER: 35,746
TELECOMPUTICATION INPORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INPORMATION FOR SEQ ID NO. 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA UVDOTHETICAL: NO
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US-08-353-476-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-353-476-21
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0
                                                               76.8%; Score 29.2; DB 2; Length 45; 91.2%; Pred. No. 0.011; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
US-08-353-476-23
; Sequence 23, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; PAPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; TITLE OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.8%; Score 29.2; DB 2; Length 45; Best Local Similarity 91.2%; Pred. No. 0.011; Matches 31; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 32606

ZIP: 32606

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
                                                                                                                                                                                                                                                                           GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainegville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECPHONE: (904) 375-8100
TELEPRAX: (904) 375-8100
TELEFAX: (904) 372-8000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                     31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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                                                                                                    Best Local Similarity
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US-08-353-476-23
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US-08-353-476-19
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US-08-353-476-20
                                                                      Query Match
                                                                                                                                         Matches
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US-08-465-590-142

| Sequence 142, Application US/08465590
| Sequence 142, Application US/08465590
| Patent No. 5824770:
| APPLICANT: Georgopoulos, Katia A.
| TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 164
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: LAHIVE & COCKFIELD |
| STREET: 60 STATE STREET, Suite 510
| CITY: BOSTON |
| STATE: MASSACHUCETTS |
| COUNTY: USA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                     Sequence 27. Application US/08353476

Patent No. 2871902

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st St., Suite A-1

CITY: Gainesville

STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,476

FILING DATE:

CLASSIFICATION: 435

ATTONEX/AGBNT INFORMATION:

NAME: Bencen, Gerard H

REGISTRATION NUMBER: 35,746

REFRENCE/DOCKFY NUMBER: 35,746

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1000 TO TELECOMMUNICATION:

TELECOMMUNICATION 1000 TO TELECOMMUNICATION:

TELECOMMUNICATION 1000 372-5800

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHRRACTERISTICS:

LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.3%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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: USA
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US-08-353-476-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32606
                                                                                                                                                                             US-08-353-476-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
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76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 32606

ZIP: 32606

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENCEN, GEART H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-8800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
              REFERENCE/DOCKET NUMBER: GP-100
                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 29; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
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US-08-353-476-21
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US-08-353-476-22
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2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30

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Sequence 142, Application US/09723909
Patent No. 6630141
GENERAL INFORMATION:
APPLICANT GEOGOPOULOS, Katia A.
APPLICANT GEOGOPOULOS, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.8%; Score 28.8; DB 3; Length 36; Best Local Similarity 93.8%; Pred. No. 0.016; Matches 30; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPRES. MA
COUNTRY: USA
ZIP: O2110-2804
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER EADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACTIBLE
OPERATING SYSTEM: Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,909
FILING DATE: 28-No. 6630141-2000
PRIOR APPLICATION NUMBER: US/08/711,417
APPLICATION NUMBER: US/08/711,417
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INCORMATION:
NAME: Myers, 14-SEP-1992
ATTORNEY/AGENT INCORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELEPHONE: 617/542-8906
                                 REFERENCE/DOCKET NUMBER: 10287/007001
TELEPHONE 107542-5070
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
IENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 1inear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
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INFORMATION FOR SEQ ID NO: 142:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-711-417C-142
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Patent No. 6228611

GENERAL INFORMATION:

APPLICANT: Georgopoulos, Katia A.

ITTLE OF INVENTION:

NUMBER OF SEQUENCES: 202

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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COUNTRY: USA
ZIP: O2110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT: INFORMATION:
NAME: Myers, Louis P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascil (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MYSTER PAUL L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.8
Best Local Similarity 93.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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US-08-711-417C-142
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Sequence 9, Application US/09522775A

Parent No. 666096
GENERAL INFORMATION:
APPLICANT: TSichlis, Philip N.
TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases
FILE REFERRNCE: OTT-3202
CURRENT APPLICATION NUMBER: US/09/522,775A
CURRENT FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 32
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Sequence 11, Application US/09522775A

Patent No. 6660906

GENERAL INFORMATION:

APPLICANT: Tsichlis, Philip N.

TITLE REPERENCE: OTT-3202

CURRENT APPLICATION NUMBER: US/09/522,775A

CURRENT PILING DATE: 2000-03-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1
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             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                       74.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 96.7
Matches 29, Conservative
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                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                           , ANTI-SENSE: NO
US-08-353-476-38
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US-09-522-775A-9
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LENGTH: 32
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0
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TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28.8; DB 6; Length 36;
Pred. No. 0.016;
0; Mismatches 2; Indels
                                       Length 36;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                       75.8%; Score 28.8; DB 3; 93.8%; Pred. No. 0.016; iive 0; Mismatches 2;
                                                                                                                            2 GGGACTITCCGCTGGGGACTITCCAGGGGAC 33
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: alingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 Carry: Gainesville
                                                                                                                                                                                                                                                   CT-US93-08743-142
Sequence 142, Application PC/TUS9308743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGACTTTCCGCTGGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.8%;
Matches 30; Conservative
                                     Query Match 75.8
Best Local Similarity 93.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Gainesvi
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US93-08743-142
US-09-723-909-142
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US-08-353-476-38
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Gaps

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Gaps

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-533-341-6
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APPLICANT: Lipton, James M.
APPLICANT: Catania, Anna P.
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
FILLE REFERENCE: 52475.8004.US00
CURRENT APPLICATION NUMBER: US 60/126,233
PRIOR FILLING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE PATENTING OFFE: 1999-03-24
NUMBER OF SEQ ID NOS: 8
SSEQ ID NO 6
LENGTH: 35
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Pred. No. 0.05;
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APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 GGGACTTTCCGCTGGGGACTTTCCAGAGGGGT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09533341 Patent No. 8603044
GENERAL INFORMATION:
APPLICANT: Zengen, Inc.
TELECOMMUNICATION INFORMATION
                           TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEGUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                72.6%;
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Best Local Similarity 96.6'
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30, Conservative
                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
NATI-SENSE: NO
US-08-353-476-26
                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 36
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Sequence 2, 7.37
Sequence 2, 7.37
Sequence 3, 7.37
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Pred. No. 0.032;
0; Mismatches 0; Indels
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100.0%; Pred. No. 0.033;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                  Query Match 73.7%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                       2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
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STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GGGGACTTTCCGCTGGGGACTTTCCAGG 35
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REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-
      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
---hes 28; Conservative
                                                          ) OTHER INFORMATION: Probe US-09-522-775A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo Sapien
US-09-440-967-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
US-08-353-476-26
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US-09-440-967-4
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nucleic acid
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APPLICANT: ZENGEN, INC.
                                    linear
                                                       MOLECULE TYPE:
                STRANDEDNESS:
TOPOLOGY: li
                                                                         HYPOTHETICAL:
                                                                                            , ANTI-SENSE:
US-08-353-476-25
                                                                                                                                                                                                                                                                                                                                                       US-09-535-066F-9
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Fatent No. 5871902

GENERAL INFORMATION:
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N. W. 41st & L., Suite A-1
CONTY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
FILING DATE:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
CMEDIUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
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                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPRONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 31; Conserv
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MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
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STATE: F]
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 38
US-08-353-476-25
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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APPLICANT: Zengen, Inc.
APPLICANT: Lipton, James M.
APPLICANT: Catania, Anna P.
TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY PEPTIDES FOR USE IN HUMAN
TITLE OF INVENTION: IMMUNOSEICIENCY VIRUS
FILE REFERENCE: 54275.8004.USO0
CURRENT APPLICATION NUMBER: US/09/533,341
CURRENT FILING DATE: 2000-03-23
PRIOR PPLICATION NUMBER: US 60/126,233
PRIOR FILING DATE: 1999-03-24
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APPLICANT: Lipton, M.J.
APPLICANT: Catania, A.P.
TITLE OF INVENTION: A LYS-PRO-VAL DIMER, FORMULATIONS AND APPLICATIONS
FILE REPERBNCE: 54275.8005.US00
CURRENT APPLICATION NUMBER: US/09/535,066F
CURRENT PILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US 60/126,233
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 9
LENGTH: 35
                                                         Gaps
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69.5%; Score 26.4; DB 3; Length 35;
Best Local Similarity 96.4%; Pred. No. 0.14;
Matches 27; Conservative 0; Mismatches 1; Indels
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Oligonuclectide probes for NF-kB
DB 2;
  Score 27.2; DB;
Pred. No. 0.072;
                                                                                                           2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
                                                                                                                                                             7 degactrirccecredegactrirccedegadec 38
                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGACTTTCCGCTGGGGACTTTCCAGG 28
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                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09535066F
Patent No. 6800291
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Patent No. 6803044
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8
SOFWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
  Query Match 71.6%;
Best Local Similarity 90.6%;
Matches 29; Conservative
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GENERAL INFORMATION:

APPLICANT: Juan Shao-Chieh

APPLICANT: Juan Shao-Chieh

APPLICANT: Wright, Samuel D.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSE: AMGEN INC

STREET: 1840 DeHavilland Drive

CITY: Thousand Oaks

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 33;
GENERAL INFORMATION:
APPLICANT: Juan, Shao-Chieh
APPLICANT: Lichenstein, Henri S.
APPLICANT: Lichenstein, Henri S.
APPLICANT: Lichenstein, Henri S.
APPLICANT: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC
STREET: Lade Declavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,397A
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.4%; Score 26; DB 100.0%; Pred. No. 0.2 iive 0; Mismatches
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; Sequence 26, Application US/08484397A
; Patent No. 5869055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-324A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Curry, Daniel R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805,447-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 33 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.43
Best Local Similarity 100.8
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 91320-1789
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                                                                                                                                                                                                                                                                                               CITY: The
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-484-397A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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Patent No. 6773705
GENERAL INFORMATION:
APPLICANT: Faustman et al., Denise L.
TITLE OF INVENTION: Mthods for disquosing and treating autoimmune disease FILE REFERENCE: 1763-1120 Kethleen M. Williams
CURRENT APPLICATION NUMBER: US/09/258,682
CURRENT APPLICATION NOWER: 1999-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                            Gaps
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                                                                    69.5%; Score 26.4; DB 3; Length 35; 96.4%; Pred. No. 0.14;
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                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                     0; Mismatches
                                                                                                                                                                                                         1 GGGGACTTTCCGCTGGGGACTTTCCAGG 28
                                                                                                                                                                                                                                                  8 GGGGACTTTCCGCTGGGGACTTTCCATG 35
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US-08-484-397A-25
; Sequence 25, Application US/08484397A
; Patent No. 5869055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                      96.4%;
                                                                                                      Best_Local Similarity 96.4
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                   RESULT 41
US-09-031-629A-5
      US-09-533-341-5
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US-09-258-682-1
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LENGTH: 32
                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGRAT INON:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEFRAX: (904) 375-5800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCAGGGGGGCTT 35
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STREET: 2421 N W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMINICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CTTTCCGCTGGGGACT
                     ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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US-08-353-476-30
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lipton, M.J.
APPLICANT: Lipton, M.J.
APPLICANT: Catania, A.P.
TITLE OP INVENTION: A LP.
TITLE OP INVENTION: US/09/535,066F
CURRENT FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US 60/126,233
PRIOR PLING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
SEQ ID NO 10
LENGTH: 35
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Patent No. 5871902

GENERAL INFORMATION:

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:

ADDRESSE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st St., Suite A-1

CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                   Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide probes for NF-kB.
US-09-535-066F-10
                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                  68.4%; bcc.
100.0%; Pred. No. ...
0; Mismatches
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US-09-535-066F-10/c
; Sequence 10, Application US/09535066F
; Patent No. 6806291
                                                                     A-324A
                REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: 32,727
REFERENCE/DOCKET NUMBER: 32,727
REFERENCE/DOCKET NUMBER: 32,727
TELECOMMUNICATION INFORMATION:
TELEPAN: 805/47-1000
TELEPAN: 805/47-1000
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTER.STICS:
LENGTH: 33 base pairs
LENGTH: 33 base pairs
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
MOLECTUE TYPE: CDNA
US-08-484-397A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ZENGEN, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Florida
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US-08-353-476-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/08479852

Sequence 44, Application US/08479852

GENERAL INFORMATION:
APPLICANT: Sherrol H: McDonough, Thomas B. Ryder,
APPLICANT: Yeasing Yang
ITILE OF INVENTION: OLIGONUCLECTER AND PROBES
TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREE: California
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM F9/2 Model 50Z or 55SX
COMPUTER: 1BM F9/2 Model 50Z or 55SX
COMPUTER: 1BM P6/2 Model 50Z or 55SX
COMPUTER: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,85Z
FILING DATE:
CLASSIFICATION NUMBER: US/08/040,745
FILING DATE:
APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
FILING DATE: 7/10/90
APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
FILING DATE: 7/11/89
ATTORNEY/AGENT INFORMATION:
NAME: Warblurg, Richard J.
REGISTRATION NUMBER: 196/189
TELECOMMUNICATION INMBER: 196/189
TELECOMMUNICATION INMBER: 196/180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 27;
                                                                                                                                                                                    DB 3; Length 25; 1.2;
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                                                              ; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 2;
Pred. No. 1.3;
                                                                                                                                                                                Query Match 63.2%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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   TYPE: DNA ORGANISM: Artificial Sequence
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
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Patent No. 6936468

GENERAL INFORMATION:
APPLICANT: Robbins, Paul D.
APPLICANT: Lu, Lina
APPLICANT: diannoukakis, Nick
TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
TITLE OF INVENTION: PRE USE OF TOLEROGENICITY IN A HOST AND METHODS FOR
TITLE OF INVENTION: MAKING THE SAME
CURRENT APPLICATION NUMBER: US/09/844,915
CURRENT APPLICATION NUMBER: 05/02/04.29

PRIOR APPLICATION NUMBER: 05/02/04.29

NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
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Sequence 2, Application US/09844915

Patent No. 6936468

GENERAL INPORMATION:
APPLICANT: Robbins, Paul D.
APPLICANT: Lu, Lina
APPLICANT: Gamnoukakis, Nick
APPLICANT: Gamnoukakis, Nick
TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
TITLE OF INVENTION: MAKING THE SAME
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ORGANISM: Artificial Sequence
27 base pairs
                             TYPE: nucleic acid
STRANDENNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
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LOCATION: (0)...(0)
OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-417
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; Publication No. US20030087848A1
; GENERAL INFORMATION:
    APPLICANT: Bratler, Robert L.
    APPLICANT: Bretzler, Robert L.
    APPLICANT: Bretzler, Robert L.
    APPLICANT: Petersen, Deanna M.
    APPLICANT: Petersen, Deanna M.
    TITLE OF INVENTION: Irmunostimulatory Nucleic Acids for the TITLE OF INVENTION: Irmannostimulatory Nucleic Acids for the TITLE OF INVENTION: Irmannostimulatory Nucleic Acids for the TITLE OF INVENTION: UTEATMENT of Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT)
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    PRIOR FILING DATE: 2000-02-03
    NUMBER OF SEQ ID NOS: 1093
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Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels
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100.0%; Score 38; DB 3; I
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CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
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SOFTWARE: PastSEQ for Windows Version 3.0
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LENGTH: 38
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US-09-78-16-2354
US-09-78-16-2354
US-10-156-306-7511
US-10-342-902-5623
US-10-669-841-10514
US-10-669-841-10693
US-10-669-841-10693
US-10-669-841-10693
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US-10-669-841-10693
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US-10-719-956-140709
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US-10-719-956-398069
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US-09-776-479-148
US-09-776-479-148
Sequence 148, Application US/09776479
Sequence 148, Application No. US20040067902A9
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
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Sequence 417, Application US/09888326
Publication No. US20030026801A1
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TILLE OF INVENTION: Methods for Enhancing Antibody-Induced
TILLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REFERENCE: C1039/7052 (AWS)

US-09-888-326-417

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FEATURE:
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Publication No. US20030050268A1

Publication No. US20030050268A1

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR

TITLE OF INVENTION: UMBER: US/10/112,653

CURRENT APPLICATION NUMBER: US 60/279,642

PRIOR APPLICATION NUMBER: US 60/279,642

PRIOR APPLICATION NUMBER: US 60/279,642

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040

SOFTWARE FEASTERQ for Windows Version 3.0

SEQ ID NO 141

LENGTH: 38
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US-10-017-995-148
Sequence 149, Application US/10017995
Sequence 140, Application US/10017995
Sequence 140, Application US/20030055014A1
GENERAL INFORMATION:
TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
FILE REFERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 38; DB 5; Length 38; Best Local Similarity 100.0%; Pred. No. 2.7e-05; Matches 38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                Length 38;
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100.0%; Score 38; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-141
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 148
LENGTH: 38
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 148
LENCTH: 38
                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                               US-09-776-479-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-10-112-653-141
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Squence 148, Application US/10831778

Publication No. US20040235774A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Pouron, Yves

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/831,778

CURRENT FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 38
                                                                          Length 38;
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Sequence 148, Application US/10314578
Sequence 148, Application US/10314578
Publication No. US20030212026A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Schetter, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/JORG (HILMAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 1145
SEQ ID NO 148
SEQ ID NO 148
                                                                                                                                                                                                      1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
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                                                                       100.0%; Score 38; DB 5; I
100.0%; Pred. No. 2.7e-05;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0;
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OTHER INFORMATION: Synthetic Sequence US-10-017-995-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

OTHER INFORMATION: Synthetic Sequence
US-10-314-578-148
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                                                                            Query Match
Best Local Similarity 100.0
Matches 38; Conservative
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APPLICANT: Weininger, Susan
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US-08-860-844-29

Sequence 29, Application US/08860844

Sequence 29, Application US/08860844

Publication No. US20030104361A1

GENERAL INFORMATION:
APPLICANT: Weininger, Susan

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st St., Suite A-1

CITY: Gainesville
STATE: Florida
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                                       100.0%; Score 38; DB 8; Length 38; 100.0%; Pred. No. 2.7e-05; ive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: END PY Compatible
COMPUTER: END PY Compatible
CORERATIOR SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 69-100C1
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION OF SEQ 1D NO: 29:
SEQUIRGNE CHARACTERISTICS:
                                                                                                                                                                        1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
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US-10-407-543-29
; Sequence 29, Application US/10407543
; Sequence 20, US20030175789A1
; GENERAL INFORMATION:
                                               Query Match 100.
Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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US-08-860-844-29
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US-10-831-778-148
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TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A SPECIFIC SEQUENCE COMPOSITION
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Publication No. US20030104361A1
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Best Local Similarity 94.1%; Pred. No. 0.019;
Matches 32; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                             NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 418t St., Suite A-1 CITY: Gainesville STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION NUMBER: US/08/860,844
FILING DATE: 09-DN-1997
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHIK, DAVIG R.
REGISTRATION NUMBER: 35,746
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,746
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Saliwanchik & Saliwanchik
2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 43 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (352) 372-5
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 9, Application US/0999495; Publication No. US20030054052A1
GENERAL INFORMATION:
APPLICANT: BLAKE, WARY E.
APPLICANT: BLAKE, WARY E.
APPLICANT: GUTTERMAN, JORDAN U.
APPLICANT: HOFFWANN, JOSEPH J.
APPLICANT: BAILEY, DAVID T.
                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 93.9%;
Matches 31; Conservative
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Matches 32; Conservative
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US-09-992-837-9
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Publication No. USCO030175789A1
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
Heininger, Arthur Meininger, Arthur Secure Composition
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COMPUTER: TEADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 09-DEC-1994
CLASSIFICATION: 435
APPLICATION NUMBER: 09-DEC-1994
CLASSIFICATION: A35
ATORNEY/AGENT INORAMINER: 35-746
REFERENCE/DOCKET NUMBER: 35-746
REFE
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ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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MOLECULE TYPE: CD
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US-10-407-543-28
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Sequence 9, Application US/09992837

Publication No. US20030039705A1

GENERAL INFORMATION.

APPLICANT: ARNTZEN, CHARLES J.

APPLICANT: BLAKE, MARY E.

APPLICANT: BLAKE, MARY E.

APPLICANT: BAILEY, DAVID T.

APPLICANT: APPLICANT: ATTERPENE COMPOSITIONS AND METHODS FOR USE THEREOF TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF; TILE REFERENCE: CLFR:006

CURRENT APPLICATION NUMBER: US/09/992,837

CURRENT FILING DATE: 2001-11-16

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: ERRIER APPLICATION NUMBER: 60/085,997

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTING DATE: LABLIER FILING DATE: 1998-05-19

SEQ ID NO 9

LENGTH: 44
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Pred. No. 0.046;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                              79.5%; Score 30.2; DB 6; 91.4%; Pred. No. 0.032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGACTITCCGCTGGGGACTITCCAGGGGGACT 34
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
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APPLICANT: JAYATILAKE, GAMINI S.
TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
FILE REFERENCE: CLFR: 006
CURRENT APPLICATION NUMBER: US/09/999,495
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 09/314,691
PRIOR APPLICATION NUMBER: 60/099,066
PRIOR FILING DATE: 1998-05-19
PRIOR PPLING DATE: 1998-05-03
PRIOR PPLING DATE: 1998-05-03
PRIOR PLING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 9
LENGTH: 44
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: GUTTERMAN, JORDAN U.
APPLICANT: HOFPWANN, JORDAN U.
APPLICANT: HOFPWANN, JORDAN U.
APPLICANT: HOFPWANN, JORDAN U.
APPLICANT: JAYATILAKE, GAMINI S.
TITLE OF INVENTION: TRITTERPENE COMPOSITIONS AND METHODS FOR USE THEREOF FILE REFERENCE: CLFR.006
CURRENT APPLICATION NUMBER: US/10/000,720
CURRENT FILING DATE: PARLIER FALLIER APPLICATION NUMBER: 09/314,691
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-05-19
PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PALENT FILING DATE: 1998-05-19
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Pred. No. 0.046;
0; Mismatches 2; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.4
Best Local Similarity 93.9
Matches 31; Conservative
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Best Local Similarity
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US-10-000-720-9
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RESULT 15

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APPLICANT: ARNYZEN, CHARLES J.
APPLICANT: BLAKE, MARY E.
APPLICANT: GUTTERMAN, JORDAN U.
APPLICANT: GUTTERMAN, JORDAN U.
APPLICANT: GUTTERMAN, JORDAN U.
APPLICANT: BAILEY, DAVID T.
TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF;
TITLE REFERENCE: CLFR:006
CURRENT APPLICATION NUMBER: US/10/238,647
CURRENT FILING DATE: 1999-009
PRIOR FILING DATE: 1999-06-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 44
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Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: ALIA SELIMANCHIK & SAliwanchik STREET: 2421 N.W. 41st St., Suite A-1

CITT: GALBERON OF NUCLEIC ACIDS WITH A

STATE: Plorida

COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIALE: FIGHTAL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
CLASSIFICATION + 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAliwanchik, David R.
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 36-100C1
TELEPHONE: (152) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.4%; Score 29.8; DB (93.9%; Pred. No. 0.046;
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Sequence 9, Application US/10238647
Publication No. US20030203049A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Matches 31, Conservative
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US-08-860-844-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-238-647-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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RESULT 18
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Publication No. US20030104361A1
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur Maininger, Arthur Mathon OF DETECTION OF NUCLEIC ACIDS WITH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 0.08;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 45;
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MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-JUN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION: 435

ATTONEY/AGENT INPORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 35,746

REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 29.2; DB 2;
Pred. No. 0.08;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                       76.8%;
91.2%;
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Best Local Similarity 91.2%;
Matches 31; Conservative
                                                             LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
INFORMATION FOR SEQ ID NO:
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lineaı
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                     US-08-860-844-19
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US-08-860-844-23
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Gaps

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2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35

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Meininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
NUMBER OF SEQUENCES: 118
                                                                                                                                                                                                         Weininger, Arthur M
IITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 0.08;
0; Mismatches 3;
7 gegacririccecregeseacririccaesesescer 40
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                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/660,844
FILING DATE: 09-DC-1994
ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
                                                                                           US-10-407-543-19; Sequence 19, Application US/10407543; Publication No. US20030175789A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/10407543 Publication No. US20030175789A1 GENERAL INFORMATION:
                                                                                                                                                                                 APPLICANT: Weininger, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.8%;
Best Local Similarity 91.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                     CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-407-543-19
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Gaps

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FEATURE:
NAME/KEY: protein bind
OTHER INFORMATION: oligonucleotide from the human immunodeficiency
OTHER INFORMATION: virus long terminal repeat containing
OTHER INFORMATION: NF-kB binding site
                                                                                                                                                                                                                            Sequence 1, Application US/10925608
Publication No. US20050080023A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE REPERENCE: D6528
CURRENT APPLICATION NUMBER: US/10/925,608
CURRENT APPLICATION NUMBER: US 60/497,841
PRIOR FILING DATE: 2003-08-26
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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APPLICANT: Singh, Sujay
TITLE OF INVENTION: Selective Inhibitors of Nuclear
TITLE OF INVENTION: Selective Inhibitors of Nuclear
TITLE OF INVENTION: Factor-?B Activation And Uses Thereof
FILE REFERENCE: D6526
CURRENT PELLICATION NUMBER: US/10/981,082
CURRENT FILING DATE: 2004-11-04
PRIOR PILING DATE: 2005-11-06
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 1
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 45;
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                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.8%; Score 29.2; DB 9; Best Local Similarity 91.2%; Pred. No. 0.08; Matches 31; Conservative 0; Mismatches 3;
                                                                                                                     10 egeactriccecreeeaactriccaeeaacet 43
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  91.2%; Pred. No. 0.08;
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: NF-kappB oligonucleotide US-10-925-608-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10981082 Publication No. US20050201976A1 GENERAL INFORMATION:
Best Local Similarity 91.2
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                            RESULT 21
US-10-925-608-1
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US-10-981-082-1
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OTHER INFORMATION: NF- B oligonucleotide from human immunodeficiency
OTHER INFORMATION: virus-1 long terminal repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10602303
; Publication No. US20040058021A1
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat
; TITLE OF INVENTION: Treatment of Human Multiple Myeloma by Curcumin; FILE REFERENCE: D6467
; CURRENT APPLICATION NUMBER: US/10/602,303
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US 60/390,926
; PRIOR PILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                              COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29.2; DB 6;
Pred. No. 0.08;
0; Mismatches 3;
               ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGGGGGACTT 35
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APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATTORNEY/ACENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-10-407-543-23
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ORGANISM: Human immunodeficiency virus-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (152) 375-8100
ELEFAK: (152) 372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
     CORRESPONDENCE ADDRESS
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Gaps

76.8%; Score 29.2; DB 7; Length 45

Query Match

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Query Match 76.39
Best Local Similarity 100.0
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-860-844-21
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US-08-860-844-22
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RESULT 23
US-08-860-844-20
; Sequence 20, Application US/0860844
; Publication No. US2003104361A1
; Publication No. US2003104361A1
; GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: BETHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik
; ADDRESSEE: Saliwanchik
; ADDRESSEE: Saliwanchik
; ADDRESSEE: Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Publication No. US20030104361A1
GENERAL INFORMATION:
APPLICANT: Weininger, Strann
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SUSTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-UN-1997

CLASSIFICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION NUMBER: 08/353,476

FILING SAILWANCHIK, DAVIG R.

REGISTRATION NUMBER: 35,746

REPERENCE/DOCKET NUMBER: GP-100C1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 46 base pairs
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F: 2421 N.W. 41st St., Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGI.
MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                                                                                                             STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO
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US-08-860-844-21
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Sequence 22, Application US/08860844

Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1

CITTLE OF INVENTION: SPECIFIC SEQUENCE COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.096; tive 0; Mismatches 0; Indels
COMPUTER: PLORY disk
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: DEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION NUMBER: 08-100C1
ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERDHONE: (352) 372-5800
INFORMATION FOR SEQ ID NO: 21:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: FIGURE

CONTRY: 105A

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/0860,844

FILING DATE: 09-UN-1997

CLASSIFICATION 1435

PRIOR APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION: 435

RICHASSIFICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INPORMATION:

NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30
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RESULT 27
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Sequence 27, Application US/08860844

Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Acthur M

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSE: Saliwanchik & Saliwanchik

STREF: 2421 N W. 41st St., Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA
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                                                                                                                                                                                                                                      76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.096; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                   7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                  GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 35,746
REPERENCE/POCKET NUMBER: GP-1(
TELECOMMUNICATION: TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                            ; ANTI-SENSE: NO US-08-860-844-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: NO
US-08-860-844-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                            RESULT 26
US-08-860-844-27
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                                              Gaps
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Weininger, Susan
Weininger, Arthur Merthur Weininger, Arthur Merthor OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
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76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; I
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                        ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.3%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
NEGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                          7 decacitricecrededeacitriceadede 35
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                                                                                                2 GGGACTTTCCGCTGGGGACTTTCCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                     US-10-407-543-20
; Sequence 20, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-407-543-21
; Sequence 21, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO
ANTI-SENSE: NO
Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-407-543-20
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TYPE: nucleic acid
STRANDEDNESS: both
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STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
US-10-407-543-27
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Medininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
                                           OF DETECTION OF NUCLEIC ACIDS WITH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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COMPUTER: TBM PC Compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543

FILING DATE: 03-Apr-2003

PRIOR APPLICATION DATA:

APPLICATION MUMBER: US/08/860,844

FILING DATE: 09-JUN-1997

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: SAI!AMAICH', DAVIG R.

REGISTRATION NUMBER: 35,746

ATTORNEY/AGENT INFORMATION:

NAME: SAI!AMAICH', DAVIG R.

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET WUMBER: 35,746
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o. 0.096;
o, Indels
                                                           SPECIFIC SEQUENCE COMPOSITION
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CORRESPONDENCE ADDRESSE:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606
COMPUTER READDALE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.3%; Score 29; DB 100.0%; Pred. No. 0.(cive 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 21:
APPLICANT: Weininger, Susan
Weininger, Arthur M
TITLE OF INVENTION: METHOD OF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONS: (352) 375-8100
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/10407543; Publication No. US20030175789A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                      NUMBER OF SEQUENCES: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                        ZIP: 32606
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 29
US-10-407-543-22
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Gaps
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TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
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COMPUTER: PLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
0.096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                    CLASSILICATION: 43-5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-001-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT TRPCHMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELEPRONE (352) 375-800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.3%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.C Matches 29; Conservative 0; Mismatches
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APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATTONEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGACTITCCGCTGGGGACTITCCAGGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/10407543 Publication No. US20030175789A1 GENERAL INFORMATION:
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LENGTH: 37 base pairs
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SEQUENCE CHARACTERISTICS:
                       Query Match
Best Local Similarity 96.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
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Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                         Score 29; DB 6; Length 46; Pred. No. 0.096; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                           Query Match 76.3%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 29; Conservative 0; Mismatches
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGACTITCCGCTGGGGACTTTCCAGGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 45.7
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPAX: (352) 372-5800
TELEPAX: (352) 372-5800
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                 REFERENCE DOCKET NUMBER: GP-
TELEPONE: (352) 375-8100
TELEPANE: (352) 375-8100
TELEPANE: (352) 372-5800
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CONA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
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Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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US-08-860-844-38
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US-08-860-844-38
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STATE:
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                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Weininger, Susan
Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Score 28.4; DB 2; Length 37; Pred. No. 0.17; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.7%; Score 28.4; DB 6; Length 37; Best Local Similarity 96.7%; Pred. No. 0.17; Matches 29; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-DC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
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(352) 372-5800
                                                                                                                                                                                                               RESULT 32
US-10-407-543-38
US-10-407-543-38
; Sequence 38, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
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72.6%;
88.2%;
Query Match 72.6
Best Local Similarity 88.2
Matches 30; Conservative
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US-10-235-682-9/c
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                       APPLICANT: David Baltimore et al.
TITLE OF INVENTION: NUCLEAR FACTORS ASSOCIATED WITH TRANSCRIPTIONAL REGULATION
TITLE OF INVENTION: NUCLEAR FACTORS ASSOCIATED WITH TRANSCRIPTIONAL REGULATION
CURRENT APPLICATION NUMBER: US/10/037,341
CURRENT FILING DATE: 2002-01-04
PRIOR PPLICATION NUMBER: 08/464364
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
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Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Arthur M
   TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: Gainesville

CITY: Gainesville

STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION WHER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: SALWAMATION: A35
ATORNEY/AGENT INFORMATION:
NAME: SALWAMATION: DATA:
REGISTRATION NUMBER: 35,746
REGISTRATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 28; Conserv
       GENERAL INFORMATION:
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US-08-860-844-26
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                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: HIV
US-10-037-341-53
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US-08-860-844-26
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LENGTH: 34
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                                                Gaps
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Weininger, Susan
Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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MEDIUM TYEE Floppy disk

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRITY APPLICATION DATA:

APPLICATION NOMBER: US/10/407,543

FILING DATE: 03-Apr-2003

CLASSIFICATION: 435

PRIOR APPLICATION UMBER: US/08/860,844

FILING DATE: 09-UW-1997

APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                Indels
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Score 27.6; DB 2;
Pred. No. 0.34;
0; Mismatches 4;
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                                                                                                                                         7 eggactriccecresesacrirccasasasecer 40
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ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.6%; Score 27.6; DB
88.2%; Pred. No. 0.34;
tive 0; Mismatches
                                                                                             2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REBERENCE/DOCKET NUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                       Sequence 26, Application US/10407543 Publication No. US20030175789A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
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Best Local Similarity 88.2
Matches 30; Conservative
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RESULT 39
US-08-860-844-25
; Sequence 25, Application US/08860844
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                                          72.1%;
83.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                     TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
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US-08-860-844-24
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Publication No. US20030104361A1

GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 NW. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: NF-kappa B DNA binding site, negative strand
US-10-235-682-9
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 27.4; DB 5; Length 35;
Pred. No. 0.41;
0; Mismatches 1; Indels
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
CLASSIFICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTONIVEY/AGRAY INPORMATION:
ATTONIVEY/AGRAY INPORMATION:
NAME: SALIWANCHIK, DAVIG R.
REGISCRATION NUMBER: 35,746
REGISCRATION NUMBER: 35,746
REGISCRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                APPLICANT: Catania, Anna P.
TITLE OF INVENTION: A CANCER TREATMENT SYSTEM
FILE REFERENCE: 8022.US01
CURRENT APPLICATION NUMBER: US/10/235,682
CURRENT FILING DATE: 2002-09-05
PRIOR PILING DATE: 2002-09-05
PRIOR FILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGACTITCCGCTGGGGACTITCCAGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGACTTTCCGCTGGGGACTTTCCATGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.1%;
Best Local Similarity 96.6%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
APPLICANT: Lipton, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: C
HYPOTHETICAL: NC
ANTI-SENSE: NO
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US-08-860-844-24
                                                                                                                                                                                                                      SEQ ID NO 9
LENGTH: 35
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US-10-407-543-24
US-10-407-543-24
Sequence 24, Application US/10407543
Publication No. US20030175789A1
GENERAL INFORMATION:
Heininger, Susan
Heininger, Arthur M
Heininger, Arthur M
SPECIFIC SEQUENCE COMPOSITION
SPECIFIC SEQUENCE COMPOSITION
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
Score 27.4; DB 2; Length 44;
Pred. No. 0.41;
0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 418t St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGIGTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-407-543-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
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FEATURE: OTHER INFORMATION: NF-kappa B DNA binding site, positive strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 44;
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                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
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Sequence 8, Application US/10235682

Publication No. US20030108523A1

GENERAL INFORMATION:
APPLICANT: Lipton, James

APPLICANT: Catenia, Anna P.
ITITE OF INVENTION: A CANCER TREATMENT SYSTEM
FILE REFERENCE: 8022.US01

CURRENT APPLICATION NUMBER: US/10/235,682

CURRENT APPLICATION NUMBER: US 60/317,514

PRIOR FILING DATE: 2002-09-05

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 8

LENGTH: 35
                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/660,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-6100
TELEPHONE: (352) 372-6100
TELEPHONE: (352) 372-6800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.5%; Score 26.4; DB Best Local Similarity 96.4%; Pred. No. 1; Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27.2; DB Pred. No. 0.49; 0; Mismatches
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.6%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ANTI-SENSE: NO
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US-10-235-682-8
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Publication No. US20030175789A1
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
Weininger, Arthur Method OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
                      GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
CLASSIFICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAILwanchik, David R.
REGISTRATION NUMBER: 35,746
REGISTRATION FORKED INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 375-8100
TELEFAX: (352) 375-8100
TELEFAX: (352) 375-8200
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
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ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
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                                                                                                                                                                                           3: Saliwanchik & Saliwanchik
2421 N.W. 41st St., Suite A-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.6%;
Matches 29; Conservative
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  Publication No. US20030104361A1
                                                                                                                                              NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                       STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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US-10-407-543-25
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Sequence 12, Application US/10659053

Sequence 12, Application US/10659053

Publication No. US20050037032A1

GRNERAL INFORMATION:

APPLICANT: ZENGEN, James M.

APPLICANT: Lipton, James M.

APPLICANT: Lipton, James M.

APPLICANT: Lipton, James M.

TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR UROGENITAL CONDITIONS

FILE REFERENCE: 54275.8005.U503

CURRENT APPLICATION NUMBER: US/10/659,053

CURRENT APPLICATION NUMBER: US 60/126,233

FRIOR RILING DATE: 2000-03-23

FRIOR PELLING DATE: 1999-03-24

FRIOR PELLING DATE: 1099-03-44

FRIOR PELLING DATE: 2003-05-21

FRIOR APPLICATION NUMBER: US 60/382,887

FRIOR PELLING DATE: 2002-05-21

FRIOR PELLING DATE: 2002-05-21
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1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                      TITLE OF INVENTION: Methods For Diagnosing Autoimmune
TITLE OF INVENTION: Disease
FILE REFERENCE: 00786/457003
CURRENT APPLICATION NUMBER: US/10/775,487A
CURRENT FILING DATE: 2004-02-10
FRIOR APPLICATION NUMBER: 09/258,682
FRIOR APPLICATION NUMBER: 09/031,629
FRIOR PILING DATE: 1999-02-26
FRIOR APPLICATION NUMBER: 09/031,629
FRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide probes for NF-kB. US-10-659-053-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.9%; Score 25.8; DB Best Local Similarity 93.1%; Pred. No. 1.8; Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.4%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCAGGG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGGACTITCCGCTGGGGACTITCCAG 27
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                                     APPLICANT: Faustman, Denise L.
APPLICANT: Havashi, Takuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: Synthetic US-10-775-487A-1
                                                                    Hayashi,
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-860-844-30
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                                                                                                                     APPLICANT: Catania, Anna P.
APPLICANT: Liptorn, James M.
TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR UROGENITAL CONDITIONS
FILE REFERENCE: 54275.8005.US03
CURRENT APPLICATION NUMBER: US/10/659,053
CURRENT FILING DATE: 2000-03-23
FRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2002-05-21
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Patent No. US20020106689A1
GENERAL INFORMATION:
APPLICANT: Faustman
APPLICANT: Hayashi
TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease
FILE REFERENCE: MGH/Faustman 17633/1030
CURRENT FILING DATE: 1998-02-21
CURRENT FILING DATE: 1998-02-21
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Oligonucleotide probes for NF-kB.
US-10-659-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L Similarity 100.0%; Pred. No. 1.5
26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGACTITCCGCTGGGGACTITCCAG 27
                           ; Sequence 11, Application US/10659053; Publication No. US20050037032A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/10775487A; Publication No. US20050158302A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.5
Best Local Similarity 96.4
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
US-10-659-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
US-09-031-629A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-031-629A-5
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US-10-775-487A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 11
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Saliwanchik & Saliwanchik
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08860844 Publication No. US20030104361A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CTTTCCGCTGGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-860-844-7
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Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
               GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Athur M
TITLE OF INVENTION: BETHOU OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N W. 41st St., Sulte A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE READABLE FORM:

MEDIUM TYPE READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: BATCHILD Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-UN-1997

CLASSIFICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION NUMBER: 09-DEC-1994

CLASSIFICATION NUMBER: 35,746

FILING SAILWANCHIK, DAVIG R.

REGISTRATION NUMBER: 35,746

REGISTRATION NUMBER: 35,746

RELECOMMUNICATION INFORMATION:

TELEBHORE, DOCKET NUMBER: 35,746

RELECOMMUNICATION INFORMATION:

TELEBHORE, SAILWANCHING INFORMATION:

TELEBHORE, SAILWANCHING INFORMATION:

TELEBHORE, SAILWANCHING SAILON

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHRARACTERISTICS:

LENGTH: 48 base pairs
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STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.3%; Score 25.2; I Best Local Similarity 90.0%; Pred. No. 3; Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
; Publication No. US20030104361A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
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US-10-407-543-30
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                                                                                                                                                                                                                                                                                           COUNTRY:
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Gaps
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APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-JUN-1997
ATORNEY/AGENT INFORMATION:
NAME: SAliwanchik, David R.
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 48;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UNN-1997
CLASSIFICATION NUMBER: 08/353,476
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATONEY/AGENT INFORMATION:
NAWE: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.3%; Score 25.2; I Best Local Similarity 90.0%; Pred. No. 3; Matches 27; Conservative 0; Mismatches
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CITY: Gainesville
STATE: Plorida
COUNTRY: USA
ZIP: 32606
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US-10-407-543-30
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; Publication No. US20030175789A1
; GENERAL INFORMATION:
    APPLICANT: Weininger, Susan
    Weininger, Atthur Meininger, American Neininger, American Specific Sequence Composition
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
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COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543

FILING DATE: 03-Apr-2003

CLASS:FICATION DATA:

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-JUN-1997

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-JUN-1997

APPLICATION NUMBER: 08/353,476

FILING DATE: 09-JEC-1994

ATORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 35,746

RECISTRATION NUMBER: 35,746

TELECOMMONICATION INDRER: 35,746

TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                         DB 2; Length 27; 3.7;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                         65.8%; Score 25; DB ilarity 100.0%; Pred. No. 3.7 Conservative 0; Mismatches
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACTTTCCGCTGGGGACTTTCCA 27
                                                                                                                                                                                                                                                                                                                                                                                          GGGACTITCCGCTGGGGACTITCCA 26
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 7:
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 27 base pairs
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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DB 6; Length 27; 3.7;
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                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
9.1;
 Query Match 65.8%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 3.7 Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.2%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 9.1 Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 16, 2006, 02:34:12
Job time : 555.471 secs
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                                                                           3 GGGACTTTCCGCTGGGGACTTTCCA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGGACTITCCGCTGGGGACTITCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGGACTTTCCGCTGGGGACTTTCC 25
                                                                                                                                       US-09-844-915-1; Sequence 1, Application US/09844915; Sequence 1, Patent No. US20020048564A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Sequence 2, Appli Sequence 6689, A Sequence 103464, Sequence 208241, Sequence 258779, Sequence 454114, Sequence 122668, Sequence 1383495, Sequence 6764, A

Sequence 213042, Sequence 767705, Sequence 2, Appli

Sequence 196232, Sequence 378884, Sequence 510666, Sequence 280766, Sequence 314081, Sequence 318283,

Sequence 11173, A Sequence 11173, A Sequence 104360, Sequence 252171, Sequence 569838, Sequence 571272, Sequence 5145, Ap Sequence 5396, Ap Sequence 2596, Ap Sequence 2596, Ap Sequence 68699, A Sequence 68699, A

Sequence 34784, A Sequence 947813, A Sequence 97013, A Sequence 93496, A Sequence 93496, Sequence 956110, Sequence 767633, Sequence 152849, Sequence 194663, Sequence 201921, Sequence 454205, Sequence 454205, Sequence 454205, Sequence 51899, Sequence 51899, Sequence 51899, Sequence 51899, Sequence 51899, Sequence 518999, Sequence 51899, Sequence 51899, Sequence 518999, Sequence 5189999, Sequence

Sequence 139984, Sequence 148772, Sequence 213033, Sequence 213054,

Sequence 255943, Sequence 264919, Sequence 264938, Sequence 295909,

Sequence 318422, Sequence 323032,

Sequence 1042809, Sequence 860573, Sequence 337618

Sequence 369219, Sequence 411393, Sequence 577777, Sequence 34784, A

Sequence 279653, Sequence 279653, Sequence 240420, Sequence 1244998, Sequence 410363, Sequence 815776, Sequence 215881,

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US-11-136-527-139991
US-11-136-527-213042
US-10-310-310-914A-767705
US-10-310-914A-29454
US-10-310-914A-29454
US-10-310-914A-29454
US-10-310-914A-1383495
US-10-310-914A-1383495
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US-10-310-914A-2963333334
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US-10-310-914A-915881
US-11-175-8859-27611
US-11-175-8859-27611
US-11-175-8859-3455
US-10-310-914A-915881
US-10-310-914A-918891
US-10-310-914A-91889
    37.9
37.9
                                  Sequence 32817, A Sequence 32817, A Sequence 3316, A Sequence 43102, A Sequence 273210, Sequence 273212, Sequence 21349, Sequence 260545, Sequence 507340, Sequence 507340,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273212,
21940, A
103498,
260545,
507340,
528104,
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                                                                                                      February 16, 2006, 02:03:53; Search time 354.248 Seconds (without alignments) 98.157 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, A Sequence 12, Sequence 13, App Sequence 2, A Sequence 6, A Sequence 1005; Sequence 2005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-175-859-16894 Sequence 16894, A US-11-175-859-29564 Sequence 29564, A US-11-175-859-78404 Sequence 78404, A US-11-175-859-108242 Sequence 108942,	US-11-175-859-111846 Sequence 111846,	US-10-310-914A-481857 Sequence 481857, c	US-10-310-914A-940417 Sequence 940417,	US-11-101-244-1342196 Sequence 1342196,	US-11-083-784-1342196 Sequence 1342196, C	US-10-310-914A-880143 Sequence 880143,	US-10-310-914A-983911 Sequence 983911,	US-10-770-726-1531 Sequence 1531, Ap	US-IO-310-914A-470528 Sequence 470528,	US-II-011-347-2195 Sequence 1223013,	US-10-310-914A-1229664 Sequence 1229664,	US-10-310-914A-515600 Sequence 515600,	US-10-310-914A-920517 Sequence 920517,	US-IU-3IU-9I4A-IZZ/854 Sequence IZZ/854, 178-11-131-848-83973 Sequence 93973 B	113-11-121-043-323-3 Sequence 323-3, A	US-11-121-849-245310 Sequence 245310,	US-11-121-849-351482 Sequence	US-11-121-849-392406 Sequence	US-11-121-849-480753 Sequence	US-11-121-849-514563 Sequence 514563,	US-11-121-849-514564 Sequence 514564,	US-11-121-849-5/4900 Sequence	US-11-136-527-52210 Sequence 52210, A	US-11-136-527-52215 Sequence 52215, A	US-11-136-527-52220 Sequence 52220, A	US-11-136-527-247224 Sequence 247224,	US-11-175-859-241 Sequence 241, App C	US-II-175-859-24603 Sequence 24603, A	US-11-1/5-859-73037 Sequence 73037, A	US-11-175-859-94754 Sequence 94754, A	US-11-175-859-114859 Sequence 114859,	US-10-310-914A-458309 Sequence 458309,	US-10-310-914A-1017158 Sequence 1017158,	US-10-310-914A-1020590 Sequence	US-10-310-914A-24012 Sequence	US-10-310-914A-1090819 Sequence 1090819,	US-10-310-914A-1298143 Sequence 1298143,	US-10-750-185-8519 Sequence 8519, Ap	US-10-750-623-8519 Sequence 8519, Ap	US-10-310-914A-166305 Sequence 166305,	US-II-121-849-29916 Sequence 29919, A US-II-121-849-50786 Sequence 50786, A	US-11-121-849-60898 Sequence 60898, A	US-11-121-849-61350 Sequence 61350, A	US-II-121-849-353099 sequence	US-11-121-849-399270 Sequence	US-11-121-849-423422 Sequence 423422,	US-11-136-527-148785 Sequence 148785,	US-11-136-527-255946 Sequence 255946,	US-11-136-527-273444 Sequence US-11-136-527-323329 Sequence	US-10-310-914A-637718 Sequence	US-11-175-859-19585 Sequence 19585, A	US-11-175-859-27865 Sequence 27865, A	US-11-175-859-34114 Sequence 34114, A	US-II-1/5-859-44652 Sequence 44652, A	US-11-175-859-66686 Sequence 66686, A	US-11-175-859-73803 Sequence 73803, A
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11 US-11-175-859-16894 Sequence 16894, A 11 US-11-175-859-29564 Sequence 29564, A 11 US-11-175-859-78404 Sequence 78404, A 11 US-11-175-859-108242 Sequence 108242,	37.9 50 11 US-11-175-859-111846 Sequence 111846,	.2 37.4 19 7 US-10-310-914A-481857 Sequence 481857, C	.2 37.4 19 7 US-10-310-914A-940417 Sequence 940417,	.2 37.4 19 9 US-11-101-244-1342196 Sequence 1342196,	2 37.4 19 10 US-11-1043-744-1342196 Sequence 1342196,	. 2 7.4 20 7 US-10-310-914A-880143 Sequence 880143,	.2 37.4 20 7 US-10-310-914A-983911 Sequence 983911,	.2 37.4 21 7 US-10-716-11531 Sequence 1531, Ap	.2 37.4 21 7 US-10-310-9144-4/0228 Sequence 4/0528,	. 37.4 21 11 US-11-001-347-2195 Sequence 2195, Ap	.2 37.4 22 7 US-10-310-914A-1229664 Sequence 1229664,	.2 37.4 23 7 US-10-310-914A-515600 Sequence 515600,	.2 37.4 23 7 US-10-310-914A-920017 Sequence 920517,	.2 37.4 23 / US-10-210-21446-122/854 Sequence 122/854,	2 3 7 4 25 11 11S-11-121-04-121890 Semiente 123890.	. 2 37.4 25 11 US-11-121-849-245310 Sequence 245310,	.2 37.4 25 11 US-11-121-849-351482 Sequence	.2 37.4 25 11 US-11-121-849-392406 Sequence	.2 37.4 25 11 US-11-121-849-480753 Sequence	.2 37.4 25 11 US-11-121-849-514563 Sequence 514563,	.2 37.4 25 11 US-11-121-849-514564 Sequence 514564,	.2 3/.4 25 II US-II-IZI-849-5/4900 Sequence	. 2 37.4 25 11 US-11-136-527-52210 Sequence 55220. A	.2 37.4 25 11 US-11-136-527-5215 Sequence 52215, A	.2 37.4 25 11 US-11-136-527-52220 Sequence 52220, A	.2 37.4 25 11 US-11-136-527-247224 Sequence 247224,	.2 37.4 50 11 US-11-17-859-241 Sequence 241, App	.2 37.4 50 II US-II-17-85-24603 Sequence 24603, A	. 37.4 50 11 US-11-17-859-7337 Sequence 7222, A	.2 37.4 50 11 US-11-175-859-94754 Sequence 94754, A	.2 37.4 50 11 US-11-175-859-114859 Sequence 114859,	36.8 22 7 US-10-310-914A-458309 Sequence 458309,	36.8 23 7 US-10-310-914A-1017158 Sequence 1017158,	36.8 23 7 US-10-310-914A-1020590 Sequence	36.8 24 7 US-10-310-914A-24012 Sequence	36.8 24 7 US-10-314A-1090819 Sequence 1090819,	36.8 24 7 US-10-310-914A-1298143 Sequence 1258143,	36.8 25 7 US-10-750-185-8519 Sequence 8519, Ap	36.8 25 7 US-10-750-623-8519 Sequence 8519, Ap	36.8 25.7 US-10-310-914A-166305 Sequence 166305.	36.8 25 11 US-11-121-849-59716 Sequence 29-10, A	36.8 25 11 US-11-121-849-60898 Sequence 60898, A	36.8 25 11 US-11-121-849-61350 Sequence 61350, A	36.8 25 II US-II-121-849-363099 sequence	36.8 25 11 US-11-121-849-399270 Sequence	36.8 25 11 US-11-121-849-423422 Sequence 423422,	36.8 25 11 US-11-136-527-148785 Sequence 148785,	36.8 25 11 US-11-136-527-255946 Sequence 25946,	36.8 Z5 II US-II-136-527-273444 sequence	36.8 28 7 US-10-310-914A-637718 Sequence	36.8 50 11 US-11-175-859-19585 Sequence 19585, A	36.8 50 11 US-11-175-859-27865 Sequence 27865, A	36.8 50 11 US-11-175-859-34114 Sequence 34114, A	36.8 50 11 US-LI-1/5-829-444052 Sequence 44057. A	36.8 50 11 US-11-175-859-66686 Sequence 66686, A	36.8 50 11 US-11-175-859-73803 Sequence 73803, A

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APPLICANT: SHISHODIA, SHISHIR
TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AN
TITLE OF INVENTION: B KINASE
TITLE OF INVENTION: ACTIVATION AND USES THEREOF
FILE REFERENCE: CLFR: 2551S
CURRENT FILING DATE: 2005-07-12
PRIOR PLICATION NUMBER: 60/587,187
PRIOR PLICATION NUMBER: 60/587,187
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 2014-07-12
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Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 38; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-141
               TILLE OF INVENTION: INVENTATION: DISEASES CURRENT APPLICATION NUMBER: US/11/127,654 CURRENT FILING DATE: 2005-005-12 PRIOR APPLICATION NUMBER: US 10/112,653 PRIOR PILING DATE: 2002-03-29 PRIOR FILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 1040 SOFTWARE: Patentin version 3.2 ENGTH: 38
      TITLE OF INVENTION: INFLAMMATORY DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/11179321; Publication No. US20060019907A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial sequence
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US-11-179-321-1
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Sequence 1225293,
Sequence 1225369,
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Sequence 1284397,
Sequence 128959,
Sequence 287193,
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Sequence 287193,
Sequence 286334,
Sequence 296334,
Sequence 319693,
Sequence 319693,
Sequence 319693,
Sequence 376371,
Sequence 572158,
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Sequence 572158,
Sequence 572158,
Sequence 576637,
Sequence 576637,
Sequence 5615, App
Sequence 5615, App Sequence 61618, App
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Sequence 1926, Ap
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Sequence 1928, Ap
Sequence 143105,
Sequence 594497,
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Sequence 1178527,
Sequence 942238,
Sequence 942238,
Sequence 1129011,
Sequence 65668,
Sequence 877624,
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Sequence 1245002,
Sequence 1364403,
Sequence 231296,
Sequence 391707,
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Sequence 823213,
Sequence 1096071,
                                               Sequence 670879,
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Sequence 1337223
      Sequence 504569,
US-10-310-914A-504569
US-10-310-914A-627070
US-10-310-914A-670879
US-10-310-914A-1179595
US-10-310-914A-1179595
US-10-310-914A-1245002
US-10-310-914A-1245002
US-10-310-914A-331296
US-10-310-914A-331296
US-10-310-914A-331707
US-11-001-347-1925
US-11-001-347-1927
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US-10-310-914A-641022

US-10-310-914A-823213

US-10-310-914A-823213

US-10-310-914A-1096671

US-10-310-914A-1096657

US-10-310-914A-1252593

US-10-310-914A-1252593

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US-11-121-849-164678

US-11-121-849-164678

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US-11-121-849-287193

US-11-121-849-37876

US-11-131-849-37878

US-11-131-849-37878

US-11-131-849-37883

US-11-131-849-37883

US-11-131-849-37883

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US-11-131-85-37-386316

US-11-136-527-36637
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US-11-175-859-5133
US-11-175-859-5133
US-11-175-859-25627
US-11-175-859-31060
US-11-175-859-48346
US-11-175-859-61618
US-11-175-859-78249
US-11-175-859-109446
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US-10-310-914A-1129011
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Sequence 5, Application US/11179321
Publication No. US20060019907A1
GENERAL INFORMATION:
APPLICANT: AGGARWAL, BHARAT
APPLICANT: SHISHODIA, SHISHIR
TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AND
TITLE OF INVENTION: A KINASE
TITLE OF INVENTION: ACTIVATION AND USES THEREOF
FILE REFERENCE: CLFR:255US US-11-179-321-5

RESULT 1 US-11-127-654-141

Sequence 141, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

ALIGNMENTS

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US-11-179-321-6
    US-11-175-815-3
                                            Query Match
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US-11-175-815-3
US-11-175-815-3
Sequence 3, Application US/11175815
Sequence 3, Application NG. US2006002932A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A METHOD FOR PREVENTING HIV-1 INFECTION OF CD4 CELLS
FILE REFERENCE: 2048/50875-DAA/JPW/AJD
CURRENT PILING DATE: 2005-07-05
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 3
LENGTH: 23
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; OTHER INFORMATION: Primer
US-11-179-321-5
                                                                                                                                                                                                                                                                                                    Score 29.2; DB 11;
Pred. No. 0.017;
0; Mismatches 3;
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US-11-116-746-12
Squance 12, Application US/11116746
Publication No. US20060020114A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin
APPLICANT: GUTTEY, Mustin
APPLICANT: Wood, William
TITLE OF INVENTION: Apo-2DCR
FILE REPERENCE: Pill OF
CURRENT APPLICATION NUMBER: US/11/116,746
CURRENT APPLICATION NUMBER: US/08/878,168
PRIOR FILING DATE: 2005-04-28
PRIOR FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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CURRENT APPLICATION NUMBER: US/11/179,321
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: 60/587,187
PRIOR FILING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 5
LENGTH: 45
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                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                      Query Match 76.8%;
Best Local Similarity 91.2%;
Matches 31; Conservative
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US-11-116-746-12
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Best Local Similarity
Matches 24; Conserva'
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US-11-179-321-2
i Sequence 2, Application US/11179321
j Publication No. US2006019907A1
j Publication No. US2006019907A1
j GENERAL INFORMATION:
j APPLICANT: AGGARWAL, BHARAT
j APPLICANT: SHISHODIA, SHISHIR
j TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AT TITLE OF INVENTION: ACTIVATION AND USES THEREOF
j TITLE OF INVENTION: ACTIVATION AND USES THEREOF
j TITLE OF INVENTION: ACTIVATION AND USES THEREOF
j CURRENT FILING DATE: 2005-07-12
j PRIOR APPLICATION NUMBER: 60/587,187
j RIOR APPLICATION NUMBER: 60/587,187
j RIOR APPLICATION NUMBER: 60/587,187
j RORPWARE: Patentin Ver: 2.1
j SEQ ID NO 2.
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| Sequence 6, Application US/11179321
| Sequence 6, Application US/11179321
| Publication No. US20060019907A1
| GENERAL INFORMATION:
| APPLICANT: AGGRAMAL, BHARAT
| APPLICANT: SHISHODIA, SHISHIR
| TITLE OF INVENTION: GUGGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AN ITLLE OF INVENTION: 1 B KINASE
| TITLE OF INVENTION: ACTIVATION AND USES THEREOF
| FILE REFERENCE: CLFR:255US
| CURRENT APPLICATION NUMBER: US/11/179,321
| CURRENT PILING DATE: 2005-07-12
| PRIOR APPLICATION NUMBER: 60/587,187
| PRIOR FILING DATE: 2004-07-12
                                                    Gaps
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60.5%; Score 23; DB 8; Length 23; 100.0%; Pred. No. 3.7; ive 0; Mismatches 0; Indels
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Pred. No. 17;
0; Mismatches 6;
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                                                                                                            2 GGGACTTTCCGCTGGGGACTTTC 24
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.6%;
Matches 25; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 45
                              Best Local Similarity 100.
Matches 23; Conservative
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Publication No. US20060024715A1
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US-11-121-849-3916/c
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                           Gaps
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-04100 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PELLING DATE: 2005-06-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 25
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTON: Method of Analysis of Human Polymorphism
FILE REFERENCE: 36001.
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
PRIOR FILING DATE: 2004-07-02
SRIOR PILING DATE: 2004-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 47.4%; Score 18; DB 11; Length 50; Best Local Similarity 66.7%; Pred. No. 3.5e+02; Matches 24; Conservative 1; Mismatches 11; Indels
                           6; Indels
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                                                                         5 ACTITICGCTGGGGACTITICCAGGGGGACTT 35
                                                                                                     13 ACTITICGCTGCTCACTITICCAGGGAGGCGT 43
     Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                         Sequence 100529, Application US/11175859; Publication No. US20060024715A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 200528, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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  Best Local Similarity 80.6%;
Matches 25; Conservative
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Best Local Similarity 86.4
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US-11-175-859-100529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial
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US-11-175-859-32817/c
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US-11-175-859-100529
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US-11-136-527-200528
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; Sequence 32817, Application US/11175859

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Sequence 3916, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Statute OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1

CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1
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Publication No. US20060024715A1

GENERAL INFORMATION:

APPLICANT: Affunctix, Inc.

APPLICANT: Affunctix, Inc.

TILE OF INVENTION: Method of Analysis of Human Polymorphism

FILE REFERENCE: 3690.11715,859

CURRENT APPLICATION NUMBER: US/11/175,859

CURRENT FILING DATE: 2005-07-05

PRIOR PILING DATE: 2004-07-02

PRIOR FILING DATE: 2004-07-02

NUMBER OF SEQ ID NOS: 116251

SOFTWARE: Patentin version 3.2

LENGTH: 50
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REPERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR PEPLICATION NUMBER: US 60/585,352
PRIOR PELLING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SEQ ID NO 32817
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 50;
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43.2%; Score 16.4; DB 11;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 20; Conservative 1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.2; DB 11;
Pred. No. 7e+02;
1; Mismatches 9;
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Best Local Similarity 68.8<sup>†</sup>
Matches 22; Conservative
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; ORGANISM: homo sapien
US-11-175-859-32817
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CORGANISM: homo sapien
US-11-175-859-66382
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Sequence 273212, Application US/11136527

Sequence 273212, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION:

FILE REPERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT PILING DATE: 2005-05-25

FRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

LENGTH: 25

LENGTH: 25
          RESULT 15
US-11-136-527-273210/c
i Sequence 273210, Application US/11136527
i Publication No. US20050287570A1
i GENERAL INFORMATION:
i APPLICANT: Wyeth
i APPLICANT: Wyeth
i TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
i TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
i TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
i TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
i TITLE OF INVENTION PATE: 2005-05-25
i CURRENT FILING DATE: 2005-05-26
i NUMBER OF SEQ ID NOS: 362830
i SOFTWARE: PatentIn version 3.2
i SEQ ID NO 273210
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Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Suoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
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41.1%; Score 15.6; DB 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.6; DB 11;
Pred. No. 2.6e+03;
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Best Local Similarity 81.8%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial
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US-11-175-859-21940/c
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US-11-121-849-565799/C
US-11-121-849-565799/C
Sequence 565799 Application US/11121849
Fublication No. US2000272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STILE REFERENCE: 3684.1
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
FRIOR PRIOR FILING DATE: 2004-05-03
FRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NOS: 673904
SEQ ID NO 565799
LENGTH: 25
LENGTH: 25
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US-11-121-849-43102
US-11-121-849-43102
US-11-121-849-43102
Sequence 43102, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: JOHN Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Momentarys
FILE REFERENCE: 3684.1
CURRENT APPLICATION WOMBER: 8011/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
NUMBER OF SEQ ID NOS: 673904
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels
                                                                                                                 Score 16; DB 11; Length 25;
Pred. No. 1.9e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16; DB 11; Length 25;
Pred. No. 1.9e+03;
0; Mismatches 5; Indels
                                                                                                                              10 CCGCTGGGGACTTTCCAGGGGGAC 33
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                                                                                                                    Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative (
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Best Local Similarity 79.2%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-43102
                                           ; ORGANISM: Homo sapien
US-11-121-849-3916
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US-11-121-849-565799
LENGTH: 25
                         TYPE: DNA
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US-11-121-849-507340

Sequence 507340, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

FILE REPERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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US-11-121-0849-528104/C
US-11-121-0849-528104/C
Sequence 528104, Application US/11121849
Sequence 528104, Application No. US20050272080A1
Sequence 528104 Application No. US20050272080A1
Sequence 528104
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  Length
                                                Indels
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Query Match
40.5%; Score 15.4; DB 11;
Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6;
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Pred. No. 3.2e+03;
0; Mismatches 6;
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                                                                                          11 CGCTGGGGACTTTCCAGGGGGACTT 35
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Best Local Similarity 76.0%;
Matches 19; Conservative (
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Best Local Similarity 76.09
Matches 19; Conservative
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CORGANISM: Homo sapien
US-11-121-849-507340
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CORGANISM: Homo sapien
US-11-121-849-528104
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US-11-121-849-260545/C
; Sequence 260545, Application US/11121849
; Publication No. US2000272080A1
; GENERAL INFORMATION:
; APPLICATION:
; APPLICATION:
; TITLE OF INVENTION: Microarray8
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION WUMBER: US/11/121,849
; CURRENT APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SEQ ID NO 260545
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 18

US-11-121-649-103498/c

US-11-121-649-103498/c

Sequence 103498, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded (FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR PAPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03
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Pred. No. 2.9e+03;
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 103498
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                       CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR PILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 CTGGGGACTTTCCAGGGGGACTTTC 37
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                                                                                                                                                                                                                                                                                                                                                                                                                37 GACTITCCTCRIGGATITIGIAG 14
                                                                                                                                                                                                                                                                                                 41.1%;
75.0%;
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; ORGANISM: homo sapien
US-11-175-859-21940
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US-11-121-849-103498
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CORGANISM: Homo sapien
US-11-121-849-260545
         FILE REFERENCE: 3690.1
                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 18; Conserv
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Sequence 2, Application US/11032236
Publication No. US20050273867A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BRULET, PHILIPPE
APPLICANT: PICAD, SANDINE
APPLICANT: PICAD, SANDINE
TITLE OF INVENTION: ON-INVASIVE REAL-TIME IN VIVO BIOLUMINESCENCE IMAGING
TITLE OF INVENTION: OF LOCAL CA2+ DYNAMICS IN LIVING ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Publication No. US20060024715A1

GENERAL INFORMATION:

APPLICANT: Affymetrix, Inc.

APPLICANT: Liu, Guoying et al.

TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.

CURRENT APPLICATION NUMBER: US/11/175,859

CURRENT APPLICATION NUMBER: US 60/585,352

PRIOR FILING DATE: 2004-07-05

NUMBER OF SEQ ID NOS: 116251

SOFTWARE: Patentin version 3.2

SEQ ID NO 66869

TENTE DAA

CORGANISM: home sapien
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                                                                                                                                                              Score 15.4; DB 7; Length 26;
Pred. No. 3.2e+03;
0; Mismatches 6; Indels
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Best Local Similarity 66.7%; Pred. No. 3.4e+03;
Matches 22; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 03495.0328
CURRENT APPLICATION NUMBER: US/11/032,236
CURRENT FILING DATE: 2005-01-11
FRIOR APPLICATION NUMBER: 60/543,659
FRIOR FILING DATE: 2004-02-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 3.3
LENGTH: 41
                                                                                                                                                                                                                                                                       6 CTTTCCGCTGGGGACTTTCCAGGGG 30
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 767705
LENGTH: 26
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                                                                                                                                                                      Query Match
Best Local Similarity 76.0%;
Matches 19; Conservative
                                                                                              ; ORGANISM: Human
US-10-310-914A-767705
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                                                                            TYPE: RNA
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Sequence 767705, Application US/10310914A

Sequence 767705, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Bhiler, Kvuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNDER: 120/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PAPLICATION NUMBER: US/11/136,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
LENGTH: 25
                                        APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
LENGTH: 25
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Pred. No. 3.2e+03;
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Pred. No. 3.2e+03;
0; Mismatches 6;
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0; Mismatches 6;
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Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Best Local Similarity 76.0%;
Matches 19; Conservative (
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Best Local Similarity 76.0%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial
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  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
US-11-136-527-213042/c
                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CEUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
LENGIH: 23
TYPE: RNA
OPCANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 454114/c
| Sequence 454114/c
| Sequence 454114/c
| Sequence 454114 Application US/11121849
| Publication No. US20050272080A1
| GENERAL INFORMATION:
| APPLICANT: John Palma
| TITLE OF INVENTION: Microarrays
| TITLE OF INVENTION: Microarrays
| FILE REPRENCE: 3684.1
| CURRENT APPLICATION NUMBER: US/11/121,849
| CURRENT FILING DATE: 2005-05-03
| PRIOR FILING DATE: 2004-05-03
| NUMBER OF SEQ ID NOS: 673804
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SEQ ID NO 454114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-310-914A-1226668

Sequence 1226668, Application US/10310914A

Sequence 1226668, Application US/10310914A

Sequence 1226668, Application US/10310914A

SEQUENCE 1226668, Application US/10310914A

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: uses thereof

FILE PERERRECE 6697,0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002.12-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.2; DB 7;
Pred. No. 3.7e+03;
6; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGACUUUUCCCUGGGAACUU 20
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55.0%;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 1226668
LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.v.
Best Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
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CORGANISM: Homo sapien
US-11-121-849-454114
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Best Local Similarity
Matches 17; Conserva
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US-10-310-914A-663779
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ORGANISM: Human
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Sequence 298241, Application US/10310914A

Sequence 298241, Papplication US/10310914A

Sequence 298241, Pagaic APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

APPLICANTION: uses thereof

FILE OF INVENTION: 1804.02

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 298241
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; Sequence 103464, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.; APPLICANT: Liu, Guoying et al.; TILE OF INVENTION: Method of Analysis of Human Polymorphism; FILE REFERENCE: 3690.1
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; RIUNG DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 103464
; LENGTH: 50
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                                                                                                                                                                     Best Local Similarity 70.4%; Pred. No. 3.4e+03;
Matches 19; Conservative 1; Mismatches 7; Indels
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US-10-310-914A-663779
; Sequence 663779, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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Best Local Similarity 70.4
Matches 19; Conservative
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US-11-175-859-103464
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US-10-310-914A-298241
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US-10-310-914A-298241
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US-11-175-859-103464
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Sequence 196212, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
FILOR PILING DATE: 2005-05-03
PRIOR PEDLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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Sequence 815249, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, 18aac
APPLICANT: Bentwich, 19aac
APPLICANT: Bentwich Isaac
CURRENT FILING DATE: 2002-12-06
SOFTWARE Patentin version 3.3
SEQ ID NO 815249
LENGTH: 24
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  APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
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LENGTH: 25
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Best Local Similarity 63.9%; Pred. No. 4.1e+03;
Matches 23; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 GGTCACTTACCTTAGAAGARGTTCAAGAGGGACTGT 42
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Pred. No. 4.5e+03;
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                                                              FILE REFERENCE: 3690.1

CURRENT APPLICATION NUMBER: US/11/175,859

CURRENT FILING DATE: 2005-07-05

PRIOR PILING DATE: 2004-07-02

NUMBER OF SEQ ID NOS: 116251

SOFTWARE: PatentIn version 3.2

LENGTH: 50
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Best Local Similarity 65.2%;
Matches 15; Conservative
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US-11-175-859-66764
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US-11-121-849-196232/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Best thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1393495
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; Publication No. US20060024715A1
; GABERAL INFORMATION:
    APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; PILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; ROTHARRE: PatentIn version 3.2
; SEQ ID NO 44456
; LENGTH: 50
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Score 15.2; DB 7; Length 26; Pred. No. 3.8e+03; 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%; Score 15.2; DB 7; Length 27; 60.0%; Pred. No. 3.8e+03;
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Pred. No. 4.1e+03;
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US-10-310-914A-1383495
US-10-510-914A-1383495, Application US/10310914A; Sequence 1383495, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
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; Publication No. US20060024715A1
; GENERAL INFORMATION:
                                                                                           1 GGGGACTTTCCGCTGGGGAC 20
                                                                                                                        7 GAGGACUTUGCCCUGGGGAC 26
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  Query Match
Best Local Similarity 65.0%;
Matches 13; Conservative
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Best Local Similarity
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US-11-175-859-43456/c
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US-11-175-859-66764
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; Sequence 280766, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
   APPLICANT: Wounts, William M
   TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
   FILE REFERENCE: 031896-041000 (AM101086)
   CURRENT APPLICATION NUMBER: US/11/136,527
   CURRENT FILING DATE: 2005-05-25
   PRIOR APPLICATION NUMBER: US 60/574,294
   PRIOR PLING DATE: 2005-05-26
   NUMBER OF SEQ ID NOS: 362830
   SOFTWARE: PatentIn version 3.2
   SEG ID NO 280766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-136-527-314081/c

i Sequence 314081, Application US/11136527

j Publication No. US20050287570A1

gENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wouth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 314081

LENGTH: 25
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APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION UMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 CGCTGGGGACTTTCCAGGGGGAC 33
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                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial
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| Publication No. US20050272080A1
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays
| TITLE OF INVENTION: Microarrays
| TITLE REFERENCE: 3684.1
| CURRENT APPLICATION NUMBER: US/11/121,849
| CURRENT FILING DATE: 2004-05-03
| PRIOR PIPLICATION NUMBER: 60/567,949
| PRIOR FILING DATE: 2004-05-03
| NUMBER OF SEQ ID NOS: 673904
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
                                                                                                                                                                                                                                                                                    Sequence 378884, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1

CURRENT APPLICATION UNMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

FRIOR APPLICATION NUMBER: 60/567,949

FRIOR APPLICATION NUMBER: 60/567,949
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                                                           Length 25;
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SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 378884
LENGTH: 25
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ches 5; Indels
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                                                         Score 15; DB 11; I
Pred. No. 4.5e+03;
0; Mismatches 0;
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                                           39.5%; Scc...
100.0%; Pre
                                                                                                                                               5 ACTITCCGCTGGGGA 19
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Best Local Similarity 78.3
Matches 18; Conservative
                                                           Query Match
Best Local Similarity 100.
Matches 15; Conservative
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, ORGANISM: Homo sapien
US-11-121-849-510666
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US-11-121-849-378884
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US-11-136-527-280766/c
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US-11-121-849-510666
                  US-11-121-849-196232
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TYPE: DNA
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TILLS OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-26
PRIOR PELICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-05
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
LENGTH: 25
                                                                                                                                                                                                                                                                                                                 Gaps
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; Sequence 11173, Application US/11175859
; Publication No. US2060024715A1
; GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.; APPLICANT: Liu, Guoying et al.; TILE OF INVENTION: Method of Analysis of Human Polymorphism FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 11773
; LENGHAR: 50
; LENGHAR: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 358480, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: US 60/574,294 PRIOR FILING DATE: 2005-05-26 NUMBER OF SEQ ID NOS: 362830 SOFTWARE: Patentin version 3.2 SEQ ID NO 318283 LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                             3 GGACTITCCGCTGGGGACTITCC 25
                                                                                                                                                                                                                                                                                                                                                                                                  2 GGACTAGCAGCTGGGGTCTTTAC 24
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CORGANISM: homo sapien
US-11-175-859-11173
                                                                                                                                   TYPE: DNA ORGANISM: Artificial
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Best Local Similarity
Matches 18; Conserv
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US-11-136-527-358480
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                                                                                                                                                                                                                                               Sequence 74560, Application US/11175859
; Sequence 74560, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; RIUNDER OF FLING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 74560
; LENGTH: 50
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US-11-175-859-104360

| Sequence 104360, Application US/11175859
| Publication No. US20060024715A1
| GENERAL INFORMATION:
| APPLICANT: Affymetrix, Inc.
| APPLICANT: Affymetrix, Inc.
| TITLE OF INVENTION: Method of Analysis of Human Polymorphism
| FILE REFERENCE: 3690.1
| CURRENT APPLICATION NUMBER: US/11/175,859
| CURRENT FILING DATE: 2005-07-05
| PRIOR APPLICATION NUMBER: US 60/585,352
| PRIOR APPLICATION NUMBER: US 60/585,352
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Score 15; DB 11; Length 50; Pred. No. 4.9e+03;
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Pred. No. 4.9e+03;
0; Mismatches 10
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                                                  0; Mismatches
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US-10-310-914A-252171/c
; Sequence 252171, Application US/10310914A
                                                                                               2 GGGACTTTCCGCTGGGGACTTTC 24
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    39.5%;
78.3%;
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SOFWARE: Patentin version 3.2
SEQ ID NO 104360
LENGTH: 50
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Best Local Similarity 67.7%;
Matches 21; Conservative
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Best Local Similarity 78.3%;
Matches 18; Conservative
Query Match
Best Local Similarity 78.33
Matches 18; Conservative
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CORGANISM: homo sapien
US-11-175-859-74560
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US-11-175-859-104360
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US-11-175-859-74560
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Sequence 571272, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

Winder: 1864.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: 06/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWAREN Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Sequence 1145, Application US/11175859

Publication No. US20060024715A1

SENERAL INFORMATION:

APPLICANT: Affymetrix, Inc.

APPLICANT: Liu, Guoying et al.

TILE OF INVENTYION: Method of Analysis of Human Polymorphism

FILE REFERENCE: 3690.1

CURRENT APPLICATION NUMBER: US/11/175,859

CURRENT FILING DATE: 2004-07-05

PRIOR APPLICATION NUMBER: US 60/585,352

PRIOR FILING DATE: 2004-07-02

NUMBER OF SEQ ID NOS: 116531

SOFTWARE: PatentIn version 3.2

LENGTH: 50
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                                                                                 Length 25;
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                                                                             Score 14.8; DB 11;
Pred. No. 5.4e+03;
0; Mismatches 2;
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Pred. No. 5.9e+03;
1; Mismatches 13;
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                                                                               Query Match 38.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                 14 TGGGGACTTTCCAGGGG
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Best Local Similarity 61.1%;
Matches 22; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-569838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapien
US-11-121-849-571272
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US-11-175-859-1145
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                              APPLICANT: Bentwitch, Isaac
APPLICANT: Bentwitch, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Baioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
LENGTH: 24
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT PILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 508663
LENGTH: 25
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; Publication No. US20050272080A1
; Publication No. US20050272080A1
; GENERAL INPORMATION:
    APPLICAMT: John Palma
; TITLE OF INVENTION: Microarrays
; TITLE OF INVENTION: Microarrays
; TITLE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR PRILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 569838
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Pred. No. 5.4e+03;
0; Mismatches 2; Indels
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88.9%;
  Publication No. US20060003322A1
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
                        GENERAL INFORMATION:
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US-11-121-849-569838
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US-11-121-849-508663
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CQ001487 Sequence
CQ00659 Sequence
CQ006700 Sequence
BD202727 Method an
AR110134 Sequence
14109 Sequence
AX15688 L. monocyto
AX3689 L. monocyto
AX058552 Sequence
AX514983 Sequence
AX514718 Sequence
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AX514717 Modulator
BD078121 Modulator
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AX213.75 Sequence
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AX15.8892 Sequence
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AX35.1114 Sequence
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CS130449 Sequence
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AX045.78 Sequence
AX045.79 Sequence
AX1043.39 Sequence
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AX4773.2 Sequence
AX6643.10 Sequence
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AXI7551 Sequence
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BD20778 Method an
ES3312 Method for
BD778154 Sequence
                                                                                               February 15, 2006, 17:51:58; Search time 479.835 Seconds (without alignments) 2369.293 Million cell updates/sec
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                GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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1 GI:13920911  construct construct uences; artificial sequences, Schetter,C. and Vollmer,J.C. mulatory nucleic acids 0 0122972-A 906 05-APR-2001; Y OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical Location/Qualifiers 120 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630"	100.0%; Score 20; DB 6; Length 20;  2y 100.0%; Pred. No. 9.7e+02;  Broative 0; Mismatches 0; Indels 0; Gaps 0;  3GGAGGGAGGGG 20	Score 20; DB 6; Length 20; Pred. No. 9.7e+02; Mismatches 0; Indels 0; Gaps 0; 20	50 bp DNA linear PAT 17-JAN-2001 WO0077250.
AX104714.  synthetic  synthetic  other seq  i Krieg, A.M  immunosti  Patent: W  UNIVERSIT  GmbH (DE)	Local Similarithes 20; Consthes 20; Coley Phair	y Match Local Similarity 100.0%; hes 20; Conservative 0; 1 AGGGAGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3 49 AX058549 50 bp TION Sequence 1 from Patent WO0077250 ION AX058549 1 G1:12310891
VERSION KEYWORDS SOURCE OURCE OUTHORS TITLE JOURNAL FEATURES FEATURES SOURCE ORIGIN	Query Matches  Qy  Db  RESULT 2  AX547767  LOCUS  DEFINITION ACCESSION VERSION	Query M Best Lo Batches Matches Qy Db	RESULT 3 AX058549 LOCUS DEFINITION ACCESSION VERSION
AX557192 Sequence AR006856 Sequence AR006858 Sequence AR06858 Sequence AR080894 Sequence AR080895 Sequence AR080895 Sequence AR080896 Sequence AR173724 Sequence AR173725 Sequence AR173726 Sequence AR173737691 Therapout CS088786 Sequence		000000000000	467 De novo 468 De novo 469 De novo 472 De novo 479 De novo
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ALIGNMENTS

DNA AX104714 20 bp I Seguence 906 from Patent WO0122972. AX104714 RESULT 1 AX104714 LOCUS DEFINITION ACCESSION

linear

PAT 30-APR-2001

Escude, C., Garestier, T., Helene, C. and Roulon, T. Method for circularizing oligonucleotides around a double stranded nucleic acid, resulting structures and uses thereof synthetic construct synthetic construct other sequences; artificial sequences. VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

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1 (bases 1 to 27)
Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
Nucleic acid transporter system and methods of use
Patent: US 5994109-A 15 30-NOV-1999;
Location/Qualifiers
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1 (bases 1 to 27)

Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.

Nucleic acid transporter systems

Patent: US 6177554-A 14 23-JAN-2001;

Location/Qualifiers
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llarity 94.7%; Pred. No. 8.8e+03;
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              Score 17.4; DB 6;
Pred. No. 8.8e+03;
0; Mismatches 1;
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Sequence 15 from patent US 6177554.
AR125630
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Sequence 15 from patent US 5994109.
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AR091425.1 GI:10018180
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            87.0%;
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              Query Match
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Matches 18; Conservative
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Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
Nucleic acid transporter system and methods of use
Patent: US 5994109-A 14 30-NOV-1999;
Location/Qualifiers
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Method for circularizing oligonucleotides around a double stranded
nucleic acid, resulting structures and uses thereof
structures and uses thereof
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LOCATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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Patent: WO 0077250-A 1 21-DEC-2000;
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(FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
LOCATION/QUALIFIERS
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iive 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:22630"
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other sequences, artificial sequences.
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                             AX058550 50 bp Sequence 2 from Patent WO0077250.
                                                                                                                            /note="Oligonucleotide"
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PAT 07-SEP-2000

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1 (bases 1 to 39)

Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.

Nucleic acid transporter system and methods of use
Patent: US 5994109-A 13 30-NOV-1999;
Location/Qualifiers
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Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.

Nucleic acid transporter systems
Patent: US 6177554-A 13 23-JAN-2001;

Location/Qualifiers
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llarity 94.7%; Pred. No. 8.7e+03;
Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Primer ON-TATADE1"
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Sequence 13 from patent US 6177554.
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Sequence 13 from patent US 5994109.
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/wol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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AR091423.1 GI:10018178
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Volumes 1 to 27)
Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
Woo,S.L.C. acid transporter systems
Nucleic acid transporter systems
Patent: US 6177554-A 15 23-JAN-2001;
Location/Qualifiers
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Pred. No. 8.8e+03;
9; Mismatches 1; Indels
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Tnf-inducible promoters and methods for using
Patent: WO 0246433-A 43 13-JUN-2002;
Saus, Juan (ES)
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/organism="synthetic construct"
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Patent: WO 0246378-A 43 13-JUN-2002;
Saus, Juan (ES)
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/mol_type="unassigned DNA"
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Sequence 43 from Patent WO0246433.
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Sequence 43 from Patent WO0246378.
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 AR125630.1 GI:14111692
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oc A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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                                                                                                                                                                                                                                                                                          24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAYCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
JAMES A MCSWIGGEN
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagant for treating diseases or conditions concerning molecule participating in vasculogenic response
Patent: JP 2002509721-A 5754 02-APR-2002;
RIBOZYME PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                               CI2N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method and reagent for treating diseases or conditions
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Location/Qualifiers
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participating in vasculogenic response
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1 (bases 1 to 20)
1 (bases 2
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Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 0;
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    .20
    /organism="synthetic construct"
/mol_type="genomic DNA"

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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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JP 2002509721-A/5754
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1 (bases 1 to 50)

Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
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Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
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89.5%; Pred. No. 1.9e+04;
tive 0; Mismatches 2; Indels
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Human Genome Sciences, Inc.; Rockville, MD Location/Qualifiers
                                                                                  linear
                                                                     Sequence 2153 from patent US 6593114.
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Sequence 2153 from patent US 6737248.
AR537591
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/organism="unknown"
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/organism="unknown"
/mol_type="genomic DNA"
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JP 2002509721-A/5754.
Homo sapiens (human)
Homo sapiens
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/organism="unknown"
/mol_type="genomic DNA"
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Biogen, Inc.; Cambridge, MA; EPX;
                           Location/Qualifiers
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89.5%;
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Best Local Similarity 89.5%;
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5%
Matches 17; Conservative
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A28678/c
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                                                                                                                                                                                 BD078154 1. 26 bp DNA linear PAT 27-AUG-2002 Modulator of DNA cytosine-5 methyltransferase and method of using
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Modulator of DNA cytosine-5 methyltransferase and method of
using the same
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Unclassified.
1 (bases 1 to 42)
Allet, B. and Kawashima, E.H.
Expression systems for overproduction of desired proteins Patent: US 5182196-A 21 26-UAN-1993;
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                                       Score 15.8; DB 6; Length 20;
Pred. No. 3.7e+04;
0; Mismatches 2; Indels
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/organism='Unidentified'
Location/Qualifiers
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29-AUG-1997 US 60/057411
NORBERT O REICH, JAMES FLYNN
CI2N9/10, CI2Q1/48//CI2N15/09
Strandedness: Double;
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Sequence 21 from patent US 5182196.
AR362756
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JP 2001514862-A/38.
unidentified
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Reich, N.O. and Flynn, J.
                                       Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                             unidentified
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Pred. No. 3.3e+04;
0; Mismatches 2; Indels
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Pred. No. 3.3e+04;
0; Mismatches 2; Indels
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Score 15.8; DB 6;
Pred. No. 3.3e+04;
0; Mismatches 2;

    43
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    .43
    forganism="synthetic construct"
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 43)
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1 (bases 1 to 43)
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2 GGGGAGGGGAGGGG 20
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Homo sapiens (human)
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CQ003487/c
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Location/Qualifiers
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                                                                                                                                                                                                                                                      1. .44
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/db_xref="taxon:32630"
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synthetic construct
other sequences; artificial sequences.
1 (bases I to 47)
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 44)
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Seguence 2126 from Patent WO0147944.
CQ003486
                                                                              A28674 44 bp dsRNA with terminal locks (comp.).
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37 GGGGGGGGAGGGGGGG 19
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Homo sapiens
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Oligonucleotide 9.
A28685
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Best Local Similarity
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CQ003486/c
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A28674/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 047944-A 2127 05-JUL-2001;
Curagen Corporation (US)
Location/Qualifiers
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                                                                                          Shimkets, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms methods of use thereof
Patent: WO 0147944-A 2126 05-JUL-2001;
Curagen Corporation (US)
Location/Qualifiers
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25. 26
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Accession number cg441131752"
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/note="Nucleotide deleted between bases 25
Accession number cg44131752"
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JP 2002509721-A/5753.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 85.0
Matches 17; Conservative
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                Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Patent: WO 014794-A 5340 05-JUL-2001;

Curagen Corporation (US)

Location/Qualifiers
                                                                    Shimkets, R. A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms and methods of use thereof.

Patent: WO 0147944-A 5339 05-JUL-2001;

Curagen Corporation (US)

Location/Qualifiers
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/note="Nucleotide deleted between bases 25 and
Accession number cg43267341"
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89.5%; Pred. No. 3.2e+04;
ive 0; Mismatches 2; Indel8
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89.5%; Pred. No. 3.2e+04;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                        1..50
/organism="Homo sapiens"
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25..26
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Sequence 5340 from Patent WO0147944.
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    .50
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 Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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ses 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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                                             Hominidae; Homo.
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Homo sapiens (human)
JP 2002509721-A/5753
02-APR-2002
24-MAR-1999 JP 2000541291
27-MAR-1999 JS 60/079678
PAMELA A PACO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT, JAMES A MCSWIGGEN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Bases 1 too 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response Participating in vasculogenic response RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                                                                                     OS Homo sapiens (human)

PN 2002509721-A/5753

PD 02-APR-2005

PF 24-MAR-1999 JP 2000541291

PR 27-MAR-1998 US 60/073678

COURTES OF THALE JARVIS, CLAIRE COESHO:

PC CI2NIS/09,A6IK31/7088,A6IK31/7125,A6IK48/00,A6IP3/10,A6IP17/06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A61P29/00,
C A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00,
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Pred. No. 5.6e+04;
0; Mismatches 3; Indels
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participating in vasculogenic response
Key
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2 from patent US 6114154.
AR110134.1 GI:12826410
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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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85.0%;
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Gaps

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METHODS OF DETECTING OR QUANTITATING NUCLEIC ACIDS AND OF PRODUCING LABELLED INVARDELLEED NUCLEIC ACIDS
PATENT: WO 9304199-A 5 G4-MAR-1993;
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Detection of genetic polymorphisms
Patent: WO 02052044-A 1181 04-JUL-2002;
Riken (JP)
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                                                                                                                                                                                                                          76.0%; Score 15.2; DB 6;
85.0%; Pred. No. 5.5e+04;
iive 0; Mismatches 3;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="Oligonucleotide"
                                                                                                                         1. .41
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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AX514983
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other sequences; artificial sequences.
1 (bases 1 to 41)
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Sequence 4 from Patent WO0077250.
AX058552
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synthetic construct
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Best Local Similarity 85.0
Matches 17; Conservative
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PATENT: WO 93104199-A 4 04-MAR-1993;
Location/Qualifiers
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Noonberg, S.B. and Hunt, C.Anthony.
In vivo oligonucleotide generator, and methods of testing the binding affinity of triplex forming oligonucleotides derived therefrom
Patent: US 5624803-A 2 29-APR-1997,
Location/Qualifiers
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    .41
    forganism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"

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L. monocytogenes HlyA gene probe-primer.
A23689
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L. monocytogenes HlyA gene probe-primer.
A23688
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 41)

    .38
    /organism="unknown"
    /mol_type="unassigned DNA"

                                                                      141099 38 bp
Sequence 2 from patent US 5624803.
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Unclassified.
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Matches 17; Conserv
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I41099/c
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BD078223 26 bp DNA linear PAT 27-AUG-2002
Modulator of DNA cytosine-5 methyltransferase and method of using
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Reich,N.O. and Flynn,J.
Modulator of DNA cytosine-5 methyltransferase and method of using the same
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29-AUG-1997 US 60/057411
NORBERT O REICH, JAMES FLYNN
C12N9/10, C1201/48/C12N15/09, C12N15/00
Strandedness: Double;
Topology: Linear;
Modulator of DNA cytosine-5 methyltransferase and method of using the same constitutions.
                Topology: Linear; Modulator of DNA cytosine-5 methyltransferase and method of
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                                                                                           organism='Unidentified'
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THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
OS Unidentified
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Pred. No. 8.4e+04;
0; Mismatches 2;
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    .26
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/db_xref="taxon:32644"

    .26
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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Strandedness: Double;
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18-SEP-2001
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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AR121366/c
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Reich,N.O. and Flynn,J.
Modulator of DNA cytosine-5 methyltransferase and method of using
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Modulator of DNA cytosine-5 methyltransferase and method of using
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Patent: WO 02052044-A 5376 04-JUL-2002;
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29-AUG-1997 US 60/057411
NORBERT O REICH, JAMES FLYNN
C12N9/10, C12Q1/48//C12N15/09, C12N15/00
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THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
OS Unidentified
PN JP 2001514862-A/55
PD 18-SEP-2001
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Sequence 5376 from Patent WO02052044.
AX519178

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 Location/Qualifiers
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JP 2001514862-A/55.
unidentified
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BD078171
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PAT 20-APR-2005

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Unknown.
Unclassified.
Unclassified.

(I (bases I to 31)

Hayashizaki,Y. and Watahiki,M.

RNA polymerase

Patent: US 6867027-A 17 15-MAR-2005;

Patent: US 6867027-A 17 15-MAR-2005;

Lich Institute of Physical and Chemical Research, Nippon Gene Co., 1td. and Nippon Genetech Co., 1td.; Wako;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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25. .26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.0%; Score 14.8; DB 6; Length 31; Best Local Similarity 88.9%; Pred. No. 8.2e+04; Matches 16; Conservative 0; Mismatches 2; Indels
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Seguence 2220 from Patent WO0140521.
AXIS8892
 Patent: US 6365350-A 31 02-APR-2002;
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Sequence 17 from patent US 6867027.
AR643452
AR643452.1 GI:62781753
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AR643452
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TITLE
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                                                                                                  Unclassified.

1 (Dases I to 30)
Murachima.K., Moriya.T., Hamaya,T., Koga,J., Sumida,N., Aoyagi,K.,
Murakami,T. and Kono,T.
Enzyme endoglucanase and cellulase preparations containing the same
Patent: US 6159720-A 18 12-DEC-2000;
Location/Qualifiers
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Systems for the mass production of proteins or peptides by microorganisms of the genus humicola Patent: US 6403362-A 25 11-JUN-2002; Meiji Seika Kaisha, Ltd.; Tokyo;
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larity 88.9%; Pred. No. 8.2e+04;
Conservative 0; Mismatches 2; Indels
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Sequence 25 from patent US 6403362.
AR213275
AR213275.1 GI:23310445
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Sequence 31 from patent US 6365350.
AR202976
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/wol_type="unassigned DNA"
Sequence 18 from patent US 6159720.
AR121366
AR121366.1 GI:14104942
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Hayashizaki,Y.
Method of DNA sequencing
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Best Local Similarity
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AR213275/c
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PAT 22-JUN-2001

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PAT 06-FEB-2002
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                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 20)

Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.

Method for generating full-length cDNA library from single cells

Patent: US 6197554-A. 2 06-WAR-2001;

Location/Qualifiers
                                                                                                                                                                                                                                        Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Lim, M.Y. and Bruice, T.W. Promoters for regulated gene expression Patent: WO 0194600-A 66 13-DEC-2001; GENELABS TECHNOLOGIES, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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larity 93.8%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 1; Indels
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llarity 84.2%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 3;
                                                                       DNA
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    .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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                                                                     25 bp
Seguence 66 from Patent WO0194600.
AX351114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR137709 20 bp
Sequence 2 from patent US 6197554.
AR137709
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/organism="unknown"
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                                                                                                                  AX351114.1 GI:18616468
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                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                             Hominidae; Homo.
                                                                                                                                                                   Homo sapiens
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Matches 15; Conserv
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Best Local Simi
Matches 16;
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FEATURES
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Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, B.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, M.Y. and Bruice, T.W.

Promoters for regulated gene expression
Patent: US 6938555-A 66 04-JAN-2005;

Genelabs Technologies, Inc.; Redwood City, CA
                                      /note="2 of 2 allelic variants (2219 is other entry)"
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Pescovitz,O.H.
Use of GRRH-RP to stimulate stem cell factor production
Patent: US 6159934-A 16 12-DEC-2000;
Location/Qualifiers
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                                                                                                                  Indels
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                                                                                   74.0%; Score 14.8; DB 6; Length 88.9%; Pred. No. 7.6e+04; ive 0; Mismatches 2; Indels
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Accession number cg39331132"
26
                                                                                                                                                                                                                                                        20 bp Sequence 16 from patent US 6159934.

    .20
    /organism="unknown"
    /mol_type="unassigned DNA"

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AR630012
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/organism="unknown"
                                                                                                                                                                   39 GGGAAGGAAGGGGAGGGG 22
                                                                                                                                               3 GGGAGGGGAGGGG 20
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AR121583.1 GI:14105159
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Best Local Similarity 93.8%,
Conservative
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                                                                                   Query Match 74.0
Best Local Similarity 88.9
Matches 16; Conservative
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Matches 15; Conservative
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Unclassified.
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AR121583/c
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AR630012
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PAT 27-APR-1998

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1 (bases 1 to 20)
Mizuguchi, M., Kurosaki, N., Makino, K., Koyanagi, Y. and Yamamoto, N.
Mizuguchi, M., Kurosaki, N., Makino, K., Koyanagi, Y. and Yamamoto, N.
Mizuguchi, M., Fanse OligoNUCLEOTIDE
Patent: JP 1997052898-4 9 25-FEB-1997;
SOYAKU GIUUTSU KENKYUSHO: KK
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MIZUGUCHI MASATSUGU, KUROSAKI NAOKO, MAKINO KEISUKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism='Artificial sequences'. Location/Qualifiers
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                                                                                                                                                                                                                                                              Length 20;
                                                                                                      /organism="synthetic construct"
|mol_type="unassigned DNR"
|db_xref="trace" trace" trace t
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Patent: WO 2005063300-A 4 14-JUL-2005;
Phenion GmbH & Co KG (DE)
Location/Qualifiers
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Anti-HTLV-1 antisense oligonucleotide.
E12675
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Sequence 55 from patent US 6339068.
AR182883.1 GI:20226090
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAMAMOTO NAOKI
CO7H21/04//A61K31/70;
strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Artificial sequences.
JP 1997052898-A/9
25-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                  2 GGGGAGGGAGGGGG 20
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hypothetical: No;
anti-sense: Yes;
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JP 1997052898-A/9.
unidentified
unidentified
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PF 09-AUG-1995
PI MIZUGUCHI MA
KOYANAGI YOSHIO,
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E12675/c
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AR182883/c
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Cosmetic or pharmaceutical preparations containing nucleic acid sequences forming a superstructure sequences forming a superstructure patent: WO 200506330-A 3 14-JUL-2005; Phenion GmbH & Co KG (DE)

Location/Qualifiers
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Immunostimulatory nucleic acid oil-in-water formulations and related methods of use
Patent: WO 2004087203-A 133 14-OCT-2004;
Coley Pharmaceutical Group, Ltd. (CA)
Location/Qualifiers
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12-JUN-2001 (first entry)

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ALIGNMENTS

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                                                                  Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour; viral infection, bacterial infection, fungal infection, parasitic infection, cancer, asthma; infections disease, allergy, immune deficiency, phosphorothioate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
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                                  Immunostimulatory nucleic acid #817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 101; Page 56; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Krieg AM, Schetter C, Vollmer J;
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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nes 20; Conservative
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                                                                                                                                                             Synthetic.
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AAF99701; AAF99701 ID AAF XX AC AAF RESULT 1

AAF99701 standard; DNA; 20 BP

4

Synthetic

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The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                   Treating non-allergic inflammatory diseases, such as psoriasis, eczeallergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
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Pred. No. 6e+02;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                        Disclosure; Page 32; 229pp; English
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  29-MAR-2002; 2002US-00112653
                                          29-MAR-2001; 2001US-0279642P
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Best Local Similarity 100.0
Whiches 20; Conservative
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                                                                                                                                                                                             WPI; 2003-521815/49.
                                                                                                                                                   Krieg AM, Berg DJ;
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(PETE/) PETERSEN D
                                                                                  (KRIE/) KRIEG A M. (BERG/) BERG D J.
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(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003087848-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, conneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
plaque neovascularisation; telangiectasia; haemophiliac joint;
angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
scleroderma; hypertrophic scar.
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                                                                                                                                                                                                                                                                                                                        (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                     14-DEC-2001; 2001WO-US048458.
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                                                                                                                                                   WO200253141-A2
                                                                                                                                                                                                                                                                                                                                                                     Bratzler RL;
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                                                                                                                                                                                             11-JUL-2002
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Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.

Disclosure; Page 17; 221pp; English

US2003050268-A1

Synthetic

ACH03240;

ACH03240 RESULT

Query Match Matches

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagoniet; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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                                                                                                                                                            Score 20; DB 9; Length 20;
Pred. No. 6e+02;
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                                                                                                                           Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;
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                                                                                                                                            100.0%; Scor.
100.0%; Pred. No. vc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fouron Y;
                                                                                                                                                                                                                                                        1 AGGGAGGGAAGGGAAGGG 20
                                                                                                                                                                                                                                   1 AGGGAGGGAGGGGG 20
                                                                                                                                                                                                                                                                                                                                                             ADU90222 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000; 2000US-0179991P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-2004; 2004US-00831778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-833006/82.
                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PETE/) PETERSEN (FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004235774-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                  ADU90222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                              Query Match
                                                                                                                                                                                                  Matches
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ADU90222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Circularizing oligonucleotide around double-stranded nucleic acid, useful e.g. for detecting mutations, using target-binding oligonucleotide with complementary end sequences.
                                                                                                                                                                                                                                                                                             Nucleic acid detection; nucleic acid labelling; gene therapy;
nucleic acid purification; androgen receptor promoter; triple helix; ss.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50 BP; 19 A; 0 C; 30 G; 1 T; 0 U; 0 Other;
 Pred. No. 6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(CNRS ) CNRS CENT NAT RECH SCI.
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100.08; 22.
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                                                                                 1 AGGGAGGGAGGGAGGG
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                                                                                                                                                                      ABL56735 standard; DNA; 50
                                                                                                                                                                                                                                    (first entry)
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                            20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-080698/09.
           Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-1999;
                                                                                                                                                                                                                                    20-AUG-2002
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                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                    ABL56735;
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ABL56735
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RESULT 7 ABL56736/c

DB 13; Length 20;

100.0%; Score 20;

Query Match

Smith LC;

COLLEGE MEDICINE

93WO-US002725.

92US-00855389

93US-00167641.

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Sottchalk S, Sparrow J, Cristiano RJ, Woo SLC,
                                                                                                                                                       (BAYU ) BAYLOR
                                                                                         14-DEC-1993;
                                                                                                                  20-MAR-1992;
                                                                                                                               19-MAR-1993;
                                       US6033884-A
                                                               07-MAR-2000
             Synthetic
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a process for circularizing an oligonucleotide around a double-stranded nucleic acid that contains a carget sequence. The method is used to detect or label nucleic acids, particularly plasmids, to detect target sequences in the nucleic acid, and to distinguish between two sequences that differ in only 1 or 2 mutations. It can be used to select, e.g. from degenerate single-stranded nucleic acids, sequences that can bind to the nucleic acid, particularly sequences that promote entry of the nucleic acid into cells or can target the nucleic acid to specific cellular compartments. The method can also be used to purify nucleic acids, particularly plasmids, and in gene therapy for specific inhibition of a gene contained in the nucleic acid. ABLS6735-36 represent a fragment of the mutine androgen receptor promoter. They were used in the course of the invention, during
                                                                                                                                                                                                                                                                                                                                                                          Circularizing oligonucleotide around double-stranded nucleic acid, useful e.g. for detecting mutations, using target-binding oligonucleotide with complementary end sequences.
                                                                                                    Nucleic acid detection; nucleic acid labelling; gene therapy; nucleic acid purification; androgen receptor promoter; triple helix; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection; ss.
                                                                             Sequence of a fragment of the murine androgen receptor promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50 BP; 1 A; 30 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 4; I 100.0%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                   & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                          Roulon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                            Helene C,
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 20; 91pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA36647 standard; cDNA; 27 BP
ABL56736 standard; DNA; 50 BP.
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                                                                                                                                                                                                                                                            99FR-00007503.
                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                          Garestier T,
                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-080698/09.
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wes 20; Conserv
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                                                                                                                                                                                                                                                            14-JUN-1999;
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                                                   20-AUG-2002
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                                                                                                                                           Synthetic.
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                         ABL56736
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                                                                                                                                                       Mus sp
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36632 and peptide sequences AAA3663-A36652 and peptide sequences AAA3665-98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for transporter stansporter acids to negate transporter and infection. The transporter cransforming cells to produce proteins, or transfecting cells in vitro carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                       System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endosomes, without requiring endosomal or lysosomal degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 17.4; DB 3; Length 27; 94.7%; Pred. No. 4.2e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                       Disclosure; Fig 15a; 108pp; English
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WPI; 2000-281993/24
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nes 18; Conserv
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Smith LC;

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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS cor (e) appecific acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The yest agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                   Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                Sparrow J,
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                                                                                                                                                             Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 15A; 107pp; English
                                                                                              (BAYU ) BAYLOR COLLEGE MEDICINE.
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93WO-US002725.
93US-00167641.
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                                                                                                                                                                Cristiano RJ,
                                                                                                                                                                                                                               WPI; 2000-038262/03.
   19-MAR-1993;
                           14-DEC-1993;
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14-DEC-1993;
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                                                                                                                                                                WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EX BY REAL STORY OF THE STORY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transport sesting). Other uses include carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro carcinogenesis or of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                 System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 17.4; DB 3; Length 27;
llarity 94.7%; Pred. No. 4.2e+03;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 27
/*tag= a
/note= "all C's are methylcytosines"
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                                                                                                                                                                                                   WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             remplate pyrimidine series sequence in a ligand.
                                                                                                                                                                                                   Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 15a; 108pp; English.
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                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGGGAGGGGAGGG 19
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                                  92US-00855389.
93WO-US002725.
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                                                                                                                                                                                                   Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                     WPI; 2000-281993/24.
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hes 18; Conserv
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                                  20-MAR-1992;
19-MAR-1993;
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Best Loca Matches

RESULT 10 AAZ39496/c

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Smith LC;

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                                                                                                                                                                                                          The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to S components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or artigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytolasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting or provided and a sessessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells animal specific acid accordingly targeted tissue culture cells specific expression into specifically targeted tissue culture cells. The second of the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen; primer; sex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.4; DB 3; Length 27;
Pred. No. 4.2e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid transporter system primer SEQ ID NO 15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cristiano RJ,
                                                                                                                                                                 Disclosure; Fig 15A; 107pp; English.
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93US-00167641.
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Best Local Similarity 94.7%
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                          WPI; 2000-038262/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001
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14-DEC-1993;
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This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a cultace ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid the nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; olotting factor; apolipoprotein; receptor; drug; oncogene; tumor autigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen; primer; ss.
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growth factors, enzymes, hormones, and tumor suppressors.
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
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                                         Disclosure; Col 97-98; 105pp; English.
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/note= "5-methylcytosine"

Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including

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Gaps

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Length 27; Indele

Score 17.4; DB 4; Pred. No. 4.2e+03; 0; Mismatches 1;

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87.0%; S nilarity 94.7%; F Conservative 0;

Query Match Best Local Similarity Matches 18; Conserv

1 AGGGGAGGGGAGGG 19

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24 AAGGGAGGGGAGGGGG 6

AAS08476/c ID AAS08476 standard; DNA; 27

RESULT 14

23-OCT-2001

AAS08476;

Pyrimidine-rich oligonucleotide #5 used in nucleic acid transport system. Nucleic acid transport, cytosis, ligand, lysis agent; spacer molecule, gene therapy, hepatocyte, muscle, bone forming cell, oligonucleotide; ss.

Location/Qualifiers

modified_base

Kev

Synthetic.

modified base

modified_base

mSc

/*tag= a /mod_base=

/*tag= b 'mod_base= m5c

mSc

/*tag= c /mod_base=

mod_base= m5c

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modified base

mod_base= m5c

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*tag=

modified base

/mod_base= m5c 21. .22 /*tag= g /mod_base= m5c

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modified base

US6177554-B1

23-JAN-2001

*tag= f

modified base

95US-00462040.

05-JUN-1995;

Disclosure; Col 97-98; 105pp; English.

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Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                             WOO SLC;
                                                                                                                                                                                                                                                                                                                                             Smith LC,
                                                                                                                                                                                                                     /*tag= n
/mod_base= Other
/note= "5-methylcytosine"
                                   *tag= h
mod_base= Other
note= "5-methylcytosine"
                     note = "5-methylcytosine"
                                                                                 note= "5-methylcytosine"
                                                                                                               note = "5-methylcytosine"
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                                                                                                                                                                          note= "5-methylcytosine"
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note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                             Sparrow J, Cristiano RJ,
                                                                 *tag= i
mod_base= Other
                                                                                                *tag= j
mod base= Other
                                                                                                                            *tag= k
mod_base= Other
       *tag= g
nod base= Other
                                                                                                                                                                  mod base= Other
                                                                                                                                                                                                                                                                                                                              (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                              93WO-US002725.
93US-00167641.
                                                                                                                                                                                                                                                                                  95US-00460971.
                                                                                                                                                          *tag= 1
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                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-049093/06.
modified base
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                             modified base
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                                                                                                                                                                                                                                                                                                                                             Gottchalk S,
                                                                                                                                                                                                                                                                                  05-JUN-1995;
                                                                                                                                                                                                                                                                                                 20-MAR-1992;
                                                                                                                                                                                                                                                                                                       19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                    US6150168-A.
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The sequence represents the pyrimidine-rich oligonucleotide #5 used in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sparrow J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith LC, Cristiano RJ, Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 15; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00855389.
93WO-US002725.
93US-00167641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOO SLC,
This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding complex comprising a ligand binding comclete caid and covalently linked to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding complex comprising a second binding complex ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor cauging parasitic antigens, and bacterial antigens. The transporter system uses lysts agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems
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Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;

AAD41066 standard; DNA; 30

RESULT 16

AAD41066

AAD41066;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the purine-rich oligonucleotide #5 used in used in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purine-rich oligonucleotide #5 used in nucleic acid transporter system.
                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gottchalk S, Sparrow J;
                                                                                                                                        ch 87.0%; Score 17.4; DB 4; Length 27; 1 Similarity 94.7%; Pred. No. 4.2e+03; 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.4; DB 4; Length 27;
Pred. No. 4.2e+03;
0; Mismatches 1; Indels
                                                                                                          Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 15, 111pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%; Scc.
94.7%; Pred
0; '
                                                                                                                                                                                                                  1 AGGGGAGGGGAGGG 19
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                                                                                                                                                                                                                                         24 AAGGGAGGGAGGGAGGG 6
                                                                                                                                                                                                                                                                                                                                            AAS08477 standard; DNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00855389.
93WO-US002725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-365933/38
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Best Local Similarity
                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6177554-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                               AAS08477;
                                                                                                                                                                                                                                                                                                            RESULT 15
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The invention relates to a tumour necrosis-factor TNP inducible promoters.

The invention is useful for identifying candidate TNP inducible promoters by aligning a test sequence consisting of a nucleic acid sequence with a comparison sequence selected from the invention, using a gap opening penalty of 50 and a gap extension penalty of 3 to define a test alignment, shuffling the nucleic sequence of the test sequence at least one hundred times, while maintaining its length and composition, to produce a series of randomised sequences, aligning the randomised sequences with the comparison sequence using a gap opening penalty of 50 and a gap extension penalty of 3, to produce a series of randomised alignments, where the average alignment quality of the randomised alignments represent an alignment expected by chance, comparing the test alignment with the average alignment quality of the randomised and identifying a test alignment with a probability value of less than to 0.05 that the alignment is obtained by chance as a candidate TNF inducible promoter. The invention is useful for identifying candidate compounds for treating or preventing autoimmune disorders or cancer. The present sequence is a primer used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel tumor necrosis-factor inducible promoter useful for identifying candidate compounds for treating/preventing autoimmune disorders/cancer, or for identifying promoters that are regulated by tumor necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                            Tumour necrosis-factor; TNF; promoter; autoimmune disorder; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                        Primer ON-TATADel used for DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                           07-DEC-2001; 2001WO-EP014412.
                                                                                                                                                                                                                                                                                                                                             08-DEC-2000; 2000US-0254649P.
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ilarity 94.7%;
Conservative (
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                                                                      30-OCT-2002 (first entry)
                                                                                                                                                               therapy; primer; ss
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                     WO200246433-A2.
                                                                                                                                                                                                                                                                                                                                                                               (SAUS/) SAUS
                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                       13-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                     Saus J;
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Gaps

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Conservative

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08-DEC-2000; 2000US-0254649P.
                                (SAUS/) SAUS J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of human DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-13, in a head-to-head arrangement with the Goodpasture antigen binding protein (GPBP). The detection of the coding sequence can be used for diagnosing an autoimmune condition and identifying cells undergoing apoptosis, and the sequences can be used in the treatment of autoimmune diseases and cancer. The present sequence is a sequencing primer
                                                                                                                                                                                                                                                                                      Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced variant of DNA polymerase kappa, useful as target for treating a patient with autoimmune disorder or cancer.
                                                    Human, pol kappa 76; Goodpasture antigen binding protein; GPBP; chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic; immunosuppressive; PCR; primer; sequencing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; Goodpasture antigen binding protein; GPBP; COL4A3BP; collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa; Goodpasture disease; cutaneous lupus; polK76; bi-directional promoter; autoimmune disease; cancer; antisense therapy; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bi-directional promoter PCR/sequencing primer ON-TATADel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.4; DB 6; Length 30;
Pred. No. 4.2e+03;
0; Mismatches 1; Indels
                                Human pol kappa 76 DNA polymerase sequencing primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                    Example; Page 15; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGGAGGGAGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                       07-DEC-2001; 2001WO-EP014409.
                                                                                                                                                                                             08-DEC-2000; 2000US-0254649P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 87.0%;
1 Similarity 94.7%;
18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACD13504 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                       described in the invention
           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                 WPI; 2002-537563/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003027165-A1.
                                                                                                                         WO200246378-A2
                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                    (SAUS/) SAUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2003
           18-SEP-2002
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                                                                                                                                                 13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACD13504;
                                                                                                                                                                                                                                           Saus J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 18
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The invention relates to an isolated pol kappa (k) 76 polypeptide (an alternatively spliced form of DNA polymerase kappa), appearing as ACD34922. The gene for AB007327 (encoded by the CDNA appearing as ACD34922). The gene for POLkappa is located on chromosome 5q12-13 in a head-head arrangement with the GDNA appearing as ACD34922. The gene for POLkappa is located on chromosome 5q12-13 in a head-head arrangement with alpha 3 binding protein (CD4A3bp), associated with autoimmune diseases alpha 3 binding protein (CD4A3bp), associated with autoimmune diseases of aisease and cutaneous lupus) i.e. has a bi-cdirectional promoter. Also included are a recombinant expression vector directional promoter. Also included are a recombinant expression vector comprising the polK76 cDNA, a host cell transfected with the vector, comprising the protein sample to be screened, contacting the protein sample to be screened, contacting the protein sample to be screened, contacting the protein sample with one or more polK76 primer, carrying out PCR to generate PCR products, and identifying the comprising contacting the sample with one or more polK76 primer, carrying out PCR to generate PCR products, and identifying the comprising providing a tissue or body fluid sample from the patient. Comprising providing a tissue or body fluid sample in which no autoimmune condition) and the tissue of body fluid sample compared to the control sample, where the increase indicates the presence of an autoimmune condition) and the tissue of body fluid sample compared to the control sample, where the increase indicates the presence of an autoimmune disorder or cancer by modifying the expression or activity of polK76 nucleic acid, such as by increasing their expression or activity of polK76 increasing produce is a PCR and/or sequencing primer used in the present sequence is a PCR and/or sequencing primer used in the analysis of bi-directional promoters of cancer are areas and indirectional promoters of cancer areas and indirectional promoters of cancer area
                                                                                                                                    New isolated DNA polymerase, pol kappa 76, useful in identifying autoimmune disorders and in treating cancer and autoimmune disorders by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour necrosis factor inducible promoter; TNF; autoimmune disorder; cancer; PCR; immunosuppressive; cytostatic; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour necrosis factor (TNF) inducible promoter PCR primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               whose structure and sequence were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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0
                                                                                                                                                                                                                                                                                       Example; Page 6; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003 (first entry)
                                                                                                                                                                                                                   modifying its expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
                                                                    WPI; 2003-479531/45.
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Matches 18; Conserv
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<u>ن</u>
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ADA97805
Saus
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAA3663-A3650 are used transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid transport system (NTS) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid transport system; NTS; cell surface receptor; cytosis nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                              endosomes, without requiring endosomal or lysosomal degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 3; Length 39;
Pred. No. 4.18+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Target sequence in a double stranded vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gottchalk S,
                                                                       Disclosure; Fig 15a; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 15A; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGGGGAGGGAGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-US002725.
93US-00167641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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14-DEC-1993;
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     CXSXLLXBXLXBXBXBXBXBXBXBXBXBXBXBXBXCX
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                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a tumour necrosis factor (TNF) inducible promoter. Also disclosed are an expression vector comprising one or more tumour necrosis factor inducible promoters and a recombinant host cell transfected with one or more expression vectors. The TNF inducible promoters, expression vectors and host cells are useful for identifying promoters that are regulated by tumour necrosis factor or for identifying candidate compounds for treating or preventing autoimmune disorders or necrosis factor. This sequence represents a PCR primer used for isolating a tumour necrosis factor inducible promoter of the invention.
                                                                                                                                                                                                                                                          New tumor necrosis factor inducible promoters, useful for identifying promoters that are regulated by tumor necrosis factor, or for identifying candidate compounds for treating or preventing autoimmune disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%; Score 17.4; DB 9; Length 30; 94.7%; Pred. No. 4.2e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid transporter system target sequence #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cristiano RJ,
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                                                                                                                                                                                                                                                                                                                                              Example; Page 7; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA36645 standard; cDNA; 39 BP
                                                                                                                         08-DEC-2000; 2000US-0254649P.
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                                                                                       07-DEC-2001; 2001US-00008721
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Best Local Similarity 94.7
Matches 18; Conservative
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                   US2003082745-A1
                                                                                                                                                         (SAUS/) SAUS
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                                                     01-MAY-2003
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                                                                                                                                                                                           Saus J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 20
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Gaps

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delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a molety that recognizes and binds to a cell surface receptor or acid or macromolecular molecule binding noiety; (d) a molety that is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a molety that is capable of moving or initiating movement through a nuclear membrane; and/or or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific ancleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells. The nucleic acid across nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The second and accordingly targeted tissue culture cells. The second according agent within the NTS avoids the problem of endosomal/lysosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel system (1) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a molecule noncovalently bound to a nucleic acid and covalently linked to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid delivery, nucleic acid transporter system, hormone, enzyme, growth factor, clotting factor, apolipoprotein, receptor, drug, oncogene, tumor antigen, tumor suppressor, viral antigen, parasitic antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into a cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transporter system for delivering nucleic acid into a cuseful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
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                                                                                                                                                                                                                                                                                                                                                                                                                               87.0%; Score 17.4; DB 3; Length 39; 94.7%; Pred. No. 4.1e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid transporter system primer SEQ ID NO 13.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith LC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 97-98; 105pp; English.
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93US-00167641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the double-stranded vector target sequence #5 used in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands, lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into hepatocytes, muscle cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targething of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, paraaitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid transport, cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell; ds.
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector target sequence #5 used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                 Match
Local Similarity 94.7%; Pred. No. 4.1e+03;
es 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                endosomal/lysosomal degradation seen with prior art systems
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Pred. No. 4.1e+03;
                                                                                                                                                                                                                      Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith LC, Cristiano RJ, Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 15, 111pp, English.
                                                                                                                                                                                                                                                                                                                                      1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                          10 AAGGGAGGGAGGGAGGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-00855389.
93WO-US002725.
93US-00167641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00462040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS08475 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-365933/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS08475;
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                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS08475
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Page

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Gaps

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Indels

Pred. No. 4.1e+03; ); Mismatches 1;

; 0

Conservative

94.78;

Best Local Similarity

18;

Matches

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artiple-helix computation tenates to mertions and computation finished a double helical nucleic acid computating first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel cried, where the oligonucleotide binds in a parallel and antiparallel cried conjectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parnogen which is not found in the genome of pathogen's host. The coligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triple-helix formation; purine-rich target sequence; double-helix DNA gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
Gaps
    ö
    Indels
    Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triple helix forming associated DNA sequence #19.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 8B; 108pp; English.
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                                                                                 1 AGGGGAGGGGAGGG 19
                                                                                                                                                               10 AAGGGAGGGAGGGAGGG 28
                                                                                                                                                                                                                                                                                                                                                                              ABK98155 standard; DNA; 39 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dervan PB, Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-536030/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK98155;
    Matches
                                                                                                                                                                                                                                                                                            RESULT 24
                                                                                                                                                                                                                                                                                                                                       ABK98155
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87.0%; Score 17.4; DB 6; Length 39;

Query Match

Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;

the present invention

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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel acid, where the oligonucleotide binds in a parallel and antiparallel configuration, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
                                                                                                                                                                                                                                                                                                                              Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; concogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 BP; 6 A; 14 C; 6 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                       Triple helix forming associated DNA sequence #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 8B; 108pp; English.
19
                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00168920.
                                           10 AAGGGAGGGAGGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-00946976.
  1 AGGGGAGGGGAGGG
                                                                                                                                                        ABK98154 standard; DNA; 39
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-536030/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6403302-B1
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                                                                                                                                                                                                                                          07-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dervan PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                   ABK98154;
                                                                                                               RESULT 25
                                                                                                                                   ABK98154/
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                                                                                                                                                                                         Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                     Gaps
                     ;
87.0%; Score 17.4; DB 6; Length 39; 94.7%; Pred. No. 4.18+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                        Triple helix forming associated oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                              (CALY ) CALIFORNIA INST OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Col 29; 108pp; English.
   87...
94.7%; Fi.
                                       19
                                                          30 AAGGGAGGGAGGGG 12
                                                                                                             BP
                                       1 AGGGGAGGGGAGGG
                                                                                                                                                                                                                                                                                                                            92US-00946976.
                                                                                                            ABK98106 standard; DNA; 43
                                                                                                                                                    (first entry)
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              respectively, for target
control gene expression.
                                                                                                                                                                                                                                                                                                                                                                  Dervan PB, Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-536030/57.
          Local Similarity
ses 18; Conserv
                                                                                                                                                                                                                                                                US6403302-B1
                                                                                                                                                                                                                                                                                                                            17-SEP-1992;
                                                                                                                                                    07-OCT-2002
                                                                                                                                                                                                                                                                                     11-JUN-2002
                                                                                                                                                                                                                                             Synthetic
                                                                                                                                 ABK98106;
  Query Match
            Best Loc
Matches
                                                                                         RESULT 26
                                                                                                   ABK98106
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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel corientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation oligonucleotides can be used to form triple-helices, and are useful to eligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA cor diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the presence of found in the genome of pathogen's host. The oligonuclectides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonuclectides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially Killing or repressing the cancer causing cell. The present sequence represents an oligonuclectide used in the the present invention methods of

Sequence 43 BP; 15 A; 6 C; 14 G; 8 T; 0 U; 0 Other;

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a triple-heltx comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel corid, where the oligonucleotide binds in a parallel and antiparallel nucleic acid, where the chuble helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The coligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific sequence bacterially bind to pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotides can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The pathogen which is not found in the genome of pathogen's host. The origin. Such therapeutic oligonucleotides are capable of forming triple-helix origin. Such therapeutic oligonucleotides are capable of forming triple contains with such sequence in cancerous cells containing the activated concepted. The present sequence represents a DNA sequence used in the methods con the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to methods and oligonucleotides for forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                                                                                                                                                                                                                                                                                                                            Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; concogene suppression; cancerous cell; cytostatic; antimicrobial; 88.
                                         Gaps
                                         ö
  43;
                                         Indels
Length
Score 17.4; DB 6;
Pred. No. 4e+03;
; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                       Triple helix forming associated DNA seguence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Col 29; 108pp; English.
                                                                                1 AGGGGAGGGAGGGG 19
                                                                                                                         14 AAGGGAGGGAGGGAGGG 32
                                      ;
0
                                                                                                                                                                                                                              ABK98104 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00168920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00946976
  87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-536030/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beal PA;
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1992;
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                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                       ABK98104;
  Query Match
Best Local 8
                                         Matches
                                                                                                                                                                                         RESULT 27
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Query Match
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                   RESULT 29
                                                                                                                                                                                                                                                                                                                                      AAQ46253
 888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Wheta gene, WhetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, graft versus host disease. Autoimmune diseases include Addison's disease, and neoplastic diseases. Autoimmune diseases include Addison's disease, arcphic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include multiple sclerosis and Li hypersensitivities such as contact with allergens that lead to doodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                             human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; leptosy; infectious disease; viral infection; HIV; fungal infection, Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                       Gaps
                                                                       ö
                                85.0%; Score 17; DB 6; Length 19; 100.0%; Pred. No. 5.9e+03;
                                                                   0; Indels
Sequence 19 BP; 5 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 699; 164pp; English.
                                                                                                                                                                                                                                                                                                                                  Human Vbeta gene repeat sequence #295.
                                                                                                       3 GGGAGGGGAGGGG 19
                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00309335,
95US-00531241,
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                                                                                                                                                                                                                            ADH70505 standard; DNA; 23
                                                                                                                                                                                                                                                                                               (first entry)
                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-059052/06
                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hood LE, Rowen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast cancer; ds.
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Б
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAR-1999;
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19-SEP-1995;
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(ROWE/) ROWEN
                                                                                                                                                                                                                                                                                               25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vbeta gene
                                                                                                                                                                                                                                                               ADH70505;
                                    Query Match
                                                                     Matches
                                                                                                                                                                                           RESULT 28
ADH70505/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was used to form a 39mer duplex an example to illustrate the invention. Oligonucleotides conforming to this sequence were 5' end radioactively labeled using T4 polynucleotide kinase and gamma 32P ATP. The annealed oligomers form a purine-rich trarget sequence to which an oligomucleotide (TFO) containing a nebularine nucleotide binds, forming a triple helix. These triplex-forming oligomers may be used to detect the presence or absence of specific sequences within genomic DNA by the formation in situ or in vivo of triple helices for diagnostic and therapeutic purposes. TFO can be selected which specifically bind to pathogenic double-stranded DNA including specific sequences required by Alternatively, TFO can be chosen to target a unique sequence of the pathogen which is not found in the genome of the host. It may include a
caused by viruses such as HIV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
                                                                           such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Voeta gene repeat sequence.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duplex; T4 polynucleotide kinase; nebularine; triple helix; triplex;
detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;
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                                                                                                                                                                         84.0%; Score 16.8; DB 12; Length 23; 90.0%; Pred. No. 6.7e+03; ive 0; Mismatches 2; Indels (
                                                                                                                                     Sequence 23 BP; 1 A; 17 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C or T"
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                                                                                                                                                                                                                                                     1 AGGGGAGGGAGGGGG 20
                                                                                                                                                                                                                                                                               AGGGGGGGGAGGTGAGGGG 4
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                                                                                                                                                                                                                                                                                                                                                                                     AAQ46253 standard; DNA; 43
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/note= "A,
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                                                                                                                                                                                             Local Similarity 90.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39mer duplex forming DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oncogene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAR-1993;
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24-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dervan PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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correct PN field.)
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                                                                                                                                                                                                                                                            25-MAR-2003
24-MAR-1994
                                                                                                                                                                                                                                                 21-OCT-2004
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                                                   Query Match
Best Local Si
Matches 17;
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                       AAQ46256;
                                                                                                                                                                      RESULT 31
                                                                                                                                                                                    AAQ46256
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                                                                                                                               셤
                                                                                                                                                                                                            The sequences given in AAQ46256-57 form a duplex which was used to evaluate the binding of trplix forming oligomers (TFO). The annealed coligomers form a purine-rich target sequence to which the TFO which contain a nebularine nucleotide binds, bind, forming a triple helix.

These triplex-forming oligomers may be used to detect the presence or specific sequences within genomic DNA by the formation in situ or in vivo of triple helices for diagnostic and therapeutic purposes. TFO can be selected which specifically bind to pathogenic double-stranded DNA or in vivo of triple helices for diagnostic and therapeutic purposes. TFO can be selected which specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence. Alternatively, TFO can be chosen to target a unique sequence of the pathogen which is not found in the genome of the host. It may include a therapeutic agent to kill the pathogen or the cell host. Triple helix technology can also be used for cancer treatment by way of triple helix suppression of specific oncogenes including those of endogenous or viral origin. (Updated on 25-MAR-2003 to
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therapeutic agent to kill the pathogen or the cell containing it. Triple helix technology can also be used for cancer treatment by way of triple helix suppression of specific encogenes including those of endogenous or viral origin. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                     T4 polynucleotide kinase; nebularine; triple helix; triplex
on; diagnosis; pathogen; bacteria; virus; virulence; cancer;
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                                                                                       Query Match 82.0%; Score 16.4; DB 2; Length 43; Best Local Similarity 89.5%; Pred. No. 8.6e+03; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
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                                                                                                                                            1 AGGGGAGGGGAGGG 19
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                                                                                                                                                                                                                                     AAQ46257 standard; DNA; 43
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/note= "A,
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                               Duplex forming DNA #2.
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24-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                       detection;
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                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duplex, T4 polynucleotide kinase, nebularine, triple helix, triplex,
detection, diagnosis, pathogen, bacteria, virus, virulence, cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triple helix formation for diagnosis and therapy - by specific recognition by oligo: nucleotide probe of target sequence in doublestranded nucleic acid.
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                                                               Length 43;
                                                                                                                           Indels
Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;
                                                            Score 16.4; DB 2;
Pred. No. 8.6e+03;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CALY ) CALIFORNIA INST OF TECHN
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                                                               82.0%;
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/note= "A,
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/mod_base=
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                                                                                           Local Similarity 89.5
nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duplex forming DNA #1.
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modified_base
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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel corientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA collected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including consideration or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogenic The pathogen which is not found in the genome of pathogen; the colligions of the pathogen which is not found in the genome of pathogen; the colligions of the colli
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treatment by way of triple helix suppression of specific oncogenes including those of endogenous or viral origin. (Updated on 25-MAR-2003 correct PN field.)
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                                                                                                                     record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regultatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                            82.0%; Score 16.4; DB 2; Length 43; 89.5%; Pred. No. 8.6e+03;
                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                          Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triple helix forming associated DNA sequence #21.
                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      1 AGGGGAGGGAGGGG 19
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                                                                                                                                                                                                                                                                                 17; Conservative
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                                                                                                                                                                                                                                                  Local Similarity
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ABK98158/
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pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix

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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel or intention, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA conditions or diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the the pathogen which is not found in the genome of pathogen's host. The
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                 origin. Such the rapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous calls containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triple-helix formation; purine-rich target sequence; double-helix DNA gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virulence; cancer; pathogenic bacteria; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                               Gaps
including those of endogenous
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0
                                                                                                                                                                                   82.0%; Score 16.4; DB 6; Length 43; llarity 89.5%; Pred. No. 8.6e+03; Conservative 0; Mismatches 2; Indels
                                                                                                                                         Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triple helix forming associated DNA sequence #3.
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                                                                                                                                                                                                                                                                        1 AGGGGAGGGAGGGG 19
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                                                                                                    the present invention
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nes 17; Conserv
suppression of
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Matches
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The present invention relates to methods and oligonuclectides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonuclectide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonuclectide binds in a parallel and antiparallel corientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonuclectides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonuclectides can be seen to pathogenic double-stranded DNA including selected to specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonuclectide can be chosen to target a unique sequence of the
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oligonucleotides can be used in cancer treatment by way of triple-helix upupression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple helices with such sequences in cancerous cells containing the activated nocogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triple-helix formation; purine-rich target sequence; double-helix DNA, gene expression; requiatory sequence; pathogenic double-stranded DNA; pathogenic bacteris; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                            Score 16.4; DB 6; Length 43;
Pred. No. 8.6e+03;
0; Mismatches 2; Indels
                                                                                                                                                                       Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triple helix forming associated DNA sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Col 35; 108pp; English.
                                                                                                                                                                                                                                                                                                  1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                 34 AAGGGNGGGAGGGAGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK98111 standard; DNA; 43 BP
                                                                                                                                                                                                            82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-00946976.
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                                                                                                                                                                                                                                     Local Similarity 89.5
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dervan PB, Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-536030/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to methods and oligonucleotides for forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             artiple-helix comprising double helical mucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively,
pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous calls containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                          82.0%; Score 16.4; DB 6; Length 43;
89.5%; Pred. No. 8.6e+03;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                 Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triple helix forming associated oligonucleotide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Col 33; 108pp; English.
                                                                                                                                                                                                                                                                                                                                    1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                             14 AAGGGNGGGAGGGAGGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00168920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK98107 standard; DNA; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-2002 (first entry)
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                       of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-536030/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK98107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
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the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triple-helix formation; purine-rich target sequence; double-helix DNA, gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; visualis; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                  Gaps
                                                                                                         cell. The present sequence represents an oligonucleotide used in the methods of the present invention
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0
                                                                                                                                                                               Score 16.4; DB 6; Length 43;
Pred. No. 8.6e+03;
0; Mismatches 2; Indels
                                                                                                                                                      Seguence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Triple helix forming associated DNA sequence #20.
                                                                                                                                                                       82.0%; Scor.
89.5%; Pred. No. e.c.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 11; 108pp; English.
                                                                                                                                                                                                                                              1 AGGGGAGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                  14 AAGGNGGGAGGGAGGG 32
                                                                                                                                                                                                                                                                                                                                                  ABK98157 standard; DNA; 45 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00168920.
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dervan PB, Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-536030/57.
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6403302-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                               ABK98157;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                      RESULT 36
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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic pursposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for

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replication or virulence, reducing their pathogenicity. Alternatively, the oligomuclectide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligomucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligomucleotides are capable of forming triple-helices with such sequences in cancercus cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA;
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                                                                                                                                                                                                                                                                                      82.0%; Score 16.4; DB 6; Length 45; 89.5%; Pred. No. 8.6e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fannon MR,
                                                                                                                                                                                                                                             Sequence 45 BP; 14 A; 7 C; 14 G; 9 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus contig SEQ ID #2153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2159; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                                                                                                                                                                                                                                                                                          1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                     AAGGGNGGGAGGGAGGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97EP-00100117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV76464 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                          Best_Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxic shock syndrome; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.aureus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV76464;
                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 37
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stability of an mRNA encoding angiogenic factor, especially ARNT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH70729;
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                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH70729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes enzymatic nuclear acts morecutes with many clearing activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a fite-2 gene. AAA16775 to AAA17621 to AAA17622 represent ribozyme sequences for ARNT, and AAA1168 to AAA17662 represent ribozyme sequences for ARNT, and AAA13168 to AAA1363 to AAA1383 and AAA19087 to Corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19155 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA20361 and AAA1561 to AAA1555 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21896 to AAA21688 represent their corresponding target sequences; AAA21896 to AAA2168 represent their corresponding target sequences; Cor integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21869 to AAA22475 and AAA23476 to AAA23362, AAA23343 to AAA2342 represent their corresponding target sequences. The ribozyme sequence integrin subunit beta 3, and AAA22476 to AAA23362, AAA2343 to AAA2342 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or
                                                                                                                                                                                             ö
                    (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribozymes for modulating the synthesis, expression and/or stability mRNA encoding an angiogenic factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes enzymatic nucleic acid molecules with RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruce augaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
for recombinant production of the polypeptides. The new DNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcswiggen JA;
                                                                                                                                            Score 16.4; DB 2; Length 50;
Pred. No. 8.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin subunit beta 3 substrate sequence SEQ ID NO:5754.
                                                                                                                                                                                      Indels
                                                                                                       Seguence 50 BP; 0 A; 46 C; 1 G; 2 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coeshott C,
                                                                                                                                                                Local Similarity 89.5%; Pred. No. 8.56 ne 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jarvis T,
                                                                                                                                                                                                                                    2 GGGGAGGGAGGGGG 20
                                                                                                                                                                                                                                                                            GGGGGGGGNGGGGAGGGG 10
                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                              82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                       AAA22528 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-591315/50.
                                                          readable medium
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                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               AAA22528;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; haddison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; infection disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Obler-Weber-Rendu syndrome, and other syndrome and diseases related to the levels of ARNT, Tie-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; T-cell associated disease; Vbeta; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 16; DB 2; Length 17; 100.0%; Pred. No. 1.3e+04; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                         Seguence 17 BP; 0 A; 13 C; 1 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 923; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Vbeta gene repeat sequence #519.
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95US-00531241,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGGAGGGGAGGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-059052/06.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast cancer; ds.
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                                                                            atrophic gastritis. Degenerative nervous system diseases include multiple soletosis and Alzheimer's disease. Hypersensitivity diseases include Type I hypersensitivities such as contact with allergens that lead to allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those present in manifested in leprosy. Infectious diseases include viral infections caused by the yeast genus Candida, parasitic infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                 including autoimmune diseases, degenerative nervous system diseases, graft versus host disease, hypersensitivity diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
rejection and diagnosing and treating T-cell associated diseases
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 12; Length 19;
Pred. No. 1.5e+04;
); Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          process for purification of oligonucleotides using liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide purification; liquid chromatography; hydrophobic protective group; deprotection; ds.
                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 1 A; 2 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGGAGGGAGGGGG 20
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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soluble organic solvent at a suitable concentration gradient to elute the deprotected oligonucleotides; and (e) removal of the solvent and the salt from the eluted oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA cytosine methyltransferase modulator containing 5-C methylcytosine used to inhibit methylation of DNA, and proliferation of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                          DNA cytosine methyltransferase; DCMTase; binding discrimination; C-5 methylcytosine; allosteric site; synthetic inhibitor; cancer cell; proliferation; development disorder; Huntington's disease;
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                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide used for screening DCMTase binding discrimination.
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                                                                                               Score 15.8; DB 4; Length 20; Pred. No. 1.5e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 2; Length 2
Pred. No. 1.4e+04;
0; Mismatches 2; Indels
                                                                                                                               2; Indels
                                                                Sequence 20 BP; 1 A; 1 C; 17 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 BP; 3 A; 1 C; 20 G; 2 T; 0 U; 0 Other;
                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Down's syndrome; Hox gene; ss.
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                                                                                                79.0%;
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                                                                                                                                                                                                                                                                               AAX40753 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                16-JUN-1999 (first entry)
                                                                                                  Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
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es 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-1997;
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                                                                                                                                                                                                                                                                                                                AAX40753;
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Matches
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Human GABA(b) receptor 1 promoter P1b primer 2058 PR1b CGVI Rev.

AAF28801 standard; DNA; 27 BP

AAF28801

09-APR-2001 (first entry)

AAF28801;

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The invention relates to novel nucleic acid molecules constituting the human gamma-amino butyric acid (GABA)B receptor 1 promoters Pla and/or Plb (AAP28781 and AAF28782). Or their functionally equivalent modified forms or active fragments. PCR primers AAF28805 were used for PCR mutagenesis of the GABA(b) promoter sequences for mutational analysis of promoter element function. Nucleic acid molecules containing the human GABAB receptor 1 promoters Pla and/or Plb are useful for screening therapeutic agents that selectively regulate the expression of GABAB receptor 1a and lb-type splice isoforms. These compounds, which are modulators of GABAB receptor 1 transcription, are potentially useful in the treatment of disorders that are related to neurally-controlled physiological responses regulated by GABAB receptors such as central nervous system (CNS) disorders, e.g. muscle relaxation in spinal apparationty, Alzheimer's disease and other dementias, psychiatric and neurological disorders, e.g. depression, anxiety or epilepsy, cardiovascular disorders, asthma, gut motility disorders, e.g. irritable
                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuroprotective; nootropic; antidepressant; tranquilizer; anticonvulsant; cardiant; primoter; cardiant; promoter; CNS; gamma-amino butyric acid B receptor 1; splice isoform; spinal spasticity; transcription modulator; central nervous system disorder; dementia; muscle relaxation; Alzaheimer's disease; depression; anxiety; epilepsy; cardiovascular disorder; asthma; irritable bowel syndrome; emesis; reflux disease; neurological disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules constituting the human gamma amino butyric acid-B receptor 1 promoters, useful for screening modulators of the receptors transcription or therapeutic agents regulating the expression
                                                                                                                                                                                                                                                                                                                                                    Human GABA(b) receptor 1 promoter P1b primer 2057 PR1b CGVI Fwd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leonardsson G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johansson T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 21; 46pp; English.
                                                                                       AAF28800 standard; DNA; 27 BP.
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                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-2000
                                                                                                                                                                          AAF28800;
RESULT 42
AAF28800/
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The invention relates to novel nucleic acid molecules constituting the human gamma-amino butyric acid (GABA)B receptor 1 promoters Pla and/or bub (AAP28781 and AAF28782). Or their functionally equivalent modified forms or active fragments. PCR primers AAF287886 were used for forms or active fragments. PCR primers AAF287886 were used for Corms or active fragments. PCR primers AAF288788 for mutational analysis of promoter element function. Nucleic acid molecules containing the human contained that selectively regulate the expression of GABAB receptor 1a- and 1b-type splice isoforms. These compounds, which are modulators of GABAB receptor 1 transcription, are potentially useful in the treatment of disorders that are related to neurally-controlled physiological responses regulated by GABAB receptors such as central nervous system (CNS) disorders, e.g. muscle relaxation in spinal nervous system (CNS) disorders, e.g. muscle relaxation in spinal coursological disorders, e.g. depression, anxiety or epilepsy, cardiovascular disorders, asthma, gut motility disorders, e.g. irritable bowel syndrome, emesis or reflux disease
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                                                                                                                             Neuroprotective; nootropic; antidepressant; tranquilizer; anticonvulsant; cardiant; antiasthmatic; antiinflammatory; human; GABA; promoter; CNS; gamma-amino butyric acid B receptor 1; splice isoform; spinal spasticity; transcription modulator; central nervous system disorder; dementia; muscle relaxation; Alzhaimer's disease; depression; anxiety; epilepsy; cardiovascular disorder; asthma; irritable bowel syndrome; emesis; reflux disease; neurological disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid molecules constituting the human gamma amino butyric
1-B receptor 1 promoters, useful for screening modulators of the
sptors transcription or therapeutic agents regulating the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johansson T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 21; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of its splice isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASTR ) ASTRAZENECA AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-024861/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid-B receptor 1
                                                                                                                                                                                                                                                                                                                           WO200068268-A1
                                                                                                                                                                                                                                                                                       Homo sapiens.
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AAL28918/c
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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; minterleukin, G-protein coupled receptor; thiossterase; interferon; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                 Human SNP oligonucleotide #5340.
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27-DEC-2000; 2000US-00173419.
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                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinasins, cytokines, interferons, interleukins, Gretofin coupled receptors and thiosesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukamai, diseases of the nervous system and an infection of pathogenic
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                                                                                                                            Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amylod protein; angiopoietin; appoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; miterleukin; Grprotein coupled receptor; thioesterase; intlammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
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Pred. No. 1.3e+04;
0; Mismatches 2; Indels
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                                                                                          Human SNP oligonucleotide #2126.
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27-DEC-2000; 2000US-00173419.
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                              (first entry)
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                                              24-JAN-2002
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AAL28918
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Leach M;

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The present invention relates to oligomucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, appprosis related proteins, cadherin, cyclin, polymerses, oncogenes, histones, kinases, colony stimulating factors, complement related proteins coupled receptors and thioseterases. The present sequence is one such oligomucleotide. The oligomucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer in the protein of pathogenic contents).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 G; S T; 0 U; 0 Other;
Claim 1; Page 2924; 4143pp; English.
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Matches 17; Conservative
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BP

AAL32132 standard; DNA; 50

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(first entry)

24-JAN-2002

AAL32132;

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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, appointed stated proceins, cadherin, polymerase, oncogenes, histomes, kinases, calony stimulating factors, complement related protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amylod protein; angiopoletin; appoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; miterfleukin; Grprotein coupled receptor; thioesterase; interferon; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin;
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Pred. No. 1.3e+04;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 11 A; 12 C; 23 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2923; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oncogenes and histones, useful for autoimmune diseases and infections.
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89.5%; Pred
0; F
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27-DEC-2000; 2000US-00173419.
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AAL28919 standard; DNA; 50
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                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2002
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apptoais related proteins, oadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins coupled receptors and thioseterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune consistency in the may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, concerned the prevented of the nervous system and an infection of pathogenic
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cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; d-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic, antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1990; 4143pp; English.
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27-DEC-2000; 2000US-00173419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-465210/50.
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Les 17; Conserv
                                                                                                                                                                         WO200147944-A2.
                                                                                                                                  Homo sapiens.
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The present interaction describes enzyments deriving activity, which specifically clave RNA encoded by an article of deaving activity, which specifically clave RNA encoded by an article of parts in integrin alpha 6 subunit gene, an integrin subunit beta 3 center an integrin alpha 6 subunit gene, an integrin subunit beta 3 corresponding target sequences for ARA1767 and AAA17661 to AAA17623 to AAA18684 represent their corresponding target sequences; AAA1865 to AAA18836 and AAA19086 and AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA1906 and AAA19155 to AAA19222 represent their corresponding target sequences; cand AAA19155 to AAA19222 represent their corresponding target sequences; corresponding target sequences; and AAA21696 to AAA21688 represent their corresponding target sequences; corresponding the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT; corresponding angiogenic factor, especially ARNT; corresponding angiogenic factor, especially as well as mediating the synthesis, expression and or corresponding angiogenic factor, especially as well as mach adactor tract cancer, diabetic retinopathy, age related mach angioting angiotic described and arthritis, as well as angiotibroma of tubercous sclerosis, pot-wine statins, Sturge Weber angiotibroma without the wine relation, and arthritis, submit and arthritish and angiotibroma without and arthritish and and angiotions and arthritish and angiotibroma without and arthritish and and angiotibroma without and arthritish and and and angiotibroma and arthritish and and angiotibroma and arthritish and and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes enzymatic nucleic acid molecules with RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human catechol-O-methyltransferase COMT gene polymorphic site, #1181.
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myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrin subunit alpha-6, or integrin subunit beta-3
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                                                                                                                                                                                                                                                                                                                                                                                                               Coeshott C,
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Matches 16; Conservative
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                                                                                                         Homo sapiens
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Sequences ABZ41217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least come polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ5087 using a crariety of detection assays, including hybridisation assays, nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ5087 using a crariety of detection assays, including hybridisation assays, nucleic acid availed by proprimers and pre-based methods. The invention also encompasses methods of avaluating and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SMPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful.

CC drugs. SNPs are also useful as polymorphism markers for discovering genes to a sequence variations metabolishing enzymes allows the customisation of fung therapies based upon the genetic profile of individual patients.

CC drug therapies based upon the genetic profile of individual patients.

CT mis would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby individual scould be selected for clinical trials only if their genetic profile aindicate that they are called drug candidates could be revived if they were matched with more appropriate patient populations. The enthed are made of drug candidates could be revived; date and compositions of the invention may therefore lead to a an increase in the number of different reactions, falled drug trials, the time patient and decreases in the number of adverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.
polymorphic site, drug evaluation, drug screening, genotyping, genetic profiling, therapeutic customisation, adverse reaction, clinical trial, drug approval, single nucleotide polymorphism, SNP, ds.
                                                                                                                                                                                 /*tag= a
/standard name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Page 83; 2785pp; English.
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                                                                                                                                                          replace (21, A)
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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Best Local Similarity
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                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                             04-JUL-2002
                                                                                                                                                          variation
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Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                            clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                            Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction;
                                                                                                                                                                                                                                                /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                            Human catechol-O-methyltransferase COMT gene polymorphic site, #5376.
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                                                                  ABZ48593 standard; DNA; 41 BP
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02-MAY-2001; 2001JP-00135256.
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comerpose and compositions for identifying individuals who have at least one polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridiation assays, nucleic acid sample using nucleic arrays and PCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of carays and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur in the above respects as they are stable in populations, occur in the above respects as they are stable in populations.

Trequently, and have lower mutation rates than other genome variations cut as repeating drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least

Claim 23; Page 169; 2785pp; English.

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Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are eapable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
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Job time : 157.744 secs
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79.0 79.0 79.0 79.0 79.0 79.0	799.0 799.0 799.0 799.0 799.0 799.0 799.0	79.0 79.0 79.0 79.0 79.0 79.0 24.9	79.0 24 9 79.0 25 9 79.0 25 9 79.0 25 11	7499.0 7499.0 7499.0 7499.0 7499.0 7499.0 7499.0	79.0 27 9	79.0 79.0 79.0 79.0 79.0 79.0 79.0 30.9	79.0 30 9 79.0 30 10 79.0 31 9 79.0 31 9	8 79.0 31 9 AZ825311 8 79.0 31 11 DR102G11S 8 79.0 32 9 AZ856053 8 79.0 33 1 AJ794963 8 79.0 33 9 AZ875613 8 79.0 33 9 AZ825930	79.0 33 10 79.0 34 1 79.0 35 9	79.0 35.9 79.0 35.9 79.0 35.9	79.0 35 9 79.0 36 9	79.0 36 9 79.0 37 1 79.0 37 9	79.0 37 10 79.0 37 10 79.0 38 9	79.0 39 9 79.0 39 10 79.0 40 10 79.0 40 11 79.0 41 8	
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.5.1.7 Biocceleration Ltd.	; Search time 1330.25 Seconds (without alignments) 703.434 Million cell updates/sec		residues	eters: 179606				results predicted by chance to have a to the score of the result being printed, of the total score distribution.	Description	AZ867169 2M0177120 AZ359724 1M0102M11 AZ958287 2M0225G02 AZ462959 1M0271G04	CL661180 PRIO139a AZ971404 2M0244G20 AZ800326 2M0061L09	AZ820833 2M0093L16 AZ375586 1M0129G03 AJ793526 AJ793526 AZ800436 2M0058L20	AZ780325 2M0017N06 AL935924 Arabidops AZ652279 1M0525K06 AZ424085 1M0203B05	AZ825536 2M0100J14 AZ877472 ZM019Z119 AI800153 TK723406.x AI597960 t804f05.x AZ447248 1M0244H23 AZ512326 1M0357118	
GenCore v Copyright (c) 1993 -	- nucleic search, using sw model February 15, 2006, 18:07:43	US-09-66 e: 20 l agggga	table: IDENTITY_NUC Gapop_10-0, Gapext_1.0 !: 41078325 seqs, 23393541228 re	oer of hits satisfying chosen parameters seq length: 0 seq length: 50	ssing: Minimum Match 0% Maximum Match 100% Listing first 300 summaries		6: gb_est5:* 7: gb_est6:* 8: gb_est7:* 9: gb_est7:* 10: gb_gss2:* 11: gb_gss3:*	No. is the number of greater than or equal derived by analysis	Query Score Match Length DB ID	20 100.0 20 9 20 100.0 35 9 4 92.0 22 9	4 87.0 28 10 4 87.0 32 9 4 87.0 33 9	4 87.0 45.9 4 87.0 47.1 4 87.0 47.1	.8 84.0 25 9 10 84.0 30 10 84.0 33 9 84.0 38 9	16.8 84.0 39 9 AZ825536 116.8 84.0 43 9 AZ877472 116.4 82.0 37 1 AI800153 116.4 82.0 46 1 AI59796 115.8 79.0 19 9 AZ44748 115.8 79.0 20 9 AZ512326	
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ORGANISM Mus musculus  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  Butheria; Buarchontoglires; Glires; Rodentia;  Sciurognathi; Muroidea; Muridae; Mus.  REFERENCE 1 (bases 1 to 20)  AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  Niederhausern, A. and Wright, D., Weises, R.  TITLE Mouse whole genome scaffolding with paired end reads from 10kb	plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	Tel: 801 585 Eax: 801 585 Email: ddunn Insert Lengt Plate: 0177 Cag primer: Class: plate: High quality	SOUICE	/Jab host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone_lib="Mouse_lokb plasmid_UUGCIM_library" /note="Vector: PWD42nv; Purified genomic_DNA from M. musculus_C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch norifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were	ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 gb AF129072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	Query Match 100.0%; Score 20; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 6.36+03; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Aggasgcgaggggagggggggg 20	Db 1 AGGGAGGGAGGGG 20  RESULT 2 AZ359724 LOCUS AZ359724 DEFINITION 1M0102M11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
AZ654733 1M0529A09 AZ654842 1M0529A09 AZ65764 1M0523P18 AZ764500 1M0560X06 AZ76450 1M0560X06 AZ76450 1M0560X09 AZ76454 2M0031M24 AZ798034 2M0049B08 AZ798894 2M0057C12	~~~~~~~~	N _		764788976680 11111111111		AZ764527 IMOS60K15 AZ764527 IMOS60K15 AZ767090 IMOS66K06 AZ782111 2M0022M0S	linear GSS 21-FEB-2001  prary Mus musculus genomic equence.
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A2359724 35 bp DNA linear GSS 02-OCT-2000 1M0102M11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0102M11 R, genomic survey sequence.
AZ359724 GI:10473424 GSSS.

ACCESSION VERSION KEYWORDS

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200 bp DNA linear GSS 21-FEB-2001
200177120R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCZM0177120 R, genomic survey sequence.
AZ867169
AZ867169.1 GI:13069207
GSS.
Mus musculus (house mouse)

ACCESSION VERSION KEYWORDS SOURCE

Euteleostomi;

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SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAP42 (gil-4732114[gb]AF129072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0271G04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0271G04 R, genomic survey sequence.
AZ462959
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84112, USA
                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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Fax: 801 585 7177
Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0225 row: G column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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                                 Mus musculus (house mouse)
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/lab host="E.
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/clone_lib="Wouse 10kb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated more state of the polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil |4732114| gb| AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0225G02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0225G02 R, genomic survey sequence.
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Plate: 0102 row: M column: 11
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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musculus (house mouse)
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Fax: 801 585 7177
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                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokee, R., Tingey, A., von Niederhausern, A. and Wright, D., Welse, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Pred. No. 4.3e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0271 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Organism="Mus musculus"
mol type="genomic DNA"
'strain="C57BL/6J"
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clone="UUGC1M0271G04"
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94.7%; Pred
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                                    Mus musculus (house mouse)
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AZ462959.1 GI:10621084
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Fax: 801 585 7177
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2M0244G20R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Tel: 801 S85 5606
Fax: 801 S85 7177
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/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
                                                                                                                                                      Appabes 1 to 28)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Mese, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: 17
Class: foomid ends.
                                                     Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                    Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 3-79, Tuebingen D-72076, Germany
Fax: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pacificus"
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llarity 94.7%; Pred. No. 4.3e+04;
Conservative 0; Mismatches 1;

    .28
    /organism="Pristionchus

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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="California"
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CL661180.1 GI:50147339
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gilfa732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plank Mol. Biol. 53 (1-2), 247-259 (2003)
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Arabidopsis thaliana T-DNA flanking sequence GK-400Al2-017894,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA f.
musculus C57BL/6J (male) was obtained from th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 33;
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94.7%; Pred. No. 4.3e+04;
tive 0; Mismatches 1;
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                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Arabidopsis thaliana
                                                                                 Plate: 0061 row: L column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                              /clone="UUGC2M0061L09"
                                                                                                                                                                     High quality sequence stop: 33.
                                                                                                                                                                                               Location/Qualifiers
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BX004665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gil4732114|gp|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                     /lab_nost="E. coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCZM library"
/note="Vector: PWD42Nv; Purified genomic DNA from M.
musculus CSTBL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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2M0061L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0061L09 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 184112, USA
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                                  Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0244 row: G column: 20
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                           Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             'db_xref="taxon:10090"
'clone="UUGC2M0244G20"
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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AZ375586/c
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                                                                                                                                                                                                                                                                          Direct Summission.

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1.3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants (TI) which were transformed with the T-DNA from vector pAC111 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
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2M0093L16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0093L16 F, genomic survey sequence.
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="GK-400A12-017894"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
ecotype="Col-0"
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                      Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A.
                                                                                               High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                         4 (bases 1 to 38)
Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
Direct Submission
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:3702"
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AZ820833.1 GI:12990741
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Best Local Similarity 94.7<sup>3</sup>
Matches 18, Conservative
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(http://www.jax.org/resourced (http://www.jax.org/resourced documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""dector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/64 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 4.3e+04;
0; Mismatches 1; Indels
                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0093 row: L column: 16
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
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/clone="UUGC2M0093L16"
                                                                                                                                                                                                                                                             High quality sequence stop: 43.
Location/Qualifiers
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GSS.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Rm. 308,
84112, US
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AZ800436
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                                                                                            FEATURES
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Antirrhinum majus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudictyledons;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone l1b="Mouse 10kb plasmid UUGCN library"
/note="Vector: PWD4ZLN; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: G column: 03
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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2M0058L20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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/clone lib="Mouse 10kb plasmid UGGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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87.0%; Score 17.4; DB 1; Length 47;
Best Local Similarity 94.7%; Pred. No. 4.3e+04;
Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                             /clone="018 3 02 ki8"
/tissue type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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                                                                                                                                      /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
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Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0058L20"
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Insert Length: 10000 Std Brro
Plate: 0058 row: L column: 20
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Fax: 801 585 7177
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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors at purified. The sheared, adaptored mouse DNA was annealed to
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2M0017N06R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0017N06 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                   adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: N column: 06
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    .25
    /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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clone="UUGC2M0017N06"
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Fax: 801 585 7177
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TITLE

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Direct Submission

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Direct Submission

Succhtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

Details on the protocols used for generation of the sequence are
described in References 1-3. Re-examination of the source from
which this sequence has been produced indicates that the sequence
is of low reliability. Therefore, no information on a potential
insertion site is deduced. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL935924 30 bp DNA linear GSS 31-MAR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-009H02-016930,
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.0%; Score 16.8; DB 9; Length 25; 90.0%; Pred. No. 6.8e+04; ive 0; Mismatches 2; Indels
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0203B05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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1 (basea 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rellay, M., Rose, M., Rose, R., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Insert Length: 10000 Std Error: 0.0
Plate: 0203 row: B column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC1M0203B05"
/sex="Male"
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                   /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequence to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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1M0525K06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Relly, M., Rose, M., Rose, M., Menen, B., Pedersen, T., Relly, M., Rose, M., Rose, M., Mesen, B., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
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                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
     http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunmegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0525 row: K column: 06
Seq primer: CACACAGGAAAACAGCTAATGACC
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/db xref="taxon:10090"
/clone="UUGC1M0525K06"
                                                                                                                                                                          /clone="GK-009H02-016930"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 33.
Location/Qualifiers
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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Insert Length: 10000 Std Error: 0.00
Sta Error: 0.00
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Class: plasmid ends
High quality sequence stop: 43.

    .43
    /organism="Mus musculus"

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Fax: 801 585 7177
Email: ddunn@genet
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Best Local Similarity
Matches 18; Conserv
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA DOLYMERSES and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 39)
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: J column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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strain="C57BL/6J"
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/sex="Male"
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Location/Qualifiers
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Fax: 801 585 7177
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gl/4732114/gl/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jac.ory/resources/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journalistations/journali
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Sciurognathi; Muroidaa; Murinae; Mus:

(Dases 1 to 43)

Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           46 bp
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/db_xref="taxon:9606"
/clone="IMAGE:2227617"
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                                                                                                                                                                                82.0%;
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                                                                                                                                                                 Query Match
Best Local Similarity 94.4%
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AI597960
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AUTHORS
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                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gqi 4722114|gbh AF12972.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clond distribution: NCI-GGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
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1 (Dases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
         /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Ov23"
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clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.0%; Score 16.8; DB 9; Length 43; 90.0%; Pred. No. 6.7e+04; ive 0; Mismatches 2; Indels
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Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity 90.0
Matches 18; Conservative
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ts04f05.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2227617 3' similar to SW:PRPB HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ; contains TAR1.t2 MSR1 repetitive element ;, mRNA sequence.
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Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (Dassa 1 to 400)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 9e+04;
0; Mismatches 1; Indels
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_pan1"
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Query Match
Best Local Similarity
Matches 17; Conserv
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                     AZ447248 19 bp DNA linear GSS 04-OCT-2000 1M0244H23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244H23 F, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                              1 (bages 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts.
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.larity 89.5%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 2; Indels
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Fax: 801 585 7177
Email: ddunn@qenetics.utah.edu
Inmert Length: 10000 Std Error: 0.00
Plate: 0244 row: H column: 23
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
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/strain="C57BL/6J"
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clone="UUGC1M0244H23"
                                                                                                                                                                                  Mus musculus (house mouse)
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AZ447248.1 GI:10599044
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Matches 17; Conserv
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfa732114 [gpl AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
AZ512326 20 bp DNA linear GSS 05-OCT-2000 1M0357118R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0357118 R, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Pred. No. 1.4e+05;
0; Mismatches 2;
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Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
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Class: plasmid ends
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/strain="C57BL/63"
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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89.5%;
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gill4]pplAR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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E (bases) 1 to 20)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tungey,A., von Contact: Robert B. Weiss

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                  GSS 14-DEC-2000
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                                                            AZ645269
1M0510B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0510B10 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UUGCM library"
/note="Vector: PWD4ZLY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0510 row: B column: 10
Seq primer: CACACAGGAAACAGCTAATGACC
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Location/Qualifiers
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RESULT 23
AZ645269/c
                                                                                                DEFINITION
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KEYWORDS
SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gp|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
                                                      AZ772707

1M0583L18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0583L18 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (Sease 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                AZ772707.1 GI:12896303
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                            Mus musculus
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RESULT 24
AZ772707/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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79.0%; Score 15.8; DB 9; Length 20; 89.5%; Pred. No. 1.46+05; ive 0; Mismatches 2; Indels

Query Match Best Local Similarity 89.5 Matches 17; Conservative

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AZ653464 linear GSS 14-DEC-2000 IMO527G11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0527G11 F, genomic survey sequence.
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Location/Qualifiers
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        2 GGGGAGGGAGGGAGGGG 20
                                                    20 GGGGAGGGGGGGGGG 2
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                                                                                                                                                          AZSB3408 13-DEC-200 21 bp DNA linear GSS 13-DEC-200 IM0378N23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0378N23 F, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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musculus C57BL/6J (male) was obtained from the Jackson
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Unpublished (2000)
Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah
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High quality sequence stop: 21.
Location/Qualifiers
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/clone="UUGC1M0378N23"
                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
20 GGGGGGGAGGGGGGGG 2
                                                                                                                                                                                                                                                                      AZ583408.1 GI:11703261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 21)
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                              RESULT 25
AZ583408/c
                                                                                                                                                                                        DEFINITION
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KEYWORDS
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse lokb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was bylordynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated for sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polymuclectide kinase. Adaptor oligomuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoresis. Vector DNA was prepared from a derivative
of pMDA2 (gil 4]4712114[9]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XIL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                               Euteleostomi;
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84112, USA
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1 Loades It of 21)
1 Loades It of 21)
1 Loader It of 21, Barber, M., Beacorn, T., Duval, B., Hamil, C.,
1 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Flate: 0527 row: G column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Best Local Similarity 89.5
Matches 17; Conservative
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Gaps

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Indels

5;

Mismatches

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17; Conservative
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AUTHORS
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COMMENT
  Matches
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/clone_lib="Wouse 10kb plasmid UUGCIM library"
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/note=="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt enderepaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                  GSS 21-FEB-2001
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                                                                                                                                                                                                               AZ871715
2M0184B13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0184B13 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Beal, T., Logagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Belan, T., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact Robert B. Weiss
University of Utah Genome Center
University of Utah
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Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: B column: 13
Seg primer: CACACAGGAAACAGCTATGACC

    .21
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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High quality sequence stop: 21.
Location/Qualifiers
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/clone="UUGC2M0184B13"
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                              2 GGGGAGGGAGGGAGGGG 20
                                                                                21 ĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÚSA
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AZ871715/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                            VERSION
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Score 15.8; DB 9; Length 21; Pred. No. 1.4e+05;

79.0%; 89.5%;

Query Match Best Local Similarity

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Disamid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                     AZ311988 29-SEP-2000
1M0060B11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0060B11 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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/clone llb="Mouse 10kb plasmid UUGCNH library"
/noce="Vector: PWD4Znr, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciurognathi, Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 22)
Dunn, D., Agogai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euto
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: B column: 11
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
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/sex="Male"
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Location/Qualifiers
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2 GGGGAGGGGAGGGG 20
                                                                 21 ddddddddddddddddd 3
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Tel: 801 585 5606
Fax: 801 585 7177
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Length 22;

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79.0%;
larity 89.5%;
Conservative 0
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  Query Match
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Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                     GSS.
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Whiversity of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                       AZ447246 2S 04-OCT-2000 1MO244E23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244E23 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone_lib="Mouse_lokb plasmid UTGCIM library." /note="Vector: PWD42nv; Purified genomic DNA from M.musculus G57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokee, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                               Gaps
                             ;
                             Indels
  89.5%; Pred. No. 1.4e+05;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: E column: 23
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                     1 GGGGGGGAGGGGGGG 19
                                                                               2 GGGGAGGGGAGGGG 20
                                                                                                                                                                                                                                                                                                                                                               AZ447246.1 GI:10599040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "sex="Male"
     Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 22)
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ORIGIN

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muscular C.7 Mouse DNA Resource
[aboratory Mouse DNA Resource
[thttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114 gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Whiversity of Utah
84112, USA
                                                                                                                                                                                                                                                                                                                                                                       AZ607348 22 bp DNA linear GSS 13-DEC-2000 1M0429D18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0429D18 R, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognachi; Muroidea; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                       Gaps
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                                                                       Indels
Score 15.8; DB 9;
Pred. No. 1.4e+05;
0; Mismatches 2;
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                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC1M0429D18"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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                                                                           17; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                          Query Match
Best Local Similarity
Matches 17; Conserv
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84112, US
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AZ488138/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                  AZ645874 22 bp DNA linear GSS 14-DEC-2000 1M0511C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0511C07 R, genomic survey sequence.
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1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Really, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unstand innerts

Unpublished (2000)
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                                                     Gaps
                                                        ö
Query Match 79.0%; Score 15.8; DB 9; Length 22; Best Local Similarity 89.5%; Pred. No. 1.4e+05; Matches 17; Conservative 0; Mismatches 2; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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'strain="C57BL/6J"
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/clone="UUGC1M0511C07"
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                                                                                                        2 GGGGAGGGGAGGGGG 20
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AZ645874.1 GI:11775791
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Fax: 801 585 7177
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AZ645874/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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Sciurognathi, Murcidea, Muridae, Murinae, Mus.

I (bases I to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Score 15.8; DB 9; Length 22; Pred. No. 1.4e+05;
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Insert Length: 10000 Std Brror: 0
Plate: 0318 row: E column: 13
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                              2 GGGGAGGGAGGGGG 20
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Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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AZ800632/c
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1M0369N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369N11 R, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                          Length 23;
                                                                                                                        Indels
and selected for ampicillin resistance."
                                                                     Score 15.8; DB 9; 1
Pred. No. 1.4e+05;
0; Mismatches 2;
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Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: N column: 11
Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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High quality sequence stop: 23.
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                                                                       Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
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Fax: 801 585 7177
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AZ581259/c
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Laboratory Mouse DNA Resources documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifica at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. We cor DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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2M0058E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0058E17 R, genomic survey sequence.
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                 Length 23
                                                                                                                                                                                                        2; Indels
                                                                                                                                     Score 15.8; DB 9;
Pred. No. 1.4e+05;
0; Mismatches 2;
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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                                                                                                                                        79.0%;
89.5%;
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Query Match
Best Local Similarity
Matches 17; Conserv
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AZ640795/C
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-eelected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis Vector DNA was prepared from a derivative
of pWNA2 (gil #772114|gb]AFL29072.1); a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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Winpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0172P09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0172P09 R, genomic survey sequence.
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                                                                                                                     Length 23;
                                                                                                                     Score 15.8; DB 9; Length 2
Pred. No. 1.4e+05;
); Mismatches 2; Indels
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: P column: 09
Seq primer: CACAGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
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/db_xref="taxon:10090"
/clone="UUGC1M0172P09"
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                                                                                                                                              1 Similarity
17; Conserva
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84112, USA
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(http://www.jaxe.pur.cog/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a lo.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|472114|ja) Aut.2010/1), a copy-number inducible derivative of plasmid R1. The vector was ligated
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clome_lib="Mouse_lokb_plasmid_UGCIN library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Insert Length: 10000 Std Error: 0.00
Plate: 0503 row: D column: 04
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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Unpublished (2000)
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Fax: 801 585 7177
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Laboratory Mouse Number, was obtained thoust the decreasing the parameters of the propure the parameters of the paramete
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                79.0%; Score 15.8; DB 9; Length 24; 89.5%; Pred. No. 1.4e+05; ive 0; Mismatches 2; Indels
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84112, USA
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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'strain="C57BL/6J"
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Location/Qualifiers
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clone="UUGC2M0036A15"
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Mus musculus
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunner
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Metacaa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metacaa, Chordata, Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.

(Dases 1 to 24)
Dunn, D., Aoyagi, M., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Miderhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.4e+05;
0; Mismatches 2;
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Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: F column: 17
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0098F17"
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89.5%;
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Fax: 801 585 7177
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/clone_lib="Mouse lokb plasmid UUGCIM library"
/clone="Weator: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Ri. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
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S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Railly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dusse whole genome scaffolding with paired end reads from 10kb plasmid inserts
L Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, U
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                             Score 15.8; DB 9; Length 24;
Pred. No. 1.4e+05;
0; Mismatches 2; Indels
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Fax: 801 585 7177
Eax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: D column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db zref="taxon:10090"
/clone="UUGCIM0281D10"
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Mus musculus
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Best Local &
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0421F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic CODE UUGC1M0421F16 F, genomic survey sequence.
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                               Score 15.8; DB 9;
Pred. No. 1.4e+05;
0; Mismatches 2;
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Insert Length: 10000 Std Error: 0.00
Plate: 0421 row: F column: 16
Seq primer: cGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0421F16"
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ilarity 89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 17; Conserv
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84112, US
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/lab host="E. coll DH108"
/lab host="E. coll DH108"
/clone lib="WAP1"
/clone lib="WAP1"
/note="Vector: pT773D-Pac (Pharmacia); Site_1: NotI;
/note="Vector: pT773D-Pac (Pharmacia); Site_1: NotI;
Site_2: EcoRI; ESTS sequenced from the T7 prining site
that_reads from the 5' end of cDNA. The NAP1 is a
directionally cloned and normalized, oligo-T prinad cDNA
library constructed from a mixture of Anopheles gambiae
developmental stages according to: Bonaldo, Lennon &
Soarse (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery, Genome Research
6, 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ307654 1inear GSS 29-SEP-2000 1M0009F22R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0009F22 R, genomic survey sequence.
  BX626114 BYP1 Anopheles gambiae cDNA clone ANGNP1181G08T7, mRNA
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Enkaryota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.

1 (Seases 1 to 26)

Lobo, N.L., Gardner, M., Romans, P. and Collins, F.H.

Anopheles gambiae EST, Center for Tropical Disease Research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                       Training
Unpublished (2003)
Unpublished (2003)
Contact: Frank H. Collins
Contact: Frank H. Collins
Contact: Frank H. Collins
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-9245
Fax: 574-631-9246
Email: frank h.collins.75@nd.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%; Score 15.8; DB 5; Length 26; 89.5%; Pred. No. 1.46+05; tive 0; Mismatches 2; Indels
                                                                                                                                                                  Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .26
/organism="Anopheles gambiae"
/mol type="mRNA"
/db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="ANGNP1181G08T7"
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Contact: Robert B. Weiss
                                                                                                               BX626114.1 GI:33552251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ307654.1 GI:10346867
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Matches 1
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AZ307654/c
LOCUS
                               DEFINITION
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD4 (gi|4732114] pd|AF129072.11), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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T. brucei Bheared genomic DNA clone 33e11, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma.
1 (bases 1 to 25)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M. A. and Barrell, B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                      Query Match
Post Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5691"
/clone="33e11"
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AL453376.1 GI:11854702
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RESULT 41 TA33E11P/c DEFINITION

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ORIGIN

ORGANISM

TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

AUTHORS REFERENCE

ACCESSION VERSION

KEYWORDS

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Gaps

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COMMENT

RESULT 42 BX626114

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Conservative
                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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          COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of puble [4732114]gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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mamalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                                                                                                                                                        Std Error: 0.00
                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Fax: 801 585 7177
Fax: 800 587 7177
Fax: 800 Fax: 800 584 Error: 0.0
Flate: 0009 Fax: F column: 22
Seq primer: CACACAGGAAACAGCTATCACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0009F22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Male"
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Best Local Similarity
Matches 17; Conserv
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gilfa732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F."
/lab host="Bell strain XL10-Gold, T1-resistant, F."
/clone lib="Mouse 10kb plasmid UUGCIM library"
/none="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource And The DNA Laboratory Mouse DNA Resource And The DNA Resource DNA Resource And The DNA Resource DNA Resource The DNA Resource 
                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0244020"
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Location/Qualifiers
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Mus musculus (house mouse)
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plasmid inserts
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/clone_lib="Mouse lokb plasmid UUGCIM library"
/clone_lib="Wouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources /documents/dnares/). The DNA
was bydrodynamically sheared by repeated epasage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated excess and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 S85 5606
Exar: 801 S85 7177
Email: ddunn@genetics.utah.edu
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Yese, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 02
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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clone="UUGC2M0076C02"
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  Unpublished (2000)
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Scilrognathi; Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=TVector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                           S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 318, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                  Plate: 0168 row: K column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db xref="taxon:10090"
/clone="UUGC2M0168K19"
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Laboratory microse was Assources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose golelectrophoresis. Vector DNA was prepared from a derivative of pwale (4732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0.001d (Stratagene) cells and selected for ampicillin resistance."
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Niederhausern, A. and Wright, D., Weiss, R.

Wouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insext Length: 10000 Std Error: 0.00
Plate: 0519 row: P column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:10090"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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Best Local Similarity 89.5
Matches 17; Conservative
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84112, USA
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AZ327022
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end arcepaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0519P18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0519P18 R, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalla; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
                                  whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Faxil: ddunn@genetics.utah.edu
Insert Length: 10000 §td Error: 0.00
                                                                                                                                                                                                                                                                                                                                                         Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .27
organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                      Plate: 0425 row: I column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
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Best Local Similarity 89.5'
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AZ649949/c
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 28)
                                                plasmid inserts
Unpublished (2000)
Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah
University of Utah
University of Utah
University of Utah
USA
84112, USA
1177
Email: ddunn@genetics.utah.edu
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                 ddunn@genetics.utah.edu
Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                Plate: 0050 row: I column: 12
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                    mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                                                                                   High quality sequence stop: 28.
Location/Qualifiers
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clone="UUGC1M0050112"
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Matches 17; Conservative
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/lab hose="B. Coli strain XL10-Gold, T1-resistant, F."
/clone_lib="Mouse lokb plasmid UUGCIM library"
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/note="Weetor: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Sequence 1, Sequence 9, Sequence 67, Sequence 67,	Sequence 321 Sequence 675	Sequence 533	Sequence 2,	Sequence 7,	Sequence 21, Sequence 67,	Sequence 14,	Seguence 3,	Sequence 36,	Sequence 36,	Sequence 673	Sequence 12,	Sequence 300	Sequence 3,	Sequence 2,	Sequence 32	Sequence 42,	Sequence 43,	Sequence 24	Sequence 43,	Sequence 42,	Sequence 43,	Sequence 3,	Sequence 43	Sequence 42,	Sequence 43,	Sequence 43,	Sequence 24,	Sequence 3,	Sequence 42	Sequence 43	Sequence 11	Sequence 3,	Sequence 1.	Sequence 3,	Sequence 4,	Sequence 3,	Sequence 3,	Sequence 4,	Sequence 22	Patent No. 5	Sequence 48	Sequence 48	Sequence 18	Sequence 18	Sequence 12	Seguence 13				
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US-08-872-446-9 Sequence 9, US-09-280-270A-9 Sequence 9, US-09-281-638-679 Sequence 675 US-09-422-978-285 Sequence 28	3 US-09-422-978-3218 Sequence 321 3 US-10-170-097-679 Sequence 679	3 US-10-131-827-5327 Sequence 53	2 US-08-872-446-2 Sequence 2,	3 US-08-729-598-7 Sequence 7,	3 US-09-894-799-21 Sequence 21, 3 US-09-863-049B-67	2 US-08-802-547-14 Sequence 14	3 US-U9-6/9-9/I-3 3 US-08-931-220-36 Semience 36	6 PCT-US95-11723-36 Sequence 36,	6 PCT-US96-05997-36 Sequence 36,	3 US-09-671-317-679 Sequence 673 2 US-08-872-446-12 Sequence 12	3 US-09-280-270A-12 Sequence 12,	3 US-10-131-827-3003 Sequence 300	3 US-10-130-792A-3 Sequence 3,	2 US-07-743-245-2 Sequence 2,	3 US-10-131-827-1882 Sequence 186	2 US-08-145-704-42 Sequence 42,	2 US-08-145-704-43 Sequence 43,	2 US-US-358-556A-24 Sequence 24,	3 US-08-987-574-43 Sequence 43,	3 US-08-535-168-42 Sequence 42,	3 US-08-535-168-43 Sequence 43,	3 US-09-43/-0/6-3 Sequence 3, 3 US-09-017-974-42 Sequence 42,	3 US-09-017-974-43 Sequence 43	3 US-08-682-255A-42 Sequence 42,	3 US-08-682-255A-43 Sequence 43, 3 US-09-429-130-42 Sequence 42,	3 US-09-429-130-43 Sequence 43,	3 US-10-352-704-24 Sequence 24,	3 US-04-704-744-3 Seguence 3, 3 US-04-097-7910-4	6 PCT-US96-11786-42 Sequence 42	6 PCT-US96-11786-43 Sequence 43,	3 US-09-230-652-117 Sequence 11'	2 US-08-424-663-3 Sequence 3,	2 US-08-424-663-4 2 US-08-424-663-5 Sequence 5.	2 US-08-872-446-3 Sequence 3,	2 US-08-872-446-4 Sequence 4,	2 03-06-6/2-446-3 Sequence 3,	3 US-09-280-270A-3 Sequence 3,	3 US-09-280-270A-4 Sequence 4,	3 US-09-280-270A-5 Sequence 5,	9 5245022-8 Patent No. 5	2 US-08-068-945A-48 Sequence 48	2 US-08-442-806-48 Sequence 48	2 US-08-145-704-18 Sequence 18	3 US-08-987-574-18 Sequence 18	3 US-08-535-168-18 Sequence 18	3 US-09-017-974-18 Sequence 18	3 US-08-682-255A-18 Sequence 18	5 US-03-423-130-18 Sequence 18 6 PCT-US96-11786-18 Sequence 18	3 US-08-976-427-12 Sequence 12	3 US-08-976-427-13 Sequence 13
9.0 45 2 US-08-872-446-9 Sequence 9, 9.0 45 3 US-09-280-270A-9 Sequence 679, 9.0 47 3 US-09-422-978-285 Sequence 678	9.0 47 3 US-10-170-097-679 Sequence 32: 9.0 47 3 US-10-170-097-679 Sequence 67:	9.0 50 3 US-10-131-827-5327 Sequence 53.	8.0 21 2 US-08-872-446-2 Sequence 2,	8.0 24 3 US-08-729-598-7 Sequence 7,	8.0 24 3 US-09-894-799-21 Sequence 21, 8.0 25 3 US-09-863-049B-67 Sequence 67,	8.0 30 2 US-08-802-547-14 Sequence 14	8.0 39 3 US-09-6/9-9/1-3 Sequence 3, 8.0 45 3 US-08-931-220-36 Sequence 36,	8.0 45 6 PCT-US95-11723-36 Sequence 36,	8.0 45 6 PCT-US96-05997-36 Sequence 36,	8.0 47 3 US-09-671-317-679 Sequence 673 8.0 48 2 HS-08-872-446-12 Sequence 12,	8.0 48 3 US-09-280-270A-12 Sequence 12,	8.0 50 3 US-10-131-827-3003 Sequence 300	7.0 22 3 US-10-130-792A-3 Sequence 3,	7.0 34 2 US-07-743-245-2 Sequence 2,	7.0 50 3 US-10-131-827-1882 Sequence 188	6.0 18 2 US-08-145-704-42 Sequence 42,	6.0 18 2 US-08-145-704-43 Sequence 43,	6.0 I8 2 US-US-358-358-54 Sequence 24,	6.0 18 3 US-08-987-574-43 Sequence 43,	6.0 18 3 US-08-535-168-42 Sequence 42,	6.0 18 3 US-08-535-168-43 Sequence 43,	6.0 18 3 US-09-43/-0/8-3 Sequence 3, 6.0 18 3 US-09-017-974-42 Sequence 42,	6.0 18 3 US-09-017-974-43 Sequence 43	6.0 18 3 US-08-682-255A-42 Sequence 42,	6.0 18 3 US-08-682-255A-43 Sequence 43, 6.0 18 3 US-09-429-130-42 Sequence 42,	6.0 18 3 US-09-429-130-43 Sequence 43	6.0 18 3 US-10-352-704-24 Sequence 24	6.0 IS 3 US-US-804-/44-3 Sequence 5, 6.0 IS 3 US-09-097-791D-4 Semience 4.	6.0 18 6 PCT-US96-11786-42 Sequence 42	6.0 18 6 PCT-US96-11786-43 Sequence 43,	6.0 19 3 US-09-230-652-117 Sequence 11'	6.0 21 2 US-08-424-663-3 Sequence 3,	6.0 ZI Z US-08-424-663-4 Sequence 4,	6.0 21 2 US-08-872-446-3 Sequence 3,	6.0 21 2 US-08-872-446-4 Sequence 4,	6.0 Z1 Z US-06-8/Z-446-3 Sequence 3,	6.0 21 3 US-09-280-270A-3 Sequence 3,	6.0 21 3 US-09-280-270A-4 Sequence 4,	6.0 24 3 US-09-280-2/0A-5 Sequence 2,	6.0 24 9 5245022-8 Patent No. 5	6.0 25 2 US-08-068-945A-48 Sequence 48	6.0 25 2 US-08-442-806-48 Sequence 48	6.0 26 2 US-08-145-704-18 Sequence 18	6.0 26 3 US-08-987-574-18 Sequence 18	6.0 26 3 US-08-535-168-18 Sequence 18	6.0 26 3 US-09-017-974-18 Sequence 18	6.0 26 3 US-08-682-255A-18 Sequence 18	6.0 26 6 PCT-US96-11786-18 Sequence 18	6.0 30 3 US-08-976-427-12 Sequence 12	6.0 30 3 US-08-976-427-13 Sequence 13
2 US-08-872-476-9 Sequence 9, 3 US-09-280-270A-9 Sequence 9, 3 US-09-441-638-679 Sequence 678 Sequence 678 Sequence 288 Sequence 288	3.8 69.0 47 3 US-09-422-978-3118 Sequence 32.3.8 69.0 47 3 US-10-170-097-679 Sequence 673	3.8 69.0 50 3 US-10-131-827-5327 Sequence 53.	3.6 68.0 21 2 US-08-872-446-2 Sequence 2,	3.6 68.0 24 3 US-08-729-598-7 Sequence 7,	3.6 68.0 24 3 US-09-894-799-21 Sequence 21, 3.6 68.0 25 3 US-09-863-049B-67 Sequence 67,	3.6 68.0 30 2 US-08-802-547-14 Sequence 14	3.6 68.0 39 3 US-U9-679-971-3 Sequence 3,	3.6 68.0 45 6 PCT-US95-11723-36 Sequence 36	3.6 68.0 45 6 PCT-US96-05997-36 Sequence 36,	3.6 68.0 47 3 US-09-671-317-679 Sequence 673 3.6 68.0 48.2 US-08-872-446-12 Sequence 12.	.6 68.0 48 3 US-09-280-270A-12 Sequence 12,	3.6 68.0 50 3 US-10-131-827-3003 Sequence 300	3.4 67.0 22 3 US-10-130-792A-3 Sequence 3,	3.4 67.0 34 2 US-07-743-245-2 Sequence 2,	3.4 67.0 50 3 US-131-827-1882 Sequence 188	3.2 66.0 18 2 US-08-145-704-42 Sequence 42,	3.2 66.0 18 2 US-08-145-704-43 Sequence 43,	3.2 66.0 IS 2 US-US-338-336A-24 Sequence 24,	3.2 66.0 18 3 US-08-987-574-43 Sequence 43,	3.2 66.0 18 3 US-08-535-168-42 Sequence 42	3.2 66.0 18 3 US-08-535-168-43 Sequence 43,	3.2 66.0 18 3 US-09-43/-0/6-3 Sequence 3,	3.2 66.0 18 3 US-09-017-974-43 Sequence 43	3.2 66.0 18 3 US-08-682-255A-42 Sequence 42,	3.2 66.0 18 3 US-08-682-255A-43 sequence 43.	3.2 66.0 18 3 US-09-429-130-43 Sequence 43.	3.2 66.0 18 3 US-10-352-704-24 Sequence 24.	3.2 66.0 18 3 08-08-804-/44-3 sequence 3,	.2 66.0 18 6 PCT-US96-11786-42 Sequence 42	3.2 66.0 18 6 PCT-US96-11786-43 Sequence 43.	3.2 66.0 19 3 US-09-230-652-117 Sequence 11	3.2 66.0 21 2 US-08-424-663-3 Sequence 3,	3.2 66.0 ZI Z US-US-4Z4-663-4 Sequence 4, 3.2 66.0 21 2 HS-08-424-663-5 Sequence 5.	3.2 66.0 21 2 US-08-872-446-3 Sequence 3,	3.2 66.0 21 2 US-08-872-446-4 Sequence 4,	3.2 66.0 21 2 03-06-8/2-446-3 Sequence 3,	3.2 66.0 21 3 US-09-280-270A-3 Sequence 3,	3.2 66.0 21 3 US-09-280-270A-4 Sequence 4,	.2 66.0 24 3 US-09-280-270A-5 sequence 5, 2 66.0 24 3 US-09-894-799-22 Sequence 22	3.2 66.0 24 9 5245022-8 Patent No. 5	3.2 66.0 25 2 US-08-068-945A-48 Sequence 48	3.2 66.0 25 2 US-08-442-806-48 Sequence 48	3.2 66.0 26 2 US-08-145-704-18 Sequence 18	3.2 66.0 26 3 US-08-987-574-18 Sequence 18	3.2 66.0 26 3 US-08-535-168-18 Sequence 18	3.2 66.0 26 3 US-09-017-974-18 Sequence 18	3.2 66.0 26 3 US-08-682-255A-18 Sequence 18	3.2 66.0 26 6 PCT-US96-11786-18 Sequence 18	3.2 66.0 30 3 US-08-976-427-12 Sequence 12	3.2 66.0 30 3 US-08-976-427-13 Sequence 13

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Gnith, Louis C.

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

COUNTRY: Los Angeles

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 87.0%; Score 17.4; DB 2; al Similarity 94.7%; Pred. No. 4.3e+02; 18; Conservative 0; Mismatches 1;
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PG7/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: PC7/US93/02725
FILING DATE: March 20, 1992
APPLICATION NUMBER: PC7/US93/02725
FILING DATE: March 20, 1993
APPLICATION NUMBER: PC7/US93/02725
FILING DATE: March 20, 1993
APPLICATION NUMBER: PC7/US93/02725
FILING DATE: March 30, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION
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MOLECULE TYPE: Other nucleic acid
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US-08-460-890A-15
Sequence 15, Application US/08460890A
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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Sequence 10, Appl
Sequence 25, Appl
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US-08460-890A-14/c
Squence 14, Application US/08460890A
Fatent No. 5994109
GENERAL INFORMATION:
APPLICANT: WOO, Savio L.C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gristiano, Richard J.
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                   US-09-052-955-7

US-09-199-507B-48

US-07-941-131C-44

US-07-314-131C-44

US-08-412-110-44

US-08-412-110-44

US-08-412-110-44

US-08-143-190-44

US-08-143-190-44

US-08-123-936-44

US-08-123-936-44

US-08-123-936-59

US-08-123-936-59

US-08-123-936-59

US-08-123-936-59

US-08-123-936-59

US-08-123-93-78-59

US-09-993-346-59

US-09-993-346-59
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US-09-400-046-10
US-09-400-0558-25
US-08-424-663-8
US-08-109-663-22
US-09-109-663-22
US-09-400-046-8
US-09-400-046-8
                                                                                                                             PCT-US92-09202-10
PCT-US93-07743-1
PCT-US93-07743-15
PCT-US93-07743-15
PCT-US93-08329-11
PCT-US96-11786-1
                                                 US-08-682-255A-1
US-08-682-255A-2
US-09-429-130-1
US-09-429-130-2
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Sequence 15, Application US/08167641C

GENERAL INFORMATIONS SHEAF

APPLICANT: Woo, Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Smith, Louis C.

APPLICANT: Gritchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCES: 65

CORRESPONDENCES: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 87.0%; Score 17.4; DB 3; Length 27; Best Local Similarity 94.7%; Pred. No. 4.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: "C" stands for 5-methylcytosine US-08-167-641C-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FERSENG CON WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIPICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INPORMATION:
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 205/012
TELECOMMUNICATION INFORMATION:
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
FEATURE:
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                                                                                                                                                                                                                                                                                                                                             TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTER.STICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-167-641C-15
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WS-08-167-641C-14/C

Sequence 14, Application US/08167641C

Patent No. 6033804

GRNERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Cristiano, Richard J.

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: ACHORS. 65

CORRESPONDENCE ADDRESS:

ADDRESSE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STREET: Suite 4700

CITY: Los Angeles

STATE: Galifornia

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: STORAGE

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

CURRENT APPLICATION DATR:

APPLICATION NUMBER: US/08/167,641C

FILING DATE: December 14, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.0%; Score 17.4; DB 2; Length 27; Best Local Similarity 94.7%; Pred. No. 4.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOSTWARE: FRAEKSQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 212/066
TELECOMMUTICATION NUMBER: 212/066
TELECOMMUTICATION NUMBER: 212/066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-08-460-890A-15
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                                                                                                               Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Srith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                  Indels
                                             "C" stands for 5-methylcytosine
                                                                                                             Query Match

87.0%; Score 17.4; DB 3;

Best Local Similarity 94.7%; Pred: No. 4.3e+02;

Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastENG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WARDLY RICHARD J.
REGISTRATION NUMBER: 32,32,2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
  MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08460971A Patent No. 6150168 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Sulte 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                  1 AGGGAGGGGAGGGA19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGGGGAGGGAGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 555-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.73
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                      FEATURE:
COTHER INFORMATION:
US-08-460-971A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                   US-08-460-971A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-460-971A-15
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US-08-460-971A-14/C
IS-08-460-971A-14/C
Sequence 14, Application US/08460971A
Patent No. 6150168

JAPLICANT: Woo, Savio L.C.
APPLICANT: Criticano, Richard J.
APPLICANT: Saith, Louis C.
CORRESPONDENCE ADDRESS: 65
CORRESPONDENCE ADDRESS: 65
CORRESPONDENCE ADDRESS: 65
CORRESPONDENCE ADDRESS: 65
CONTRY: LOS ARGESS
STREET: Suite 4700
CITY: LOS ARGESS
CONTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 31 Work at Compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: 31 Congatible
COMPUTER TRADABLE FORM:
MEDIUM TYPE: 31 Congatible
COMPUTER: MIN Compatible
COMPUTER: MIN Compatible
COMPUTER: MIN Compatible
COMPUTER: ALING OFFICE J. 1995
CLASSIFICATION NUMBER: US/08/460,971A
FILING DATE: Date: 07/855,389
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INDORMATION:
MAPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INDORMATION:
MARE: Watch 19, 1993
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                                                                                                                                                                                                                                                                                                                87.0%; Score 17.4; DB 3; Length 27; 94.7%; Pred. No. 4.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AAGGGAGGGAGGGGGG 22
                      | TELEPHONE: (213) 489-1600
| TELEX: (7-213) 955-0440
| TELEX: (7-3510
| TELEX: (7-3510
| TELEX: (7-3510
| SEQUENCE CHARACTERISTICS:
| LENGTH: 27 base pairs
| TYPE: nucleic acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: CDNA
| US-08-167-641C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELER: (7-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 Date pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.77
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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TOPOLOGY: 1:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-462-040-15
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                                                                                                                                               Sequence 14, Apt.
Sequence 16, Apt.
Sequence 16, Apt.
Septicant Series 16, Septen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: NETFOOS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
STREET: 633 Mest Fifth Street
STREET: 634 Mest Fifth Street
CITY: 108 Ancels
COUNTRY: 12.8 Ancels
COUNTRY: 12.8 Ancels
COUNTRY: 12.8 Ancels
CONPUTER READELE FORM:
MEDIUM TYPE: 30. Diskette, 1.44 Mb
MEDIUM TYPE: 18.0 Diskette, 1.94 Mb
MEDIUM TYPE: 18.0 Diskette, 1.94 Mb
MEDIUM TYPE: 18.0 Diskette, 1.93
COMPUTER: Setence
COMPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-462-040-15
Sequence 15, Application US/08462040
; Partent No. 617554
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                                 4 AAGGGAGGGAGGGAGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AAGGGAGGGAGGGGG 6
Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-462-040-14
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APPLICANT: WOO, SAYO, L.C.
APPLICANT: WOO, SAYO, L.C.
APPLICANT: CHIEFLAND E.C. CHIEFLAND C.C. C
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Gaps
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; Sequence 13, Application US/08460971A
; Sequence 13, Application US/08460971A
; Patent No. 6150168
; Patent No. 6150168
; APPLICANT: Woo, Savio L.C.; APPLICANT: Cristiano, Richard J. APPLICANT: Gritchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

ADDRESSEE: Lyon & Lyon
; ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.0%; Score 17.4; DB 3; Length 39; Best Local Similarity 94.7%; Pred. No. 4.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: CALLLOLLING
COUNTRY: CAS.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPALIAL
COMPUTER: IBM COMPALIAL
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: JUNE 5, 1995
PRIOR APPLICATION OBJAR:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: POT/855,389
FILING DATE: MARCH 20, 1992
                                    GOFTWARE: FastESD tow Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US3/02725
APPLICATION NUMBER: PCT/US3/02725
ATTONNEY AGENT INPORMATION:
NAME: WALDULG, RICHARD J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
YSTEM: IBM P.C. DOS 5.0 FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AAGGGAGGGGAGGGGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: CDNA US-08-167-641C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
TELEX: 6'
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Patent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES 65

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: Suite 4700

STREET: Suite 4700

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.0%; Score 17.4; DB 2; Length 39; 94.7%; Pred. No. 4.3e+02; Live 0; Mismatches 1; Indels
                                                                                                                     COUNTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TEASTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTEM: IBM P.C. DOS 5.0
SOFTWARE: TASTEM: IBM P.C. DOS 5.0
SOFTWARE: JAMES STORAGE
FILING DATE: JUNE 5, 1995
CLASSIFICATION NUMBER: 08/167,641
FILING DATE: DECEMBER: 1993
PILING DATE: MARCH 20, 1993
APPLICATION NUMBER: C7/655,389
FILING DATE: MARCH 20, 1993
APPLICATION NUMBER: PCT/US93/02725
RILING DATE: MARCH 19, 1993
ATTORNEY, AGENT INPORMATION:
"NAME: Was-hurr Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEXT: (213) 955-0440
TELEX: (5-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYRE: nucleic acid
STRANDENNESS: double
  633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGGGGAGGGAGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.75
Marches 18; Conservative
                            T: Suite 4700
Los Angeles
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-167-641C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-460-890A-13
                                                                                                             COUNTRY:
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/note= "Sticky single-stranded end
from base 1 to 4. Double stranded from base 5 to
43 to complementary strand, SEQ ID NO:3."
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                                                                                                                                                                                                                                                     87.0%; Score 17.4; DB 3; Length 39; 94.7%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2. Application PC/TUS9302352

GENERAL INFORMATION:

APPLICANT: California Institute of Technology,

APPLICANT: Pasadena, California 91125, U.S.A.,

TITLE OF INVENTION: Triple helix recognition of DNA

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard F. Trecartin

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02352
FILING DATE: 19930311
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/850,503
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: TECATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: 415,781-1989
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
TELEFAX: (415) 789-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  1 AGGGGAGGGAGGG 19
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                                      LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLLGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc binding LOCATION: 5..43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.07
Best Local Similarity 89.55
Matches 17; Conservative
                                                                                                                                                                                                                                                                                     Best Local Similarity 94.7
Matches 18; Conservative
            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: /1 / OTHER INFORMATION: /1 / OTHER INFORMATION: £1 / CT-US93-02352-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 43 base par
TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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PCT-US93-02352-2
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US-08-462-040-13
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GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Wath, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Getterlano, Richard J.
APPLICANT: Getterlano, Richard J.
APPLICANT: Getterlano, Richard J.
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Galifornia
COUNTRY: U.S.A.
ZIP: 108 Angeles
STRYEE: Galifornia
COUNTRY: U.S.A.
ZIP: 108 Angeles
STRYEE: Suite 4700
CITY: LOS Angeles
STRYEE: Suite 4700
CITY: LOS Angeles
STRYEE: 108 Compatible
COUNTRY: U.S.A.
ZIP: 108 Angeles
STRYEE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 0.00 SOURCE
MEDIUM TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.0%; Score 17.4; DB 3; Length 39; 94.7%; Pred. No. 4.3e+02; tive 0; Mismatches 1; Indels
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELEFRAN: (213) 489-1600
TELEFAX: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDENDESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08462040; Patent No. 6177554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGGGAGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AAGGGAGGGGAGGG 28
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-460-971A-13
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US-08-462-040-13
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Gaps

CORRESPONDENCE ADDRESS:

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TELEFAX: (301) 309-8439
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SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-956-171E-2153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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OTHER INFORMATION: from base 1 to 4. Double-stranded from base 5 to OTHER INFORMATION: 37 to complementary strand, SEQ ID NO:2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: California Institute of Technology,
APPLICANT: Pasadena, California 91125, U.S.A.
TITLE OF INVENTION: Triple helix recognition of DNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02352
FILING DATE: 19930311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/850,503
FILING DATE: 13-MAR-1992
ATTONNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
REGISTRATION NUMBER: 13,801
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3:
LENGTH: 43 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-956-171E-2153/C
% Sequence 2153, Application US/08956171E
% Patent No. 659314
% GENERAL INFORMATION:
% APPLICANT: Charles Kunsch
% Patrick S. Dillon
Patrick S. Pollon
***Charter Charles Charter Char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGGGGAGGGGAGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc binding LOCATION: 5..43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
PCT-US93-02352-3/c
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US-08-781-986A-2153/c

Sequence 2153 Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
CORPUTER: HP Vectra 486/33
COPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION NUMBER: 06/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

WEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
OPERATING SYSTEM: MSDOS Version 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.0%; Score 16.4; DB 3; Best Local Similarity 89.5%; Pred. No. 9.8e+02; Matches 17; Conservative 0; Mismatches 2;
ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
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Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: primer bind
; LOCATION: (1)..(22)
US-09-118-752-2
                                                                                                                     TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESIRED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 42
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                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                       82.0%; Score 16.4; DB 3; Length 50;
89.5%; Pred. No. 9.8e+02;
iive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09622745B
Patent No. 6933124
| GENERAL INFORMATION:
APPLICANT: Actracence AB
APPLICANT: Edlund, Anders
APPLICANT: Donase
APPLICANT: Leonardsson, Thore
APPLICANT: HUMAN GABA B RECEPTOR I PROMOTERS
| TILE OF INVENTION: HUMAN GABA B RECEPTOR I PROMOTERS
| CURRENT APPLICATION NUMBER: US/09/622,745B
| CURRENT FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Edlund, Anders
APPLICANT: Estrand, Jonas
APPLICANT: Estrand, Jonas
APPLICANT: Estrand, Jonas
APPLICANT: Leonardsson, Goran
TITLE OF INVENTION: HUMAN GABA B RECEPTOR 1 PROMOTERS
FILE REFERENCE: 1103326-0633
CURRENT APPLICATION NUMBER: 08/09/622,745B
CURRENT APPLICATION NUMBER: PCT/SE00/00878
PRIOR APPLICATION NUMBER: PCT/SE00/00878
PRIOR APPLICATION NUMBER: PCT/SE00/00878
PRIOR APPLICATION NUMBER: PCT/SE00/00878
PRIOR PRIOR PRIOR APPLICATION NUMBER: OF SEQ ID NOS: 26
SEQ ID NO 20
SEQ ID NO 20
LENGTH: 27
                         NAME: BEHBOIL, BULL
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301,309-8514
TELEPAX: (301) 309-8514
TELEFAX: (301) 309-8516
SEQUENCE CHRACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09622745B
Patent No. 6933124
PARERAL INCRWATION:
APPLICANT: AstraZeneca AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: P R 1b GCVI Fwd
US-09-622-745B-20
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                   US-08-781-986A-2153
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US-09-622-745B-20/c
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US-09-622-745B-21
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; Sequence 2, Application US/09118752
; Patent No. 6114154
; GENERAL INFORMATION:
; APPLICANT: Li, Huiwu
; TITLE OF INVENTION: Direct Construction and Isolation Full Length Target
; TITLE OF INVENTION: CDNA MOLECULe from an mRNA Population
; TITLE OF INVENTION NUMBER: US/09/118,752
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 37
                                                                                                                                                                                                                                                                                                                                 Gaps
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;Patent No. 5182196
APPLICANT: ALLET, BERNARD;KAWASHIMA, ERIC H.
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR OVERPRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: primer
                                                                                                                                                                                                                                                                            Score 15.8; DB 3; Length 27;
Pred. No. 1.6e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8; DB 9; Length 42;
Pred. No. 1.6e+03;
0; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: PCT/SE00/00878
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,281
FILING DATE: 27-UW-1989
PRIOR APPLICATION NUMBER: 53,398
FILING DATE: 18-MAY-1987
APPLICATION NUMBER: 785,4987
FILING DATE: 09-OCT-1985
                                                                                                                                                                                                       ; OTHER INFORMATION: P R 1b GCVI Rev US-09-622-745B-21
                                                                                                                                                                                                                                                                                                                                                                             1 AGGGGAGGGGAGGG 19
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Meiji Seika Kaisha, Ltd.

APPLICANT: Meiji Seika Kaisha, Ltd.

APPLICANT: Moriya, Tatsuki
TITLE OF INVENTION: Systems for the Mass Production of Proteins or Peptides by Microo
TITLE OF INVENTION: of the Genus Humicola
FILE REPERENCE: VX990054

CURRENT APPLICATION NUMBER: US/09/230,225B

CURRENT FILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.1

SEQ ID NO 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                  TITLE OF INVENTION: ENZYME ENDOGLUCANASE AND CELLULASE PREPARATIONS
TITLE OF INVENTION: CONTAINING THE SAME
FILE REFERENCE: 99-0055*/LC (WMC)/144
CURRENT APPLICATION NUMBER: US/09/230,222A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                           Length 30;
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Fatent No. 6365360
GENERAL INFORMATION:
FAPLICANT: HAYASHIZAKI, Yoshihide
TITILE OF INVENTION:
FILE REFERENCE: 024705-080
CURRENT APPLICATION NUMBER: US/09/254,352B
CURRENT FILING DATE: 1999-11-10
FRIOR APPLICATION NUMBER: OT/JP98/03039
FRIOR FILING DATE: 1998-07-06
FRIOR FILING DATE: 1998-06-04
FRIOR FILING DATE: 1998-06-04
FRIOR APPLICATION NUMBER: JP 9-196478
FRIOR APPLICATION NUMBER: JP 9-196478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/09230225B Patent No. 6403362
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                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
  APPLICANT: KONO, TOSHIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-230-225B-25/c
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                                                                                                                                                                                                                                                  TYPE: DNA
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Patent No. 5624803

GENERAL INFORMATION:
APPLICANT: HOND:
AND TITLE OF INVENTION:
TITLE OF INVENTION: OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREE: 755 PAGE MILL ROAD
CITY: PALO ALTO
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76.0%; Score 15.2; DB 3; Length 37; 85.0%; Pred. No. 2.6e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 813-5600
TELECOMMUNICATION INFORMATION:
TELEPX: (415) 494-0792
TELEPX: (415) 494-0792
TELEPX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TURNGTH: 38 base pairs
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Patent No. 6159720
                                                                                                  1 AGGGGAGGGAGGGG 20
                                                                                                                                                16 AGGGAAGGGGGGGGGGGGG 35
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APPLICANT: MORIAY, TAYSUKI
APPLICANT: HAMAYA, TORU
APPLICANT: KOGA, JINICHIRO
APPLICANT: SUMIDA, NAOMI
APPLICANT: AOYAGI, KAORU
APPLICANT: AOYAGI, KAORU
APPLICANT: MURAKAMI, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AGGGGAAGGGAAGGG 8
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Best Local Similarity 85.0 Matches 17; Conservative
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                       Best Local Similarity
Matches 17; Conserv
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US-09-230-222-18/c
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Query Match
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Gaps

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APPLICANT: LIN, SHI-LUNG
APPLICANT: LIN, SHI-LUNG
CHONG, CHENG-MING
YING, SHAO-YAO
TITLE OF INVENTION: Method for Generating Full-Length CDNA
Library from Single Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lacour. Berek R.
APPLICANT: Thomas, Rita L.
APPLICANT: Thomas, Rita L.
APPLICANT: Kongpachith, Ana
APPLICANT: Sheppach Liana T.
APPLICANT: Lim, Moon Young
APPLICANT: Lim, Moon Young
APPLICANT: Lim, Moon Young
TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
FILE REFERENCE: 54600-8135.U500
FILE REFERENCE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,549
PRIOR APPLICATION NUMBER: US 60/209,549
PRIOR APPLICATION NUMBER: US 60/209,549
NUMBER OF SEQ ID NOS: 246
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FRAELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.0%; Score 14.4; DB 3; Length 25; Best Local Similarity 93.8%; Pred. No. 5.2e+03; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                 Query Match 72.0%; Score 14.4; DB 3; Length 20; Best Local Similarity 93.8%; Pred. No. 5.2e+03; Matches 15; Conservative 0; Mismatches 1; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: David & Raymond Patent Firm
STREET: 108 N. Ynez Ave., Suite 128
CITY: Monterey Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66, Application US/09875453B
Patent No. 6338556
GENERAL INFORMATION:
APPLICANT: Starr, Douglas B.
APPLICANT: Tarm, Albert W.
APPLICANT: Laurance, Megan E.
APPLICANT: Michelotti, Emil F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 2, Application US/09197951
Patent No. 6197554
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         5 GAGGGGAGGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                     GAGGGGAGGTGAGGGG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wichelotti, Emil
Velligan, Mark D.
Patentin Ver. 2.0
                                                                                           TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
COUNTRY: USA
                                                                                                                                                           US-08-777-708C-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-875-453B-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-875-453B-66
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US-09-197-951-2/c
                           SEQ ID NO 16
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 66
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                8
                                                                                           FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: T7 RNA polymerase (WT)
NAME/KEX: misc feature
LOCATION: (25)
COTHER INFORMATION: Nucleotide 25 is n wherein n = any nucleotide.
US-09-254-352B-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-011.6.0

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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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LOCATION: (1)..(31)

OTHER INFORMATION: Mutant T7 RNA polymerase wild type.

NAME/KEY: misc_feature

LOCATION: (25)...(25)

OTHER INFORMATION: Nucleotide 25 is "n" wherein "n" = any nucleotide.
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                                                                                                                                                                                                                                                                                                                          Score 14.8; DB 3; Length 31;
Pred. No. 3.7e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-13-14-14

US-09-13-14-17, Application US/09254344

Patent No. 6867027

GENERAL INFORMATION:

APPLICANT: WATAHIKI, MARANCTI

TITLE OF INVENTION: RNA Polymerase

TILE REFERENCE: 024705-077

CURRENT APPLICATION NUMBER: US/09/254,344

CURRENT FILING DATE: 1999-09-03

PRIOR PLILING DATE: 1998-07-06

PRIOR APPLICATION NUMBER: JP 9/180883

PRIOR PLING DATE: 1998-07-07

PRIOR APPLICATION NUMBER: JP 10/155759

PRIOR PLING DATE: 1998-06-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PATENT VERSION 3.0

SEQ ID NO 17

LENGTH: 31
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                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                       74.0%;
ilarity 88.9%;
Conservative
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Thes 16; Conservat
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US-09-254-344-17
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   LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps

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US-09-965-101-55/c
; Sequence 55, Application US/09965101
; Patent No. 6821957
20 GGGGGGGGGGGGGG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Davis, Heather I.
APPLICANT: Davis, Heather I.
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1039/7009
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT APPLICATION NUMBER: US 60/047,233
PRIOR FILING DATE: 1997-05-20
PRIOR PILING DATE: 1997-05-20
PRIOR PILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.0%; Score 14.2; DB 3; Length 20; 84.2%; Pred. No. 6.1e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.0%; Score 14.2; DB 3; Length 20; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                         NAMÉ: Chan, Raymond Y.C.
REGIGGTRATION NUMBER: 37,484
REFERENCE/DOCKET NUMBER: USP8462A-SL(3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 571-9812
TELEPHONE: (626) 571-9813
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: synthetic oligonucleotide US-09-082-649B-55
                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,951
FILING DATE: 20-NO. 6197554-1998
CLASSIFICATION: CURROWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-082-649B-55/c
; Sequence 55, Application US/09082649B
; Patent No. 6339068
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                     COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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Best Local Similarity
Matches 16; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Evide, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: Cl039/7057 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/965,101
CURRENT FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.0%; Score 14.2; DB 3; Length 20; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Harmann, Gunther
APPLICANT: Brazaler, Robert L.
APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
FILE REPERENCE: C1039/7004
FILE REPERENCE: C1039/7004
CURRENT APPLICATION NUMBER: US/09/672,126B
CURRENT FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 169
SEQ ID NOS: 169
SEQ ID NOS: RatSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Synthetic Oligonucleotide US-09-672-126B-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: synthetic oligonucleotide US-09-965-101-55
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; Sequence 134, Application US/09672126B
; Patent No. 6949520
; GRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGGAGGGAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 42, Application US/08403888A

| Patent No. 5952490
| GENERAL INFORMATION:
| APPLICANT: Hancak et al.
| TITLE OF INVENTION: Sequence
| TITLE OF INVENTION: Sequence
| NUMBER OF SEQUENCES: 146
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
| STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Pred. No. 6.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM FC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,888A
FILING DATE: 12-JUN-1995
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/954,185
FILING DATE: 29-SEP-1992
ATTONNEY/AGENT INPORMATION:
NAME: PAUL K. LEGGARA
REGISTRATION NUMBER: 38,534
                                                                                                                                                                                                        COMPUTER: IBM
COMPUTER: IBM
COMPUTER: WORDERFECE 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,964
FILING DATE: June 8, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 128D-1175A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
                      2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGGAGGGGAGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
STREET: 25v.
CITY: Pullerton
STATE: California
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US-08-257-964-3
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                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reddy, Parameswara M.
APPLICANT: NORMATION: Methods and Reagents
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: Oligonuclecting
TITLE OF INVENTION: Oligonuclectides
NUMBER OF SEQUENCES:
ADDRESSE: Beckman Instruments, Inc.
STREFT: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08257964

Patent No. 5518651

GENERAL INFORMATION:

APPLICANT: Reddy, Parameswara M.
APPLICANT: Hanna, Naeem B.

TITLE OF INVENTION: Methods and Reagents

TITLE OF INVENTION: for Cleaving and

TITLE OF INVENTION: Opigonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTEX: USDAY

ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: ISM
COPERATING SYSTEM: MS.DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/873,915A
FILING DATE: 19920424
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BURGOOM, RICHARD P.
REGISTRATION NUMBER: 128D-111
TELECOMMUTATION INFORMATION:
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beckman Instruments, Inc.
                                                                                                                                    Sequence 3, Application US/07873915A
Patent No. 5348868
                         1 GGGGGGGGGGGGGG 19
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 84.2*
Matches 16; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ANTI-SENSE: no
US-07-873-915A-3
                                                                                                                     US-07-873-915A-3
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US-08-257-964-3
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                                                                                                                                                                                                                                                      Score 14.2; DB 2; Length 21;
Pred. No. 6.1e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 91101
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Matson, Robert S.
APPLICANT: Matson, Peter J.
APPLICANT: Coassin, Peter J.
APPLICANT: Cassin, Peter J.
APPLICANT: Cassin, Jang B.
APPLICANT: Cassey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABALdon & Mak
STREET: 225 South Lake Avenue, 9th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUKKENT APPLICATION DATE

CUKKENT APPLICATION NUMBER: US/08/863,639A

FILING DATE: May 28, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532

REFERENCE/DOCKET NUMBER: 20,532

REFERENCE/DOCKET NUMBER: 11859-1

TELECOMMUNICATION INFORMATION:
TELEPAN: (626) 795-6321

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
  ISIS-1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 35
US-08-863-639A-11/c
US-08-863-639A-11/c
Sequence 11, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
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REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                           Query Match 71.0%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                          TELEFAX: 215-568-3439
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
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Matches 16, Conservative
                                                                                                                                                                           single
                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasadena
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Sequence 4484, Application US/09696791
; Sequence 4484, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: SKIN AND EYE DISEASE
; TITLE OF INVENTION: SKIN AND EYE DISEASE
; TITLE OF INVENTION: SKIN AND EYE DISEASE
; TITLE OF INVENTION WOMBER: US/09/696,791
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4484
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                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
                                                               APPLICANT: MARSON, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Coassin, Peter J.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
, OTHER INFORMATION: PDGF A ribozyme recognition site US-09-696-791-4484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2; DB 2;
Pred. No. 6.1e+03;
                                                                                                                                                                                                                                                     STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: COREL Wordberfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: MAY 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
Sequence 12, Application US/08863639A, Patent No. 5981185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGGAGGGAGGGGG 20
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Pest Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                         USA
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Query Match 71.0%; Score 14.2; DB 6; Length 23; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10770
FILING DATE: 19921211
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE, INDIVIDUAL ISOLATE: 12/C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10792
FILING DATE: 19921211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Jayasena, Sumedha D.
TITLE OF INVENTION: (PuNPyN) - (PuNPyN) Tracts
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SRI International
STREET: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 9-2962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 859-4850
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          ADDRESSEE: SRI International
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGGGAGGGAGGGG 20
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                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                    ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                   STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 40
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                      71.0%; Score 14.2; DB 3; Length 21; 84.2%; Pred. No. 6.1e+03; Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/808,452
FLING DATE: 19911213
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Fabian, Gary R.
REFERENCE/DOCKET NUMBER: 8255-008
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMUNICATION INFORMATION:
TELEFONMUNICATION INFORMUNICATION:
TELEFONMUNICATION INFORMUNICATION INFORMUNICATION INFORMATION:
TELEFONMUNICATION INFORMUNICATION INFORMUNICATION INFORMATION INFORMUNICATION INFORMUNICATION INFORMUNICATION INFORMUNICATION INFORMUNICATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application PC/TUS9210770
Sequence 15, Application PC/TUS9210770
SEMERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on TITLE OF INVENTION: RNA-Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
TITLE OF INVENTION: RNA-Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
STREET: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                             RESULT 38
US-07-308-452-15
Sequence 15, Application US/07808452
; Patent No. 6063612
                                                                                                                                                         2 GGGGAGGGAGGGGG 20
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
         Query Match
Best Local Similarity 84.2*
***rhes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 49, Application US/08486421
| Patent No. 5672479
| GENERAL INFORMATION:
| APPLICANT: JOHNSON, Edward M. APPLICANT: JOHNSON, CLONING AND EXPRESSION OF PUR PROTEIN INTERPRESSION OF PUR PROTEIN CORRESPONDENCES: 51
| CORRESPONDENCES: 51
| ADDRESSEE: Pennie & Edmonds | STREET: 1155 Avenue of the Americas | CITY: New York |
                                                                                                                     Length 24;
                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: O'-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION WHERE: US/08/486,421
FILING DATE: 06-JUN-1995
ATPONDEN/AGENT: 06-JUN-1995
ATPONDEN/AGENT: NFORMATION:
ANDER APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-JUN-1995
ATPONDEN/AGENT: NFORMATION:
                                                                                                                     Query Match 71.0%; Score 14.2; DB 2; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.0%; Score 14.2; DB 2; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3;
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-470-911-49
; Sequence 49, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGGGAGGGGAGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A. 742
REGISTRATION NUMBER: 60,742
REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION:
                          MOLECULE TYPE: DNA (genomic) US-08-014-943A-7
unknown
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TOPOLOGY:
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US-08-014-943A-7

Equence No. 554551

GENERAL INFORMATION.

APPLICANT: Johnson, Edward M.

APPLICANT: Johnson, Edward M.

APPLICANT: Bergeman, Andrew D.

TITLE OF INVENTION: Cloning And Expression Of PUR Protein NUMBER OF SEQUENCES: 26

CORRESPONDENCES: 26

CORRESPONDENCES: 26

CORRESPONDENCES: Aborne of the Americas

GITY: New York

STATE: New York

STATE: New York

COMPUTR: IS Now York

COMPUTR: TIMP C COMPATION:

MEDIUM TYPE: Flopy disk

COMPUTR: Patentin Release #1.0, Version #1.25

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/014,943A

FILING DATE: 02)FEB)1992

CLASSIFICATION: 435

ATTORNEY/AGETRATION: 435

REGISTRATION NUMBER: 0523-033

TELEFHONE: 212 790-9090

TELEFHONE: 212 790-9090

TELEFAX: 6141 PENNIE

INFORMATION FORDER

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                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,934
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: FIGURE 10, C-1
                                                                                                                                                                                                                                                NAME: Pabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: P-314
TELECOMMUNICATION INPORMATION:
TELEPAX: (415) 859-3880
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: Single
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LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 130 Water Street
CITY: Boston
STATE: MA
                                              ATTORNEY/AGENT INFORMATION:
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LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA
US-08-486-809-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           usa
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US-08-960-190A-31
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US-08-960-190A-31
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APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCES: 51
CORRESPONDENCES: 51
CORRESPONDENCES: 61
STREET: 1155 Avenue of the Americas
CITY: New York
CULTY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470, 911
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: 30,742
FILING DATE: O6-JUN-1995
CLASSIFICATION NUMBER: 30,742
FILERANCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
NAME: COLUZZ, LAURA A:
RESERRUE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELECHAN: (212) 869-9741/8864
TELECHAN: (212) 869-9741/8864
TELECOMMUNICATION NUMBER: 30,742
SEQUENCE CHARACTERISTICS:
LENGRATION POR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGRATION POR SEQ ID NO: 49:
ERNGRATION POR SEQ ID NO: 49:
TELEFAX: (112) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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| Sequence 49, Application US/08486809
| Patent No. 5869622
| GENERAL INFORMATION:
| APPLICANT: Johnson, Edward M. APPLICANT: Bergemann, Andrew D. TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
| CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Edmonds | STREET: 1155 Avenue of the Americas | STREET: New York | STATE: New York | COUNTRY: U.S.A. |
| COUNTRY: U.S.A. |
| COUNTRY: IN SALDABLE FORM: | MEDIUM TYPE: Floppy disk | COMPUTER: IRADABLE FORM: | MEDIUM TYPE: Floppy disk | COMPUTER: PatentIn Release #1.0, Version #1.30 |
| CURRENT APPLICATION DATA: APPLICATION DATA: OCHAPLE OF PATENT OF APPLICATION DATA: OCHAPLE OF APPLICATION DATA: OCHAPLE OF APPLICATION AND APPLICATION: AND A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGGGAGGGGAGGGG 20
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Best Local Similarity
Matches 16; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
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US-08-486-809-49
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71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-OCT-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 39-OCT-1997
CLASSIFICATION NUMBER: ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48002
TELEROMUNICATION INFORMATION:
TELERPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Burkhardt, Martin
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
RELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPAX: (212) 790-9090
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 64141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/08960190A
Patent No. 6232445
GENERAL INFORMATION:
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(602) 495-9475
                              JS-09-896-650C-26/c
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Head, Steven R.
APPLICANT: Goelet, Philip
APPLICANT: Goelet, Philip
APPLICANT: Border-Jacino, Michael
TITLE OF INVENTION: De No. 63371880 or "Universal" Sequencing Array
FILE REFERENCE: 04990.0049
CURRENT APPLICATION NUMBER: US/09/648,312
CURRENT FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 25
                                                                                                                                                                                                                                                                               APPLICANT: Head, Steven R.
APPLICANT: Head, Steven R.
APPLICANT: Geolet, Philip
APPLICANT: Geolet, Philip
APPLICANT: Warn, Jonathan
APPLICANT: Boyce-Jacino, Michael
TITLE OF INVENTION: De No. 63229680 or "Universal" Sequencing Array
FILE REFERENCE: 04990.0049
CURRENT APPLICATION NUMBER: US/08/976,427A
CURRENT FILING: DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PastSEQ for Windows Version 3.0
SED ID NO 26
LENGTH: 25
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              71.0%; Score 14.2; DB 3; Length 24; 84.2%; Pred. No. 6.1e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.0%; Score 14.2; DB 3; Length 25; 84.2%; Pred. No. 6.1e+03; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                 US-08-976-427-26/c
; Sequence 26, Application US/08976427A
: Patent No. 6322968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-976-427-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Synthetic primer US-09-648-312-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09648312
Patent No. 6337188
                                                                                        2 GGGGAGGGAGGGG 20
                                                                                                                  3 GGGSGGGSGGGSGGG 21
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.29
Matches 16; Conservative
Query Match
Best Local Similarity 84.2;
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| Patent No. 5389531 | GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: METHODS TO REPLICATE DNA in vitro USING TITLE OF INVENTION: PRDI-CATALYZED DNA REPLICATION SYSTEMS NUMBER OF SEQUENCES: 89 CORRESPONDENCE ADDRESS: 89 CORRESPONDENCE ADDRESS: ADDRESSE: CAHILL'S PATENT: LSS Park One, 2141 E. Highland Ave. CITY: Phoenix STATE: Arizona COUNTRY: U.S.A. COUNTRY: U.S.A. COUNTRY: U.S.A. COUNTRY: U.S.A.
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MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
COMPUTER: Packard Bell (IBM PC/AT compatible)
COMPUTER: Packard Bell (IBM PC/AT compatible)
COMPUTER: Packard Bell (IBM PC/AT compatible)
COBERATING SYSTEM: MS-Dos, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,486
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/208,486
FILING DATE: April 14, 1992
APPLICATION NUMBER: Japan 240525/91
FILING DATE: April 14, 1992
ATTORNEY AGENT INFORMATION:
FILING DATE: August 26, 1991
ATTORNEY AGENT INFORMATION:
TELEPHONE: GO2) 485
REFERENCE/DOCKET NUMBER: #3954-A-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (602) 459-9475
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
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TYPE: nucleic acid
STRANDEDNESS: single
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10: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCONB.seq:*
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             GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-08-781-986A-2153
US-10-329-624-2153
US-09-263-959-923
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US-10-314-578-906
US-10-831-778-906
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Sequence 906, Application US/09776479
; Sequence 906, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Pouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Immunostimulatory
; FILE REFERENCE: CLO37/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2000-02-03
; RIOR FILING DATE: 2000-02-03
; SEQ ID NO 906
; SEQ ID NO 906
; LENGTH: 20
                                                                                                                                                                              Query Match 100.0%; Score 20; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 20; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
FRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                           ; OTHER INFORMATION: Synthetic Sequence US-09-776-479-906
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                                                                                                                                                                                                                              1 AGGGAGGGAGGGGG 20
                                                                                                                                                                                                                                             1 AGGGAGGGAGGGAGGGG 20
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                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Matches 2
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Sequence 228006,
Sequence 250515,
Sequence 267219,
Sequence 356771,
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1882, Ap
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24, Appl
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26, Appl
26, Appl
34, Appl
3759, Ap
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Sequence 240365,
Sequence 248970,
Sequence 249389,
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Sequence 133786,
Sequence 183495,
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Sequence 26, Appl
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Sequence 166862,
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Sequence 291543,
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Sequence 2
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US-10-313-22-182

US-10-723-947-2

US-09-949-744-3

US-09-949-744-3

US-09-949-748-2

US-09-949-748-2

US-10-849-072-24

US-10-849-072-24

US-10-849-072-24

US-10-849-072-24

US-10-949-338

US-09-918-889-26

US-09-918-889-26

US-09-918-889-26

US-09-918-889-26

US-09-918-889-26

US-10-112-653-559

US-09-918-889-26

US-10-917-95-559

US-09-918-889-26

US-10-917-95-559

US-10-956-157-176142

US-10-956-157-176142

US-10-956-157-176142

US-10-956-157-176142

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US-10-956-157-176142

US-10-956-157-176142

US-11-036-317-155963

US-11-036-317-155963

US-11-036-317-28909

US-11-060-756-249399

US-11-060-756-249399

US-11-060-756-229353

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US-11-060-756-229353
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US-10-112-653-875

Sequence 875, Application US/10112653

Sequence 875, Application Wo. US2003005026841

Publication No. US2003005026841

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES

TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES

TITLE OF INVENTION: UNMBER: US/10/112,653

CURRENT APPLICATION NUMBER: US/10/112,653

CURRENT PILING DATE: 2002-03-29

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040
1 AGGGGAGGGAGGGGG 20
                                                1 AGGGAGGGAGGGGG 20
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Sequence 906, Application US/09776479
Publication No. US20030087848A1
GENERAL INFORMATION:
APPLICANT: Brateler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immalatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy

US-09-776-479-906

ALIGNMENTS

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Gaps

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100.0%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 3e+02; ative 0; Mismatches 0; Indels

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Publication No. US2003055014A1
GENERAL INFORMATION:
APPLICANT: Brataler. Robert L.
TILLE REFERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,534
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PRESENCE OF Windows Version 3.0
SEQ ID NO 906
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Krieg, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jones
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 2000-08-23
                                                                                                                        ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-875
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 875 LENGTH: 20
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 906
LENGTH: 20
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                                                                TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 20, Conservative
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Matches 20; Conserv
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US-10-314-578-906
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US-10-010-920-43

US-10-010-920-43

Sequence 43, Application US/10010920

Sequence 43, Application US/10010920

Publication No. US20030027165A1

PUBLICANT: Saus, Juan

TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences

TITLE OF INVENTION: and methods for using

TITLE OF INVENTION: And methods for using

FILE REPERENCE: 98,723-83

CURRENT FILING DATE: 2001-12-07

PRIOR PELING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 102

SEQ ID NO 43

LENGTH: 30
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JOSTICA APPLICATION US/10831778

Sequence 906, Application US/10831778

Publication No. US20040235774A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Fouron, Yves

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT FILING DATE: 2004-04-23

PRIOR PAPLICATION NUMBER: US 60/179,991

PRIOR APPLICATION NUMBER: US 60/179,991

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

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                                                                                                                                               0; Indels
                                                                                             Query Match 100.0%; Score 20; DB 6; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 20; Conservative 0; Mismatches 0
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Pred. No. 3e+02;
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; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-906
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Query Match
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Sequence 159, Application US/10971736

Publication No. US20050227251A1

GENERAL INFORMATION:

APPLICANT: darnell, robert

APPLICANT: jensen, kirk

APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-TATADE1
US-10-008-721-43
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                                                                                                                                                                                                                                         Sequence 43, Application US/10008721

Sequence 43, Application No. US20030082745A1

GENERAL INFORMATION:

APPLICANT: Saus, Juan

ITLLE OF INVENTION: TNF-Inducible Promoters and Methods for Using

FILE REFERENCE: 98, 723-E1

CURRENT APPLICATION NUMBER: US/10/008, 721

CURRENT FILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-08

NUMBER: OF SEQ ID NOS: 102

SEQ ID NO 43

LENGTH: 30
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94.7%; Pred. No. 2.2e+03;
tive 0; Mismatches 1; Indels
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lery E.
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1 AGGGGAGGGGAGGG 19
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Best Local Similarity 94.7'
Matches 18; Conservative
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US-09-263-959-699/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
ADDRESSEE: Seed and Reventions
ADDRESSEE: Seed and Reventions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SSCTWARE: PatentIn version 3.2
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%; Score 16.8; DB 3; Length 23; 90.0%; Pred. No. 3.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
                                                                                                                                                       E: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 220152, Application US/11060756 Ubblication No. US20050221354A1 GENERAL INFORMATION:
APPLICANT: Wyeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFRENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGGAGGGAGGGAGGGG 20
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                              STREET: 6300 CCCTY: Seattle
STATE: Washington
COMMENT. WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Matches 17; Conserv
                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 98104-7092
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US-11-060-756-220152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: probe US-11-060-756-220152
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TOPOLOGY:
US-09-263-959-699
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Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Famon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
CORRESPONDENCE S. 2556
CORRESPONDENCE BLUMAN Genome Sciences, Inc.
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Sequence 2153, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 2555
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 16.4; DB 2; Length 50; 89.5%; Pred. No. 4.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 90,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2153, Application US/10329624
Publication No. US200440043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGGAGGGAAGGGAGGGG 20
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Best Local Similarity 89.5-
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville
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    US-08-781-986A-2153/c
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US-10-329-624-2153/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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Sequence 923, Application US/09263959

Sequence 923, Application US/09263959

Sequence 923, Application US/09263959

Sequence 10 Courant No. US2002015081A1

SERVERL INFORMATION:

APPLICANT: Rowen, Lee

APPLICANT: Seatle

CORRESPONDENCE ADDRESS:

ADDRESSES: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seatle

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seatle

STREET: 6300 Columbia Center, 701 Fifth Avenue

COUNTRY: US

COUNTRY: US

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DESCRIPT: D
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Pred. No. 4.2e+03;
0; Mismatches 2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mark J. Hyman
REGISTRATION NOWBERS: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 2153: US-10-329-624-2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGGAGGGAGGGGG 20
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STRANDEDNESS: double
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Best Local Similarity 89.5%;
Matches 17; Conservative 0
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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19 base pairs

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Sequence 41, Application US/10407449
Publication No. US20040005601A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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METHYLTRANSFERASE AND METHODS FOR USE THEREOF
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                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: CA
                                                                                                                                                      ;
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                                                                                                        Query Match 79.0%; Score 15.8; DB 3; Length 19; Best Local Similarity 89.5%; Pred. No. 9.3e+03; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%; Score 15.8; DB 5; Length 26; 89.5%; Pred. No. 8.4e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIE: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKETEN: DOS
SOFTWARE: FASTER: DOS
SOFTWARE: FASTER: DOS
CURRENT APPLICATION NUMBER: US/10/010,476
FILING DATE: 07-Dec-2001
CLASSIFICATION CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/485,071
FILING DATE: 12-JUN-1998
APPLICATION NUMBER: 60/057,411
FILING DATE: 29-AUG-1997
ATTORNEY/AGRAT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/10010476
Publication No. US20030114402A1
GENERAL INFORMATION:
APPLICANT: Flynn, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Canady, Karen S
REGISTRATION NUMBER: 39,927
REFERENCE/DOCKET NUMBER: 30794.30W001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEFRAX: 310 445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                       1 GGGCGGGGAGGGCGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGGAGGGAAGGGAGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGAGGGAGGGAGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.5:
Matches 17; Conservative
  ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-10-010-476-38
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RESULT 16 US-10-407-449-41

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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US-10-407-449-44

Sequence 44, Application US/10407449

Publication No. US20040005601A1

GENERAL INFORMATION:
APPLICANT: Hutley, Laurence
APPLICANT: Farrell, Thomas
APPLICANT: Beares, David
TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
FILE REPERENCE: 53223-20004.00
CURRENT APPLICATION NUMBER: US/10/407,449

CURRENT PILING DATE: 2003-04-04

PRIOR PILING DATE: 2002-08-04

PRIOR PILING DATE: 2002-08-04

PRIOR FILING DATE: 2002-08-05

PRIOR FILING DATE: 2002-08-05

PRIOR FILING DATE: 2002-08-05

NUMBER: OF SEQ ID NOS: 64

SOFTWARE: FSSESQ for Windows Version 4.0

SEQ ID NO 44

LENGTH: 22

TWODE: NAME 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Generalized quadruplex structure for RET
US-10-407-449-41
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Hurley, Laurence
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Bears, David
TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
FILE REFERENCE: 53223-20004,00
CURRENT APPLICATION NUMBER: US/10/407,449
CURRENT APPLICATION NUMBER: US 60/404,966
PRIOR PILING DATE: 2002-08-04
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/370,358
PRIOR PLING DATE: 2003-04-05
PRIOR PLING DATE: 2003-04-05
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FeatsEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGGAGGGGAGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
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1 Accecececececececes 20
TYPE: DNA
ORGANISM: Zea mays
US-10-931-077-28
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                                                                                                                      Sequence 5, Application US/10820487

Publication No. US20050004160A1

GENERAL INFORMATION:

APPLICANT: WHITTEN, Jeffrey P.

APPLICANT: WHATTEN, Jeffrey P.

APPLICANT: WORAN, Terrance

ITILE OF INVENTION: HETEROCYCLIC SUBSTITUTED

ITILE OF INVENTION: 1,4-DIMYDRO-4-OXO-1,8-NAPTHTHYRIDINE ANALOGS

ITILE REFERENCE: 5322320401200

CURRENT APPLICATION UNMBER: US 60/461,205

FRICK FILING DATE: 2003-04-07

PRIOR APPLICATION NUMBER: US 60/519,569

FRICK FILING DATE: 2003-11-12

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 22
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### Sequence 5, Application US/10903975

### Publication No. US20050085468A1

### APPLICANT: WHITTEN, Jeffrey P.

### APPLICANT: SCHWAEBE, Michael

### APPLICANT: SIDDIQUI-JAIN, Adam

### APPLICANT: SIDDIQUI-JAIN, Adam

### APPLICANT: MORAN, Terrance

### ITLE OF INVENTION: SUBSTITUTED QUINOBENZOXOZINE ANALOGS

FILE REFERENCE: 532132001120

### CURRENT FILING DATE: 2004-07-30

### PRIOR PPLICATION NUMBER: US 10/821,243

### PRIOR PPLICATION NUMBER: US 60/461,271

### PRIOR PPLICATION NUMBER: US 60/463,171

### PRIOR PPLICATION NUMBER: US 60/519,535

### PRIOR PPLICATION NUMBER: US 60/519,535

### PRIOR PPLICATION NUMBER: US 60/532,727

### PRIOR PPLING DATE: 2003-11-12

### PRIOR PPLING DATE: 2003-12-23

### NUMBER OF SEQ ID NOS: 20

### NUMBER OF SEQ ID Windows Version 4.0
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     1 AGGGGGGGGGGGGGGG 20
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Best Local Similarity 85.0%;
Matches 17; Conservative (
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Best Local Similarity 85.0
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-10-820-487-5
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US-10-903-975-5
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APPLICANT: Multani, Dilbag
APPLICANT: Multani, Dilbag
APPLICANT: Multani, Dilbag
APPLICANT: Niu, Xiaomu
APPLICANT: Niu, Xiaomu
APPLICANT: Tomes, Dwight T
APPLICANT: Xu, Deping
TITLE OF INVENTION: BRZ AND DW3 PROMOTERS AND METHODS OF USE
FILE REFERENCE: 035718/281933
CURRENT APPLICATION NUMBER: US/10/931,077
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: 60/499,580
PRIOR FILING DATE: 2003-09-02
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: RET quadruplex-forming nucleotide sequence US-10-407-449-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.2; DB 9; Length 27; Pred. No. 1.48+04; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.0%; Score 15.2; DB 6; Length 24; Best Local Similarity 85.0%; Pred. No. 1.4e+04; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                   GENERAL INFORMATION:

APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Starcell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Bersell, Thomas
APPLICANT: Bersel, David
TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
FILE REFERENCE: 5323-20004.00
CURRENT APPLICATION NUMBER: US/10/407,449
CURRENT FILING DATE: 2003-04-04
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR PLING DATE: 2002-04-05
PRIOR PLING DATE: 2003-03-20
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
LENGTH: 24
Sequence 43, Application US/10407449
Publication No. US20040005601A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/10931077; Publication No. US20050204432A1; GENERAL INFORMATION:
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85.0%;
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Best Local Similarity 85.0%
Matches 17; Conservative
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Sequence 4, Application US/10239176

Sequence 4, Application US/10239176

Sequence 4, Application No. US20040086856A1

Sequence 4, Application No. US20040086856A1

GENERAL INFORMATION:
APPLICANT: TAKAHASHI, MASAYOSHI

APPLICANT: OKADA, JUN
APPLICANT: OKADA, JUN
TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF

TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME
FILE REFERENCE: 228765US0SRDPCT
CURRENT APPLICATION NUMBER: US/10/239,176

CURRENT APPLICATION NUMBER: US/10/239,176

CURRENT APPLICATION NUMBER: DCT/JP02/08670

PRIOR PILING DATE: 2002-03-03-19

PRIOR PILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 4

LENGTH: 48

LENGTH: 48
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Patent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Ben F.
ITILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.0%; Score 15.2; DB 7; Best Local Similarity 85.0%; Pred. No. 1.1e+04; Matches 17; Conservative 0; Mismatches 3;
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REPERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGGAGGGAGGGAGGGG 20
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       21 AGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
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Sequence 3, Application US/10239176

Publication No. US20040086856A1

GENERAL INFORMATION:
APPLICANT: TAKAHASHI, MASAYOSHI

APPLICANT: OKADA, JUN

APPLICANT: OKADA, JUN

TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF

TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME

FILE REPERENCE: 228763USOSRDPCT

CURRENT FILING DATE: 2003-03-19

PRIOR APPLICATION NUMBER: DCT/JP02/08670

PRIOR APLLICATION NUMBER: DF 2002-01-8

PRIOR FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 3

LENGTH: 39
                                                                                                                                                                                                                                                 APPLICANT: OKADA, JUN
APPLICANT: OKADA, JUN
APPLICANT: HASHIMOTO, KOJI
TITLE OF INVENTION: NUCLEIC THE PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF
TITLE OF INVENTION: NUCLEIC THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME
FILE REFERENCE: 228763USOSRDPCT
CURRENT APPLICATION NUMBER: US/10/239,176
CURRENT FILING DATE: 2003-03-19
PRIOR FILING DATE: 2003-03-19
PRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTION OF SEQ ID NOS: 18
SOFTWARE: PATENTION OF SEQ ID NOS: 18
LENGTH: 35
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                                                                                                                                                 Sequence 13, Application US/10239176; Publication No. US20040086856A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGGGGAGGGGAGGGG 20
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26 AGGGAGAGGAGGAGGGG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: synthetic DNA US-10-239-176-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic DNA US-10-239-176-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                    RESULT 22
US-10-239-176-13/c
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US-10-239-176-3/c
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TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5
METHYLTRANSFERASE AND METHODS FOR USE THEREOF
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METHYLTRANSFERASE AND METHODS FOR USE THEREOF
NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,476
FILING DATE: 07-Dec-2001
CLASSIFICATION: <u >CUNKNOWN></u>
                                                                                                         Sequence 55, Application US/10010476
Publication No. US20030114402A1
GENERAL INFORMATION:
APPLICANT: Reich, No. US20030114402Albert O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.0%; Score 14.8; DB 5; 88.9%; Pred. No. 1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reich, No. US20030114402Albert O. Flynn, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30794.30W001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/485,071
FILING DATE: 12-Jun-1998
APPLICATION NUMBER: 60/057,411
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-010-476-55
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 39,927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 107, Application US/10010476 Publication No. US20030114402A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Canady, Karen S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 310 445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
10 GGAAGGGAGGGRAGGGG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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Best Local Simi
Matches 16;
                                                                RESULT 28
US-10-010-476-55
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                                                                                                                                                    ore 15; DB 3; Length 15;
red. No. 1.9e+04;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1181, Application US/10035833A

Publication No. US20040072156A1

GENERAL INFORMATION:
APPLICANT: Nakamurz Yuho
APPLICANT: Sexine, Akihiro
APPLICANT: Saito, Vuho
APPLICANT: Saito, Osamu
ITLE OF INVERTION: Detection of Genetic Polymorphisms
FILE REFERRICE: FORS-06904
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFTWARE: Patentin version 3.2
SEQ ID NO 1181
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 376, Application US/10035833A

Sequence 376, Application US/10035833A

Publication No. US20040072156A1

GENERAL INFORMATION:

APPLICANT: Nakamura, Yuho

APPLICANT: Iida, Aritoshi

APPLICANT: Salto, Osamu

TILLE OF INVENTION: Detection of Genetic Polymorphisms

FILE REPRENCE: FORS-06904

CURRENT APPLICATION NUMBER: US/10/035,833A

CURRENT PILING DATE: 2001-12-27

NUMBER OF SEQ ID NOS: 7669

SOFTWARE: PATENTIN VERSION 3.2

SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                       Score 15;
Pred. No.
                                                                                                                                    75.0%; Scur
100.0%; Pre
0; 1
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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US-10-035-833A-1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                                                         STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                         US-09-263-959-443
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APPLICANT: Socos, John
APPLICANT: Rienhoff, Jr., Hugh
APPLICANT: Rienhoff, Jr., Hugh
APPLICANT: Guida, Marco
APPLICANT: Guida, Marco
APPLICANT: Curran, Mark
TITLE OF INVENTION: Polymorphisms Associated with Ion-Channel Disease
FILE REFERENCE: DNA-334022
CURRENT APPLICATION NUMBER: 10/224,683
PRIOR APPLICATION NUMBER: 10/224,683
PRIOR APPLICATION NUMBER: 60/314,331
PRIOR APPLICATION NUMBER: 60/314,331
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-05-06
NUMBER: 0F SEQ ID NOS: 185
SOFTWARE: PatentIn version 3.1
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Pred. No. 1.6e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nakamura, Yuho
APPLICANT: Sekine, Akihiro
APPLICANT: Sekine, Akihiro
APPLICANT: Iida, Aritoshi
APPLICANT: Saito, Osamu
TITLE OF INVENTION: Detection of Genetic Polymorphisms
TITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: FORS-06904
CURRENT APPLICATION NUMBER: US/10/035,833A
CURRENT APPLICATION NUMBER: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFTWARE: Patentin version 3.2
SEQ ID NO 6318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.0%; Score 14.8; DB 9; Best Local Similarity 88.9%; Pred. No. 1.7e+04; Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: (21)...(21)
; OTHER INFORMATION: c is present or absent.
US-10-035-833A-6318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-035-833A-6318/c
; Sequence 6318, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
                                                                                                                                               ; Sequence 93, Application US/10942561A; Publication No. US20050089905A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGGAGGGGAGGG 19
2 GGGGAGGGAGGGAGGG 19
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Best Local Similarity 88.9%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-942-561A-93
                                                                                                                               US-10-942-561A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 93
LENGTH: 40
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Fublication No. US20030162192A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stoos, John
APPLICANT: Curran, Mark
APPLICANT: Curran, Mark
TITLE OF INVENTION: Polymorphisms Associated with Ion-Channel Disease
FILE REFERENCE: 4389-33
CURRENT APPLICATION NUMBER: US/10/224,683
CURRENT PILING DATE: 2002-01-06
PRIOR PILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-06-6
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 93
LIENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.7e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%; Score 14.8; DB 5; Length 26; 88.9%; Pred. No. 1.9e+04; Live 0; Mismatches 2; Indels
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,476
FILING DATE: 07-Dec-2001
CLASSIFTCATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/485,071
FILING DATE: 12-Jun-1998
APPLICATION NUMBER: 60/057,411
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Canady, Karen S
REGISTRATION NUMBER: 39,927
REFERENCE/DOCKET NUMBER: 30794.30W001
TELECOWNUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEFAX: 310 445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGGGGAGCGGAGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
  CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-10-224-683-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-10-224-683-93
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APPLICANT: Sheppard. Liana T.
APPLICANT: Sheppard. Liana T.
APPLICANT: Lim, Moon Young
APPLICANT: Lim, Moon Young
TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
FILE REPERENCE: 4600-0.135.30
CURRENT APPLICATION NUMBER: US/09/875,453
CURRENT FILING DATE: 2001-06-06
PRIOR PILING DATE: 2000-06-06
NUMBER: OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.0%; Score 14.4; DB 3; Length 25; Best Local Similarity 93.8%; Pred. No. 2.7e+04; Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Neville, Matt
APPLICANT: de Arruda Indig, Monika
APPLICANT: Cao, Feng
APPLICANT: Claenburg, Mary C.
APPLICANT: Koelbl, Jim C.
APPLICANT: Alzenstein, Brian D.
APPLICANT: Alzenstein, Brian D.
APPLICANT: Alzenstein, Brian D.
APPLICANT: Alzenstein, Brian D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REPERENCE: FORS-08195
CURRENT APPLICATION NUMBER: US/10/617,070
CURRENT FILING DATE: 2003-07-10
PRIOR PELING DATE: 2003-04-11
PRIOR PLING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 60/371,819
PRIOR PLING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 529
SOFTWARE: Patentin version 3.2
SEQ ID NO 431
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 431, Application US/10617070 Publication No. US20040096874A1 GENERAL INFORMATION:
          Sequence 66, Application US/09875453
Publication No. US20030027320A1
GENERAL INFORMATION:
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                                                                                                                                                       Laurance, Megan E
Michelotti, Emil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic US-10-617-070-431
                                                                                  APPLICANT: Kim, Jungsuh P.
APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
                                                                                                                                                                                                          Velligan, Mark D.
                                                                                                                                                                                                                                  Latour, Derek R.
Thomas, Rita L.
Kongpachith, Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-875-453-66
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US-09-943-944E-100/C

Sequence 100, Application US/09943944E

Publication No. US20040014036A1

GENERAL INFORMATION:

APPLICANT: Petashne, et al.,

TITLE OF INVENTION: Therefor

FILE REFERENCE: 0342941-0065

CURRENT APPLICATION NUMBER: US/09/943,944E

CURRENT APPLICATION NUMBER: US/09/943,944E

SOFTWARE: PAGENT NOS: 238

SOFTWARE: PAGENT NOS: 238

SOFTWARE: PAGENTIN Ver. 2.1

SOFTWARE: PAGENTIN Ver. 2.1

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.0%; Score 14.4; DB 3; Length 18; Best Local Similarity 93.8%; Pred. No. 3e+04; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (32) ... (32)
OTHER INFORMATION: This residue is a non-paired base.
Sequence 9, Application US/10397943
; Publication No. US20040053876A1
; GENERAL INFORMATION:
; APPLICANT: Turner, David L.
; APPLICANT: Yu, Jenn-Yah
; TITLE OF INVENTION: siRNAa and Uses Thereof
; FILE REPERENCE: UN-7885
; CURRENT APPLICATION NUMBER: US/10/397,943
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 9
; LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NOCATION: (1)..(22)
OTHER INFORMATION: n is a, c, g, or u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (42); (43); OTHER INFORMATION: n is a, c, g, or u US-10-397-943-9
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                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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PRIOR APPLICATION NUMBER: US 09/627,249
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 9
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-431
                                                                                                                                                                                                                                                                                                                                                  5 GAGGGGAGGGGGG 20
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                                                                                                                                                                                                                                          Best Local Similarity 93.8 Matches 15; Conservative
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US-10-956-507-432
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Sequence 672.432
Sequence 672.432
Sequence 672.433
Sequence 673.433
Sequence 672.433
Sequen
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Sequence 411, Application US/10956507

Sequence 421, Application No. US20050196771A1

GENERAL INCORMATION:

APPLICANT: Neville, Matt

APPLICANT: Ge Arruda Indig, Monika

APPLICANT: Cao, Feng

APPLICANT: Cao, Feng

APPLICANT: Alzenstein, Brian D.

APPLICANT: Koelbl, Jim C.

APPLICANT: Koelbl, Jim C.

APPLICANT: Folsonstein, Brian D.

APPLICANT: Paizenstein, Brian D.

APPLICANT: Davey, Keith

TITLE OF INVENTION: Characterization of CYP2D6 Genotypes

FILER REFERENCE: FORS. 08195

CURRENT PLING DATE: 2004-10-01

PRIOR APPLICATION NUMBER: US/10/617,070

PRIOR PLING DATE: 2003-04-11

SOFTWARE: Patentin version 3.2

SSEQ ID NO 431

LENGTH: 39
                                       1; Indels
   93.8%; Pred. No. 2.3e+04; tive 0; Mismatches 1
                                                                                                        S GAGGGGAGGGGGG 20
                                                                                                                                                   23 GTGGGGAGGGAAGGG 38
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Best Local Similarity 93.88
Matches 15; Conservative
   Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                              RESULT 37
US-10-617-070-432
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US-10-956-507-431
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Sequence 2, Application US/09916369A
Publication No US20020058802A1
Fublication No US20020058802A1
GENERAL INFORMATION:
APPLICANT: Dellinger, Douglas J
APPLICANT: Dellinger, Marvin H
APPLICANT: Caruthers, Marvin H
APPLICANT: Betley, Jason R
TITLE OF INVENTION: Synthesis of Polynucleotides Using Combined Oxidation/Deprotectic
TITLE OF INVENTION: Chemistry
FILE REFERENCE: 10003669-1
CURRENT APPLICATION NUMBER: US/09/916,369A
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72.0%; Score 14.4; DB 9; Length 39; 93.8%; Pred. No. 2.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nevillo, Matt
APPLICANT: de Arruda Indig, Monika
APPLICANT: Cao, Feng
APPLICANT: Cao, Feng
APPLICANT: Oldenburg, Mary C.
APPLICANT: Nevelbl, Jim C.
APPLICANT: Aizenstein, Brian D.
APPLICANT: Davey, Keith
TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
FILE REFERENCE: FORS-08195
CURRENT APPLICATION NUMBER: US/10/617,070
PRIOR PILING DATE: 2003-07-10
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-11
SRIOR FILING DATE: 2003-04-11
SRIOR PLILING DATE: 2003-04-11
SRIOR FILING DATE: 2003-04-11
                                                                              Indels
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RESULT 43
US-09-920-313-133
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; Better No. US20020156033A1
; GENERAL INFORMATION:
   APPLICANT: Bratiler: Robert L.
; APPLICANT: Bratiler: Robert L.
; APPLICANT: Detersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
   TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
; TITLE OF INVENTION: Cancer:
; FILE OF INVENTION: Cancer:
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Sequence 133, Application US/09895007A

Sequence 133, Application

GENERAL INFORMATION:

APPLICANT: Scheter.

APPLICANT: Scheter.

APPLICANT: Petersen, Deanna M.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE

TITLE OF INVENTION: TREATMENT OF ANEMIA, THROMBOCYTOPENIA, AND NEUTROPENIA

FILE REFERENCE: C1041/7014 (AMS)

CURRENT APPLICATION NUMBER: US/09/895,007A

CURRENT APPLICATION NUMBER: US 60/214,368

PRIOR APPLICATION NUMBER: US 60/214,368
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 133
LENGTH: 20
                                                                                                                                                                                                                                                       ; OTHER INFORMATION: synthetic sequence US-09-916-369A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Synthetic Sequence US-09-800-266A-133
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SOFTWARE: PatentIn version 3.1
                                                                                                                         TYPE: DNA
ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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                                        SEQ ID NO 2
LENGIH: 20
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Best Local S:
Matches 16
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| Sequence 168, Application US/09888326
| Publication No. US20030026801A1
| GENERAL INFORMATION:
| APPLICANT: Weiner, George
| TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
| TITLE OF INVENTION: Methods for Enhancing Cancer
| TITLE OF INVENTION: Methods for Enhancing Cancer
| TITLE OF INVENTION: Coll Lysis and Treating Cancer
| FILE REFERENCE: Cl039/7052 (AWS)
| CURRENT APPLICATION NUMBER: US/09/888,326
| CURRENT FILING DATE: 2001-06-22
| PRIOR APPLICATION NUMBER: US 60/213,346
| PRIOR FILING DATE: 2000-06-22
| NUMBER OF SEQ ID NOS: 848
| SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 133, Application US/09920313
; Publication No. US20020198165A1
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
LENGTH: 20
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; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-133
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LOCATION: (0)...(0); LOCATION: (0)...(0)
US-09-888-326-168
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Query Match
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NAME/KEY: misc_feature
LOCATION: (0) ...(0)
OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-169
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NAMB/KEY: misc_feature
LOCATION: (0) ... (0)
OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
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                                                                                                                                                                                                                                                                      Sequence 169, Application US/0988326; Bedlication No. US20030026801A1; GENERAL INFORMATION:
APPLICANT: Weiner, George; APPLICANT: Weiner, George; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced; TITLE OF INVENTION: Methods for Enhancing Cancer; FILE REFERENCE: C1039/7052 (AMS); CURRENT APPLICATION NUMBER: US/09/888,326; CURRENT FILING DATE: 2001-06-22; PRIOR PRILING DATE: 2000-06-22; NUMBER OF SEQ ID NOS: 848; SOFTWARE: FRAISEQ for Windows Version 3.0
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APPLICANT: Hartmann, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REPERENCE: Closs/7062 (AWS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 429
LENGTH: 20
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71.0%; Score 14.2; DB 3; Length 20; 84.2%; Pred. No. 3.4e+04; ive 0; Mismatches 3; Indels
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                          Best Local Similarity
Matches 16; Conserv
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LENGTH: 20
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Publication No. US20030087848A1;
GENERAL INNORMATION:
APPLICANT: Bratzler, Robert L.,
APPLICANT: Petersen, Deanna M.,
APPLICANT: FOURDN: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy;
FILE REFERENCE: C1037/7013 (HCL/MAT);
CURRENT APPLICATION NUMBER: US/09/776,479;
CURRENT FILING DATE: 2001-02-02,
PRIOR APPLICATION NUMBER: US 60/179,991
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weiner, George
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
ITILE OF INVENTION: Methods for Enhancing Antibody-Induced
ITILE OF INVENTION: Cell Lysis and Treating Cancer
ITILE OF INVENTION: Cell Lysis and Treating Cancer
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 430
LENGTH: 20
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Length 20;
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71.0%; Score 14.2; DB 3;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3;
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Pred. No. 3.4e+04;
Score 14.2; DB 3;
Pred. No. 3.4e+04;
0; Mismatches 3;
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; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-430
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 257
LENGTH: 20
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                                                                                                                                                                                                                                                                     Sequence 430, Application US/09888326; Publication No. US20030026801A1; GENERAL INFORMATION:
                                                                                                  2 GGGGAGGGAGGGGG 20
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84.2%;
  Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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US-09-776-479-530/c

Sequence 530, Application US/09776479

Sequence 530, Application US/09776479

Sublication No. US20030087848A1

GENERAL INFORMATION:

APPLICAMY: Betarler, Robert L.

APPLICAMY: Petarsler, Nobert L.

APPLICAMY: Petarsler, Yes

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Tractment of Asthma and Allergy

FILE REFERENCE: C103777013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT APPLICATION NUMBER: US 60/179,991

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
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US-09-776-479-531

i Sequence 531, Application US/09776479

i Publication No. US20030087848A1

i GENERAL INFORMATION:

i APPLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

APPLICANT: Pouron, Yves

ITILE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Tracment of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
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71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels
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3; Indels
0; Mismatches
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COTHER INFORMATION: Synthetic Sequence
US-09-776-479-531
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-310-914A-776151/c
Sequence 776151, Application US/10310914A
Sequence 776151, Baac
APPLICANT: Bentwich. Reaac
APPLICANT: Bentwich. Kvuzat
TITLE OF INVENTION: uses thereof
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwin 10x
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE REPERENCE: 06087.0200.CPUS01
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1295111
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TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-03-29
FRIOR APPLICATION NUMBER: US 10/112,653
FRIOR FILING DATE: 2002-03-29
FRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: PACENTIN VEYSION 3.2
LENGTH: 20
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Best Local Similarity 100.0
Matches 20; Conservative
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ORGANISM: Human
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Sequence 76617, A
Sequence 348779,
Sequence 444004,
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1302921,
273461,
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Sequence 80883, A
Sequence 172569,
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Sequence 497156,
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Sequence 840057,
Sequence 993088,
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Sequence 840058,
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US-10-310-914A-455466
US-10-310-914A-455466
US-10-310-914A-1302921
US-10-310-914A-172752
US-10-310-914A-172752
US-10-310-914A-172752
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US-10-310-914A-172753
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US-10-310-914A-191746
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US-10-310-914A-191746
US-10-310-914A-191854
US-10-310-914A-191874
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US-10-310-914A-191874
US-10-310-914A-191874
US-10-310-914A-191876
US-10-310-914A-367876
US-10-310-914A-39883
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US-10-310-914A-367876
US-10-310-914A-443940
US-10-310-914A-443940
US-10-310-914A-443940
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US-10-310-914A-443940
US-10-310-914A-993073
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US-10-310-914A-682082
US-10-310-914A-840058
US-10-310-914A-845336
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US-10-310-914A-76617
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TYPE: RNA

Sequence 875, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

RESULT 1 US-11-127-654-875

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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 60687.0240.CURNER: 2020.CURNER: 2011.02410.0310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1162719
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Fublication No. US20060003322A1
Fublication No. US2006000332A1
Fublication No. US2006000332A1
Fublication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
LENGTH: 21
LENGTH: 21
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Sequence 1162726, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: USES thereof
TITLE OF INVENTION: USES thereof
TITLE OF INVENTION: USES thereof
CURRENT APPLICATION UNMERS: US/10/310,914A
CURRENT APPLICATION
CURRENT APPLICATION
SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 116726
LENGTH: 21
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100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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US-10-310-914A-1295143
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ORGANISM: Human
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| Sequence 776152/c
| Sequence 776152, Application US/10310914A
| Publication No. US20060003322A1
| Publication No. US20060003322A1
| Publication No. US2006000332A1
| Publication No. US2006000332A1
| Publication No. US2006000332A1
| APPLICANT: Bentwich, Isaac
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| FILE REFERENCE: 06087.0200.CPUS01
| FILE REFERENCE: 06087.0200.CPUS01
| CURRENT RPLING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 776152
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich. Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200. CPUSOI;
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 739686
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95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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thes 0; Indels
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
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US-10-310-914A-739686
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US-10-310-914A-739686
            ; ORGANISM: Human
US-10-310-914A-776151
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ORGANISM: Human
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APPLICANT: Bentwich, Isaac
APPLICANT: Biller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: 0500.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1295149
LENGTA: 23
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 066087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 739676
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Sequence 1162727, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 1167727
LENGTH: 27
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Best Local Similarity 100.0
Watches 19; Conservative
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Best Local Similarity 100.8
Matches 19; Conservative
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US-10-310-914A-1162727/c
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; ORGANISM: Human
US-10-310-914A-1162727
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Wuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1295144
LENGTH: 21
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
USes thereof
TITLE OF INVENTION:
USES 12002-12-06

NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN version 3.3
SEQ ID NO 1295148
LENGTH: 23
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Pred. No. 1.3e+02;
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Mismatches 0; Indels
                                                                                  0; Indels
                                         DB 7; Le
1.3e+02;
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                                      95.0%; Score 19;
100.0%; Pred. No.
:ive 0; Mismatch
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100.0%; F1.
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                                         Query Match
Best Local Similarity 100.
Matches 19; Conservative
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Matches 19; Conservative
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Matches 19; Conservative
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US-10-310-914A-1295149
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US-10-310-914A-1295148
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US-10-310-914A-1295143
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Human
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Sequence 16294, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06007.0200.0PUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 162974
APPLICANT: Shiler, Kwizat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 162906
LENGTH: 24
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Publication No. US2006000332A1

GENERAL INFORMATION:
GENERAL INFORMATION:
I APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087,0200, CPUS01

FILE REFERENCE: 06087,0200, CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

CURRENT FILING DATE: ASSOCIATION NOWER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3
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Pred. No. 2.1e+02;
0; Mismatches 1;
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Best Local Similarity 95.04
Matches 19; Conservative
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Best Local Similarity 95.0
Matches 19; Conservative
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ORGANISM: Human
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Sequence 1162700, Application US/10310914A

Fublication No. US2060003322A1

Sequence 1162700, Application US/10310914A

Fublication No. US206000332A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Briller Kruzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: USES thereof

TITLE OF INVENTION: USES thereof

CURRENT APPLICATION WHORER: US/10/310,914A

CURRENT RILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 1167700

LENGTH: 28

LENGTH: 28
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Publication No. US2060003322A1
Rublication No. US206000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087,0200.CPUS01
CURRENT FAPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1155402
LENGTH: 20
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   Length 27;
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                                                                         0; Indels
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   DB 7; Le
1.3e+02;
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95.0%; Pred. No. 4.1.
0; Mismatches
Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 19; Conservative 0; Mismatches
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US-10-310-914A-162906
; Sequence 162906, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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Matches 19; Conservative
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Best Local Similarity 95.0
Matches 19; Conservative
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; ORGANISM: Human
US-10-310-914A-1155402
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ORGANISM: Human
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Page 7

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1295146
LENGTH: 22
TYPE: pw.
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APPLICANT: Benewich, Isaac
APPLICANT: Benewich, Isaac
APPLICANT: Biller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 739675
LENGTH: 23
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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Pred. No. 2.9e+02;
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100.0%; Pre
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100.08; FL.
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Best Local Similarity 100...
Best Local Similarity 100...
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Best Local Similarity
Matches 18; Conserv
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US-10-310-914A-739675
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kwuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Youxat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087,0200,CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 905589
LENGTH: 19
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Pred. No. 2.1e+02;
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Best Local Similarity 95.0%; Pred. No. 2.1e
Matches 19; Conservative 0; Mismatches
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APPLICANT: Bentwich, Isaac
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Matches 19; Conservative
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US-10-310-914A-906589
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; ORGANISM: Human
US-10-310-914A-906589
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US-10-310-914A-282266
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Best Local S:
Matches 18;
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION VMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 152912 LENGTH: 19
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US-10-314A-386825

Sequence 386825, Application US/10310914A

Publication No. US20060003322A1

Publication No. US2006000332A1

APPLICANT: Bentwich, Isaac

APPLICANT: Bantwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNDER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOGTWARE: PatentIn version 3.3

SEQ ID NO 386825

LENGTH: 19
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 66087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
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Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Best Local Similarity 94.75
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Best Local Similarity
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US-10-310-914A-386824
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US-10-310-914A-386825
                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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                                                                                                                                                                                                            Sequence 100302, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Baioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 100302
LENGTH: 19
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Sequence 148888, Application US/10310914A

Sequence 148888, Application US/10310914A

Publication No. US20060003322A1

GRNERAL INFORMATION:

APPLICANT: Shiler, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNDER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

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LENGTH: 19
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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  Pred. No. 2.9e+02; Mismatches 0;
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US-10-310-914A-162912
Sequence 162912, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kouzat
    Best Local Similarity 100.0%; P)
Matches 18; Conservative 0;
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Best Local Similarity 94.7%;
Matches 18; Conservative
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hes 18, Conservative
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US-10-310-914A-148888
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ORGANISM: Human
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Sequence 628864, Application US/10310914A

Foguence 628864, Application US/10310914A

Fublication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 628864
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: Bentwich, Isaac
APPLICANT: Biller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1155411
LENGTH: 20
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Pred. No. 4.6e+02;
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ilarity 94.7%; Pred. No. 4.6e+02;
Conservative 0; Mismatches 1;
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TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06007.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 588532
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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US-10-310-914A-1155411
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                                                                                                                                                                                          TYPE: RNA
ORGANISM: Human
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                                                                                                                                                                LENGTH: 20
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 288225
LENGTH: 20
                                                                                                                                                                                                                                                                                                   APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE OF INVENTION: uses thereof
FILE REFERENCE: 06.087_00.CPUS.0.1
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 388850
LENGTH: 19
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) Publication No. US20060003322A1

) GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

) APPLICANT: Shiler, Kvuzat

) TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
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Pred. No. 4.6e+02;
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    1; Indels
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94.7%; Pred. No. ...
0; Mismatches
    0; Mismatches
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APPLICANT: Benewich, Isaac
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Matches 18, Conservative
       18; Conservative
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US-10-310-914A-288225
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ORGANISM: Human
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ORGANISM: Human
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US-10-310-914A-386839
US-10-310-914A-386839
Sequence 386839, Application US/10310914A
Sequence 386839, Application US/20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 60687.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 386839
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Fublication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOCTWARE: PatentIn version 3.3
SEQ ID NO 386841
LENGTH: 21
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              CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 288227
LENGTH: 21
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FILE REFERENCE: 06087.0200.CPUS01
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Matches 18; Conserv
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US-10-310-914A-288227
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US-10-310-914A-386841
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; ORGANISM: Human
US-10-310-914A-386841
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Best Local
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                                                                                                                                                                   Sequence 100342, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USES TO COUNTY
CURRENT APPLICATION UNBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 100342
LENGTH: 21
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Publication No. US20060003322A1
RUDICALINCRMATALINCRMATACH, ISAAC
APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 288226
LENGTH: 21
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US-10-310-914A-288227
Sequence 288227, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
PAPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
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Matches 18; Conservative
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US-10-310-914A-100342/c
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US-10-310-914A-100342
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; ORGANISM: Human
US-10-310-914A-288226
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Publication No. US20060003322A1

Publication No. US2006000332A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087, 0200, CPUS01;
CURRENT APPLICATION NUMBER: US/10/310,914A

NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 366862
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NOWEL: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 282307
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                                                                                                                                                                                       Score 17.4; DB 7; Length 21;
Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 1345469 LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 282307, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-310-914A-282307
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ORGANISM: Human
                                                                                                                 TYPE: RNA
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                                                                                                                       Sequence 659280, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kwuzat
TITLE OF INVENTION: US uses thereof
FILER REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 659280
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Sequence 1345469, Application US/10310914A
Sequence 1345469, Application US/10310914A
Sequence 1345469, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
   1 AGGGGAGGGAGGGG 19
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Best Local Similarity 94.7%
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Best Local Similarity 94.7
Matches 18; Conservative
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; ORGANISM: Human
US-10-310-914A-659280
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                                                                                                                 US-10-310-914A-386851
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US-10-310-914A-386851
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US-10-310-914A-1345363/C

Sequence 1345363, Application US/10310914A

Fublication No. US2060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses (18/10/310, 914A)

CURRENT APPLICATION NUMBER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1345363

LENGTH: 22

LENGTH: 22
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105-310-310-3145-1345365/c
105-310-310-3145-1345365, Application US/10310914A
1 Sequence 1345365, Application US/10310914A
1 Fublication No. US20060003322A1
1 GENERAL INFORMATION:
1 APPLICANT: Bentwich, Isaac
1 APPLICANT: Bentwich, Isaac
1 APPLICANT: Biller, Kvuzat
1 TITLE OF INVENTION: uses thereof
1 TITLE OF INVENTION: uses thereof
1 FILE REPREBUCE: 06087.0200.CPUS01
1 CURRENT APPLICATION NUMBER: US/10/310,914A
1 CURRENT PILLIO DATE: 2002-12-06
1 NUMBER OF SEQ ID NOS: 1388402
1 SOFTWARE: PatentIn version 3.3
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87.0%; Score 17.4; DB 7; Length 22;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
0; Mismatches 1;
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87.0%; Score 17.4; DB 7;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1;
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 659284
LENGTH: 22
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-310-914A-1345363
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US-10-310-914A-1345365
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US-10-310-914A-659284
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LENGTH: 22
                                                                                                                    TYPE: RNA
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                                                                                                                         Sequence 560684, Application US/10310914A
Publication No. US20060003322A1
GENERAL IPCORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNDERS: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NOS: 1388402
SEQ ID NOS: 206884
LENGTH: 22
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US-10-310-914A-659284

US-10-310-914A-659284, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Benewich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof

TITLE REFERENCE: 06087.0200.CPDUS01

CURRENT APPLICATION NUMBER: US/10/310,914A
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94.7%; Pred. No. 4.6e+02;
iive 0; Mismatches 1;
4 AGGGAAGGGAGGGAGGG 22
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Best Local Similarity 94.77
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-310-914A-560684
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; ORGANISM: Human
US-10-310-914A-628966
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US-10-914A-162972

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US-10-914A-162972

US-10-914A-162972

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Benewich, Kauac

APPLICANT: Benewich, Kauac

APPLICANT: Benewich, Kauac

APPLICANT: Benewich, Council and Counc
                                                                                                                                                                     US-10-914A-100318/c
Sequence 100318, Application US/10310914A
Sequence 100318, Application US/10310914A
Sequence 100318, Application US/10310914A
Sequence 100318, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Shiler, Kuzat
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION WHOBER: US/10/310,914A
CURRENT APPLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 100318
LENGTH: 23
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19 GGGAGGGGAGGGCGGGG 1
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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; ORGANISM: Human
US-10-310-914A-162972
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; ORGANISM: Human
US-10-310-914A-100318
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